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CGTTGAGCCA AATGAAGCTG GAGAAACACG CTTTACCTAT GCCACTTATG GTGAGGGAAA	180
GCTTCCAGAA GGTCTGACCA TTTCCCTCCAA GGAGAGTGCA GAAACGAGTG ATTTATTAGG	240
GTCTTACTTG ATTGTATCAG GAAGTTTGGG TGGAGTGAGC TTACAGACCA CCTTGAAAGA	300
GCTTGGTTAT CAAGGCTTTG TTTCGAATGG AGAAGATCCA TTTTCGATAG TCTTACTATT	360
GACGGCCACC CCTATGGTGC TACTGAGTTT AGCTATTTTT CTGCTGACCT TTATGAGTCT	420
GACCCTGATT TATCGGATCA AATCCCTTCG TCAGGCAGGG ATTCGCTTAA TAGCTGGTGA	480
GAGCTTGTTT GGAGTTGCTC TCAGACCAGT GTTAGAAGAT GTGAGACAGC TTATCTGCTC	540
AGTGCTGGTA TCCAGTCTTT TGGGATTGGG GATTCTCTGG TATCAAGGTG CCTTGTTTAT	600
GGCAACGGTG CAACTGGTCA TCATTGCTCT TCTACTTTAT GGATTGACCT TGGCAGGGAT	660
TTCTACCTTA CTAAGTGTCTG TCTATCTACT TGGTTTACAG GAAAATAGTC TGGTGGATCT	720
ATTGAAAGGG AAACCTCCCTC TCAAACGTAT GATGACATTG ATGATGGTGG GGCAACTCTT	780
AGCTGTATTG GTGGTCGGAT CGAGTGCGAC AGCTCTCCTA CCCCCTACC GTGAAATGCA	840
GGAAATGGAG AGAGCTAGCA ATAAATGGAG CCAGTCCTCA GACCGTTACC GTCTATCCTT	900
TGGTTGGTCT AGTGCATTTG CCGATGAAGA AGGAACGCGT AAGGATAATC GTGAGTGGCA	960
GACATTTACT GAAGAACGGT TAGCCAATAC AGACTCTTTT TATATTATGA GCAATGTTGA	1020
CAATTTCTCA GATGGAGCAG AAGTGGACCT AGATGGCAAT CGTCTCAGTG ACTACACACC	1080
GTCAGGGAAT GTTATCTATG TCTCACCGCG CTATCTGATA GAAGAAAAGA TTACCGTTTC	1140
TTGAGAGCTTG CGAGAGCAGT CTGTCTACTA CCAAGGATTG TTTACAGATT ACCTGCAAAA	1200
CTTTTCATCT GAAAGTGTAG AAGTGACGAG TCAGAAACAC TACCTCCCAC AGGTAAGGCT	1260
AGCTTTTACA GAAACAGGAC AGGAACGTTT CCTCTATAAT GATGGGTACA AGACAACACG	1320
CCAGTACCTA AAAGATCCGA TTATTGTAGT TCTAACGCCG CAAGCGACTG GAACAAGACC	1380
TGTTGCAGGG ATGTTGTGGG GAACTACGGC TAATAGTGCC TTGAAACTAG ATCGATATGG	1440
AGACAGCATC ACAGCTCTAA AAGAGAAAGG TCTGTATCAC AAGGTTTCTT ACTTGGTAAA	1500
AAGCCAGCTA TTTTTTGCCA AGGTACTAAA TGACAAACGG GTGGAGTTTT ACTCTCTCCT	1560
TATTGGGACG ATTTTGACCC TGTCTACGGC TATCTTGTTA TTTGATTCCA TGAATCTTCT	1620
CTATTTTGAG CAGTTCAGAC GGGAACCTAT GATTAAACGT CTTGCTGGTA TGACAATCTA	1680
TGAGCTTCAT GGCAAGTATT TACTGGCGCA AGGAGGAGTT CTCTTGCTTG GCCTAGTCCT	1740
ATCTAGTATT TTGACAAGAG ATGGTTTGAT TAGCGCTCTA GTTGTAGCTT TGTTTACGCT	1800
	1860

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ATTGAAAGGA	AAATAAGATG	ATTGATATTC	AAGGATTGGA	AAAGAAATTT	AATGACCGCG	1980
CGATTTTCTC	TGGTTTGAAT	CTCAAGCTGG	AGAAGGGCAA	GGTTTATGCC	TTAATCGGAA	2040
AGAGTGGAAG	CGGAAAGACG	ACGCTGCTGA	ATATCTTGGG	AAAGCTAGAA	AAGATAGATG	2100
GTGGAAGGGT	TCTCTATCAG	GGGAAAGATT	TAAAAACCAT	TCCCACCTCGT	GAGTATTTTC	2160
GAGACCAGAT	GGGCTATCTC	TTTCAAAATT	TCGGCCTCTT	AGAAAACCAA	TCAATCAAAG	2220
AAAATTTGGA	TTTGGGTTTT	GTTGGTCAGA	AAATCTCAAA	AGTAGAACGT	TTGGAAAGGC	2280
AAGTGGGGGC	TTTAGAAAAA	GTTAATCTAG	GGTATTTGGA	TTTAGAACAA	AAAATCTATA	2340
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CCTTGATTTT	GGCAGATGAA	CCAACAGCAG	CTCTTGATCC	TGAAAAATTCA	GAGGAGGTTA	2460
TGAATCTCTT	GGTGGATTTG	AAAGATGAAA	ATCGAATTAT	CATCATTGCG	ACCCATAATC	2520
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AAAATCCGTA	TTCGCAGGGT	ATCTGATTAT	CCTAGTGCCA	GAGGTGGTTT	AGAAGATATC	2640
CTCATCATGG	AAAATATGAC	CAATCATCTC	CTTTTGGTTC	AAATCCGAGT	GCATGGCTAT	2700
TTGCTTGATT	TTGCTAGTAT	TGAAGGGCAA	AGGCAAAAGC	ATTATCGTTT	GAAAAATTTA	2760
CCTCAGACGG	TTGAACTGAC	AGTGGATGAT	GTGGAGGAGG	ATGTGGATTT	GACCCTACCT	2820
GAAAATCGAA	GTTATCAAGA	AGCTGATTTT	TTTGAACGCA	TGTTTCGAGA	GAACTGCTAA	2880
GGCCACTTTT	AAAGATTTCC	AAGACTATCT	TTCTTCATGA	GGAAAGATAG	TTTTTTGGTA	2940
TGATTTTCAT	TCCCAAAATA	CAAGGGGAAT	GTGTTACAAT	AGTAGTAACA	GATAATAGAA	3000
AAGAGAATAG	ATGAGAATTG	CAGATTATAG	CGTGACCAAG	GCAGTGCTGG	AGCGTCACGG	3060
TTTTACCTTT	AAAAAGTCCT	TTGGGCAAAA	TTTTTTGACG	GATACCAATA	TCCTTCAAAA	3120
AATTGTGGAT	ACGGCTGAAA	TTGATGATCA	GGTCAATGTC	ATCGAAATCG	GGCCAGGTAT	3180
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CCACCGTTTG	GTGCCAATTT	TGGCAGATAC	CCTGCGTGAT	TTTGATAATG	TGACCGTAGT	3300
TAACGAAGAT	ATTCTCAAGG	TTGATTTGGC	GCAACATATC	CAGAATTTTA	AAAATCCTGA	3360
CCTGCCAATC	AAGGTAGTGG	CTAATTTGCC	TTACTACATC	ACGACGCCTA	TTCTCATGCA	3420
CTTGATTGAG	AGTGGCATTG	CTTTTTGTGA	GTTTGTGGTC	ATGATGCAGA	AAGAAGTAGC	3480
GGACCGCATT	TCAGCCCAGC	CTAACACCAA	GGCTTACGGT	AGCTTGTCTA	TCGCCGTGCA	3540
GTATTACATG	ACAGCCAAGG	TTGCCTTTAT	CGTGCCTCGT	ACGGTCTTTG	TGCCAGCGCC	3600
AAATGTGGAT	TCAGCCATCT	TGAAAATGGT	GCGTCGTCCA	GAGCCAGCCG	TAGCAGTAGA	3660

1001

AGATGAGAAC	TTTTTCTTTA	AGGTTTCCAA	GGCTAGTTTT	ACCCATCGCC	GCAAGACCTT	3720
GTGGAATAAC	TTGACAGGTT	ACTTTGGTAA	GACTGAAGAG	GTCAAGGACA	AGCTGACCAA	3780
GGCTTTGGAC	CAGGCAGGCT	TGTCACCAAG	TGTGCGTGGG	GAAGCTCTCA	GCTTGGCAGA	3840
ATTTGCCGGT	CTAGCAGACG	CACTTAAAGG	GCAAGGACTC	TAAGATGCAG	GGACAAATCA	3900
TTAAAGCCTT	GGCAGGTTTC	TACTATGTGG	AGAGTGATGG	CCAGGTTTAT	CAAACACGCG	3960
CGCGTGGGAA	TTTCCGTAAA	AAAGGCCATA	CCCCTTATGT	TGGGGACTGG	GTAGATTTCT	4020
CTGCCGAGGA	AAATTCAGAA	GGCTATATCC	TCAAAATTCa	CGAACGGAAA	AACAGTCTGG	4080
TTCGTCCGCC	TATTGTCAAT	ATCGATCAAG	CTGTAGTAAT	CATGTCCGTC	AAGGAACCTG	4140
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CCATTGTCTA	TATTTCCAAA	ATGGATTTGT	TGGAAGATAG	GGGAGAAGTG	GATTTTACC	4260
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TCAATAAAAT	CGCACCAGAC	CTCAATCTTG	AAACGGGAGA	AATTCAGAC	AGTCTAGGTC	4440
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ATACACCAGG	ATTTTCATCC	TTGGACTATG	AAGTATCAAG	GGCTGAAGAC	CTCAATCAGG	4560
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ATGAGCCGTC	TTGTGCCGTC	AAACCAGCTG	TTGAAGAGGG	TGTTATTGCA	ACCTTCCGTT	4680
TTGACAATTA	CCTGCAATTC	CTTAGTGAAA	TTGAAAATCG	TAGAGAAACC	TATAAAAAAG	4740
TCAGCAAAAA	AATTCCAAAA	TAAGGAGAAA	CCTATGTCTC	AATACAAGAT	TGCTCCGTCA	4800
ATTCTGGCAG	CAGATTATGC	CAACTTTGAA	CGTGAAATCA	AACGTCTAGA	AGCAACTGGG	4860
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ATCCATGTAG	AAGCAACGCC	TCATATTCAT	GGCGCCCTCC	AAAAAATTCG	TTCACTCGGA	5100
GTTAAGCCTT	CAGTCGTTAT	CAATCCTGGC	ACATCAGTTG	AAGCCATCAA	GCACGTCCTT	5160
CATCTAGTTG	ACCAAGTTTT	AGTCATGACG	GTTAATCCAG	GTTTTGGTGG	GCAAGCCTTT	5220
CTGCCAGAAA	CCATGGATAA	GGTCCGTGAG	TTGGTTGCTC	TTCGTGAGGA	AAAAGGTTTG	5280
AACTTTGAAA	TCGAAGTGGA	TGGTGGGATT	GATGACCAAA	CTATTGCTCA	AGCCAAAGAA	5340
GCCGGTGCGA	CTGTTTTTGT	AGCAGGTTC	TATGTCTTTA	AGGGAGAAGT	CAATGAGCGA	5400

1002

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GGAAGAAGAC	TTACCTCTTG	CTCTAGCAGT	CGGAGATTTT	GATTCTGTGA	CGGAAGAAGA	5580
GCGACAGGTG	ATTCAAAAAG	GTGCCCAGTA	TTTTGTCCAA	GCACGACCAG	AAAAGGATGA	5640
TACAGATCTG	GAATTGGCTC	TCTTAACCAT	CTTTGAACAA	AATCCTCAGG	CTCAGGTCAC	5700
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GGTAACTTGC	CCAGATGGTT	ATGTGGTCGT	ACTGCATAGC	AAGGACAGGA	GGTAGGATGG	6060
AAAGTTTACT	TATTCCTATTA	TTAATTGCCA	ATCTAGCTGG	TCTCTTTCTG	ATTTGGCAAA	6120
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TGACCCAAGT	CCGTCAAGAA	ATGACAGATA	ATCTCCTCCA	AACTAGAGAC	AAGACAGACC	6360
AACGTCTCCA	AGCCTTGCAG	GAATCAAATG	AGCAACGTTT	GGAACAAATG	CGCCAGACGG	6420
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CTAAACAAC	GGAGTCTGTC	AATCGTGGCC	TTGGAGAAAT	GCAGACAGTT	GCCCGTGATG	6540
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CAAGCGTCAA	GCGCTTTGCT	AGGGATATTA	GGAACAAGTA	CATAGCACCA	CCTCGGACGA	6900
CCAATTTTGG	AGTTTGTGTT	GTTCCGACAG	AAGGTCTCTA	CTCAGAAATC	GTCCGCAATC	6960
CGGTCTTCTT	TGATGATTTG	AGACGGGAAG	AACAGATTAT	TGTTGCAGGA	CCAAGTACCC	7020
TATCAGCCCT	TCTTAACTCC	CTATCAGTTG	GTTTCAAGAC	CCTTAATATC	CAAAAGAGTG	7080
CCGACCATAT	CAGCAAGACT	CTTGCCAGTG	TCAAGACCGA	GTTTGGCAAG	TTTGGTGGTA	7140
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1003

ACCGTCGTAC	CATAGCTATC	GAGCGGACGC	TCCGTCACAT	TGAGTTGTCA	GAAGGTGAGC	7260
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CTGCCTCAAG	CTGGTGAACC	CAATGACCCA	GCTGATTTCA	AGGTCAAGTC	ACCAGTTGAT	7620
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CGTTTGGCAG	ACGCTATTAG	CGAAGTTTAT	CCTCAGCTCA	ATAAGAGCCT	GCTCTATGCG	7860
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ACAGTTATGG	AACTCGGCAT	CGATGATACC	AAGGAAGAAG	TCGTTTTGCT	TCGTCATGTC	8040
ATCCTCAGTC	ACCACGGCTT	GCTTGAGTAT	GGAAGCCCAG	TCCGTCCACG	CATTATGGAA	8100
GCAGAGATTA	TCCATATGAT	TGACAATCTG	GATGCAAGCA	TGATGATGAT	GTCAACAGCT	8160
CTTGCTTTGG	TGGATAAAGG	AGAGATGACC	AATAAAATCT	TCGCTATGGA	TAATCGTTCC	8220
TTCTATAAAC	CAGATTTAGA	TTAATAATTT	AAGAAAAATG	AGCATTTTTT	AGGATAAGAA	8280
TGTTCGTTTT	TTTATGTGAA	TATGGTATAA	TAAGTAAAAG	ACAAAAATGA	ATACTCTTCG	8340
AAAATCTCTT	CAAAC TAGGG	TAGTATCGCC	TTGTCTGATG	TATATATGCA	GGTATATTAC	8400
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GAAGAAGTGA	TCGGATGGTT	GTCATTTCCA	ACTATTTGAT	TAATAATCCT	TATAAACTAA	8580
CTAGTCTCAA	TACTTTTGCT	GAAAAGTATG	AGTCTGCTAA	ATCATCCATC	TCAGAAGATA	8640
TCGTCAATTAT	CAAACGCGCC	TTTGAGGAAA	TTGAAATCGG	TCATATCCAG	ACAGTGA CTG	8700
GGGCTGGCGG	AGGTGTCATC	TTACACCCGT	CTATTTTCGAG	TCAGGATGCT	AAGGAAATGG	8760
TTGAAGACTT	GCGTACCAAG	TTGTCAGAAA	GTGACCGTAT	CTTGCCAGGT	GGTTATATCT	8820
ATCTGTCTGA	TTTGCTTAGC	ACACCAGCCA	TCTTGAAAAA	TATTGGTCGT	ATTATTGCCA	8880
AAAGCTTTAT	GGACCAAAAA	ATTGACGCGG	TTATGACCGT	AGCAACTAAG	GGTGTGCCAC	8940

1004

TTGCAAATGC	AGTTGCCAAT	GTCCTCAATG	TCTCTTTTGT	CATTGTGCGC	CGTGACCTGA	9000
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ATGACTTCTT	GAAAGGTGGC	GGAACGGTCA	ATGGTATGAT	TAGTCTCTTG	CGCGAGTTTCG	9180
ACTCAGAACT	GGCAGGTGTA	GCGGTCTTTG	CGGACAATGC	CCAAGAAGAA	CGTGAAAAGC	9240
AGTTTGACTA	CAAGTCACTC	TTGAAGGTAA	CCAATATTGA	TGTCAAGAAC	CAAGCCATCG	9300
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CGATTGTCCC	AGCCTTTCTT	TGCAAACAGA	ATAGAAGGAA	GCTTATGAAA	ACACCATT'TA	9420
TCAATAGAGA	AGAGTTAGAA	GCGATTGTTG	CCGAGTTCCC	GACTCCCTTT	CACTTGTATG	9480
ATGAGAAGGG	GATTCGTGAG	AAGGCAAGAG	CCGTCAACCA	AGCTTTTTTCG	TGGAACAAGG	9540
GCTTTAAGGA	ATATTTTGCA	GTTAAGGCTA	CTCCAACCTC	AGCTATTTTG	AAAATTCTCC	9600
AAGAAGAAGG	TTGTGGTGTG	GACTGCTCTA	GTTATGTAGA	GCTTTTGATG	AGCCATAAAC	9660
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CCTATGCACG	TGAATTGGGT	GCGACCATTA	ACTTGGATGC	CTTTGAAGAT	ATTGAACATC	9780
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TTGAACTGGG	GACAGACATT	ATGGACAATC	CTGGGGAGGC	TAAGTTTGGC	ATGACCAAGG	9900
ACCAGCTCTT	TGAAGCCTTT	GCTATCTTGA	AGGAAAAAGG	AGCCAAGACT	TTTGGGATTC	9960
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TCTTTGAACT	GGCTGTTGAA	ATCAAGGAAA	AGTTGGGCAT	TTGCTAGAC	TTTATCAATC	10080
TTTCTGGCGG	TATTGGTGTT	AATTATCATC	CAGACCAGGA	GCCGAACGAT	ATCGCCTTGA	10140
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ACCTCATGCG	TCCAGCTATG	TACGGAGCTT	ACCATCATAT	TAGCAACGTG	ACCCATCCAG	10380
ATGGACCAGC	TGAAGTG GTA	GATGTGGTGC	GTTCACTCTG	TGAAAACAAT	GATAAATTTG	10440
CAGTTAATCG	CGAACTGCCT	CATACAGAAA	TCGGTGATTT	GCTGGTCATT	CATGATACAG	10500
GTGCCCACGG	ATTTTCAATG	GGCTACCAGT	ATAATGCCAA	ATTACGTTCT	GCGGAAATCC	10560
TCTATACCGA	AGAAGGTAAA	GCCCCGTCAA	TCCGCCGTGC	AGAGCGCCCT	GAGGACTATT	10620
TTGCAACCTT	ATATGGCTTC	GATTTTGAAG	AATAATCTGA	TAATAGATTG	AAAATGAAAT	10680
TGAAAAACAG	ATTGCTTTCT	AAAAAATAGG	CAAAAATCTT	GTTTTTCCTT	CAAGTCGTGA	10740

1005

TATAATAAAA	CTATAAACG	TTTTCAAGGA	AGGTAACGAT	ATGTCTGAAG	AAACAATTGA	10800
TTATGGACAA	GTGACAGGAA	TGGTGCATTC	GACAGAAAGC	TTTGGGTCAG	TAGATGGGCC	10860
TGGTATTTCGC	TTTATTGTCT	TTTTGCAGGG	CTGTCACATG	CGTTGCCAGT	ATTGCCACAA	10920
CCCAGACACT	TGGGCTATGG	AGTCCAATAA	GTCACGTGAA	CGGACGGTAG	ATGATGTCTT	10980
GACAGAGGCC	TTGCGCTACC	GTGGTTTCTG	GGGAAATAAG	GGTGGGATTA	CAGTCAGTGG	11040
AGGAGAAGCT	CTCTTGCAGA	TTGATTTCCCT	GATTGCTCTC	TTCAACCAAGG	CTAAGGAACA	11100
AGGAATCCAC	TGTACCTTGG	ACACCTGTGC	TCTTCCTTTC	CGTAATAAAC	CACGTTACCT	11160
TGAGAAGTTT	GACAAACTCA	TGGCTGTCAC	TGACTTGGTT	CTTTTGGATA	TCAAGGAAAT	11220
CAACGAAGAA	CAGCACAAGA	TTGTCACTAG	CCAAACCAAT	AAAAATATCT	TGGCTTGTGC	11280
CCAGTATCTA	TCAGATATTG	GAAAACCTGT	CTGGATTTCG	CACGTGCTAG	TTCCAGGATT	11340
GACAGACAGA	GATGATGACT	TGATTGAACT	TGGTAAGTTC	GTCAAGACCC	TCAAAAATGT	11400
TGATAAGTTT	GAAATTCTAC	CTTATCACAC	CATGGGTGAG	TTCAAGTGGC	GTGAACTTGG	11460
AATTCATAT	TCCCTCGAAG	GAGTCAAACC	ACCAACAGCA	GATCGCGTCA	AGAACGCTAA	11520
ACAACTCATG	GATACCGAAA	GTTATCAAGA	TTATATGAAA	CGTGTACATG	GATAGAAAAG	11580
AAGCCTGATG	GAAACATCGG	GCTTTTGA	TGCAAAAAGA	CTTAGCAAAT	CAGCTAAGCC	11640
TTTTTCTTCT	TATCTCGAAC	GTTGTTTTCC	AGCGTTGCGA	TTTTTGTGTT	TTTTCTTGCT	11700
TGTGATAGCA	GTTGGTTGTT	CAGGGGTAAC	GTCTTTTCGT	CCACTTGGTT	TAGAGAAAGC	11760
ACTTGCTTTT	GGTGGTTCT	TGGCTAGTTC	TTCACGGACT	TTTTTGC	GAA GTTTGGACG	11820
AACGATATAG	TTGACGATAA	ACTGTTGGAG	AATCATCATG	AAACCACCGA	CAACCCAGTA	11880
AAGTGTGACA	CTAGCTGGTG	AGAAGAGGGA	GAAGACGACG	ATCATGAGTG	GGCTCATGTA	11940
AATCATTTTC	TTGATTTGTT	CTCTTTGCAT	TTCATCTTCT	ACTCCGTGAA	GTGAAAGGAG	12000
CGATTGAAGA	TAGTAAAGGA	CACCAGCACA	GGCAACCAA	ATCATACTTG	GAGAACCTAG	12060
AGGAATGCCT	AGGTAGCTTG	CTTGAGCAAC	CCCTTCAGTA	TGTTGGGCAG	CAAAGTAGAT	12120
AGCAGAGAAG	AAAGGCATTT	GAAGGAGGAT	AGGGAAACAT	CCTACACCGC	CAAACATGCT	12180
GATACCGTGC	TCTTTTGAG	CAGCAAAGAG	AGCTTGTTGG	GCTTCGAGTT	TTTCTTCTTG	12240
AGTAGTCGCT	TCTTTGAGAC	GCGTTTGGTG	TGGCTCAAGG	ACGTGCTTGA	GGGCGTTCAT	12300
CTTTTCAGAG	TGAAGCGTTG	CCTTCCATGA	TTGGTAGATA	CCAAGTGGTA	AGATAATCAA	12360
GCGTACGATA	ATGGTTACGA	TAATGATAGC	GACACCAAAG	CCTAGACCTT	TATCAGTAGC	12420
GAAGTACTTG	ATGGCTTCAG	CCATAGGCGC	TCCGATCGTA	TTCCAAATAA	ATCCTGTTGG	12480

1006

CTGACCTGTG GTTTTATCGA CATTGACACA GCCAGTCAAG ACAAGCAACA TAGCCACTCC	12540
CATAGCCGAG AGTGCAAAAT CGGGGT	12566

(2) INFORMATION FOR SEQ ID NO: 150:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

TGACACTCTG TAGGATTGTC GTTAATTGAT TGCTCGTACT CTCTACAATA ACCACCAAAG	60
TAAAAACGAC ATAGAAAGAT AGCATCAGCT GTAGCCATAG CGCCTTTGAC ACCTTCTGGA	120
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GTTTTTCGCAT AAAAACCACA GTCCATGATC CAAGCACATG GAGAAATACG CATAGCTGAT	240
CCATTCCCAA AGCTATTATA AGGCTCACGG TTATCGCTGT TTAGCCATGC ATTAAACCGA	300
GCACCGTAAT CAGCATTCGG ATACATTCTG CCATATTTCT TCATCGCGTC AATGAAGTCA	360
TCTTTTTGTC CACCATTCAT AATTGCTTCT GCAACAGCAC AGGTCATAAC CGTGTCATCT	420
GTAAAAAAGC AGTCCTTCCG AAATAAAGGA AAGTCCTTTG TTTTGATATT GTTCCATTCG	480
TAAACAGAAC CGACAATATC TCCAATAATT GCTCCAAGCA TCAGATTCCT CTTGTTTCAT	540
TTTGATGCTT TTTATATTGG TTATCTACCA TATTTATTTT AGAAAATAAC ATCCTGTTGG	600
ATTTTAAAAA TTTCATTTTT TTCAAAATAG GGTTTTACCA TTTCTTTCCA CCTAGCTCTA	660
TGAAAATTGA TTGATTTTAA AGGAGATAGG CCATAATTTT CCAATGCATA ACCATCATTT	720
ACTTCAACAA CAAGTGTCTT GCCATCGCGA GTAACACCGA TATCTAGTCC ATAAGCTATT	780
GGCGCATCTT TCCAACATGA TATCGCTTCA TCAATTACAC TTGCATCAAA TTGTGCATGA	840
TAATCACCTG TATAGGGTCG AACATCTAAT ACGCGACCAT CTAACACAAA ACAACGCCAT	900
TCAGCTATGA ATTCTACAAC CTCACTAATC CATATAGGAT AGTCGAAAGG TAGACCAATA	960
CCTATTAAAT CATGGGTTCC ATTAACAACCT CTTCCAGTAA AGACTTTTGA ACCAGCTTTA	1020
GGCTTAATAA ATTTTCCCCA ATTATCAGGT ATATTCACAA TCTCTCCTAA AATACCAGCA	1080
TAAATCTTTC GACCATAAAA CTCTTTAAGC TCAATAGGAT AGTCATGAAC CGGAACGTTT	1140
AAGCCCATCA TTTTtagTAA TGCTCTAGTC TCCATTATAT AATCTACAAC TATATCTTCA	1200
CTTGTTAACT CTTTtATTTC AGAAAAAGAT TGATATAAAA TAACTTCTTC TCCTTGTAAG	1260
TAGGCACCTA CTTGAGCATT GTATTTATTA ATTGAAACCT CACTTGGTAA TTTACTTTGT	1320

1007

CTAATATAAA	CAACCATTTT	ATCACTCCTA	TATCACTAGT	GTTACACCAA	TTTGTAAAAA	1380
ATAATAGCAA	TTTGTCTCTT	ATTTTTTTGA	GTAAATAGCC	CCCATAATAT	CATCGAAATA	1440
ATCAACGGTA	TTTAGGAGTA	ATTCAATAAC	CTGGGACTTT	GTTAGTCGCA	TTCCCCTTCT	1500
ATCTCTAGCA	TCTTCTACTA	AATTTTCAAG	TTTCTCTAGA	TTTTTATCAT	CCAAGCTAAT	1560
CATTATTCTA	TTTTTATCGG	TTGCCATTTT	CATCACCTCA	AGTTAATTCT	ATCACAGGTG	1620
TAACACTAGT	GTCAACTGGC	TTTTATAATA	CATTAGTTTA	AAAGTGGAGA	GGATTTTTTA	1680
CACAGTAACT	TTAAATCTTT	GGTATTAAAA	AATTTTCACA	ATATTTATAG	AAATAAAATC	1740
TGTCTCAAAT	CAGTTATCAA	ATCTAGTATA	AATTATGAGC	GGCTACTCTA	ATACTTTCCC	1800
TCTAAACAAG	AAAAAGACTT	ACACTCAAGG	GTTTTCTTCC	CCCCCTTCGT	TATAACGTTT	1860
TGACTCTTTT	ACTAGCAAAG	GTATATACTC	ACAAGGAACT	TTGGTTGACT	ATTGAATCTC	1920
TCCAACCTTCT	TCTTTAACAT	ATCCTTCTAC	ATCTTCAATC	TCTACAAACA	TTGGGTCTAA	1980
GTGACACAAG	AAATGCCAAA	CTTCGATCCC	TTTTTTTCTG	TAAAGAATCG	CTTCACCGTC	2040
TTCACTTCCG	AAAAAGCTTC	TGTCGATTTT	ATATCCGCGG	CTTCTAAGA	AGTCTTTTGC	2100
TTTACGATAG	TTCGTTTCTC	TTGTTTCGAC	ATAGGCTTTA	ACTTCATGGT	TGTTAACGAC	2160
ATATGCATCA	ATTTTTGAAT	ATCCTTCGAT	CACTCTATCA	TTTTTGAGGG	ATAAATTTGA	2220
AATCTCTTTC	CAAATAATGT	TTACATTTTC	CTCAGGATCG	AACATAAATT	TAGATAAAGG	2280
AACAATATTT	CCGTAAAAA	TAATTTCCAT	ATAATCCGGT	ATGTTTTTAG	GATTAAAATA	2340
CTCCACTTCA	AAACCATCTT	CTGTTTCCAG	AGTGTATCCC	GGGATTTGAG	CTACAAAGGC	2400
TTTCCCATCT	TCTATGGAAT	CAAATGCTAC	TAAATCTTTA	GAATAATCAT	TTTGGTACAA	2460
TTCCAATATA	ACCATCGATA	ATCTCTCCAT	TTTCATTATC	AGGCTAATGT	AAATAAGCAC	2520
GTCACCTGAC	CAATTCAGGC	TCTCTGTATC	ATCTCATCAT	ATTTCCCTACT	TACTTTACGA	2580
GTCTTATACC	CAGAACACAC	CTTATCGACC	TTCGGTCTCA	CCTCGTCGCA	TTGGCTGAAC	2640
ATCTACTTTT	ACTTTGCTGA	TGCTTCAACT	CGTACAAGCA	GTGATACCGC	CTCAGCGTGA	2700
TGCGTCAGTG	GGACTCAAAA	GGTTCGGGGA	ACCTTTTGAG	GATTAACTAC	GTTTCTCTAA	2760
TAAACTTACA	CATTCAACTT	GTTCATCATT	GTCCAAACCT	ATGTTGAGAT	TTTCTTCTAT	2820
AATTGGTAGC	TTAAAAGTAA	TGGATTTTAG	CCATTGTCCG	TTAGATTGTT	TTTCTTCATA	2880
AACTTGAATT	TCAGAAATCA	AAGCTGAAAT	TAACTGCCTA	CGCTCTACAT	CATTCATGAC	2940
TTTATAGAGC	TTATCAAAAT	AGATCAGAAC	CTTATATATG	TTATCTCCTG	TAAGCTTTTC	3000
AGCTTCAATA	GTCTGTTTCT	TTGCTTTCGC	ATCAATTAGT	GATGATTCTA	ATTCATCTAG	3060

1008

TTTGTCATAC	ATACGATATA	GTCTATCATC	TAAATCCTGT	TTCCTTCTCT	TATAATGCTT	3120
ATCTTCAACA	TCTAAATTAT	CTATTTCCCTC	AATTAGCTTA	AACTTTGTAG	AATGACTCTT	3180
TCTCAATTCC	TTTTGGTAAT	TATCTATTTT	TTTTTCTATT	TCAGAGGTAT	CCACCTTCAT	3240
GTGATTTTTT	TCTTGCATCA	TAGAAGCAAA	TTTCGGATTA	CTTACTATCT	TGACAATCAC	3300
CTCTGCAACA	GCATCATCTA	ACAATTCTTC	TCTAATTTGC	TTACTGAATG	TACACTTATT	3360
ACCTCTTATC	ATCTGCCTAT	GGTTACAACC	ATAGTAATAA	AAATCTTTAT	ACTTTGTGCC	3420
ATCTTTCTTT	TTCTTGATAC	ACTTGTTCCT	AAACATTCCC	ACTCCACATA	TCGGGCATTT	3480
TACAATTCCA	GAAAGCAAGT	GTGTGCGTGT	ATCTTTTCCT	TTATTACACAT	GCTCATATTT	3540
CTTTGCTTGA	GATTTTAGCT	TAACCTGAGC	AGCTTGCCAA	ACTTCATCGG	AACTATAGC	3600
TTCATGTATC	CCTTCAGATA	TTAGATATTC	ATCTTGTTCA	ACCTGCTTAT	ATTCATTTCT	3660
TGTACCATGA	ACTTTTTCTA	AAGTTCTTCT	TCCAAATGCT	ATTTTCCCAT	TATATACAGG	3720
ATTCTTTAAT	ATCTTTCTTA	TAAGACCTGC	ATCAAACAAA	GGATTCTTAC	CATTCTGTCT	3780
TGGGATTTTT	CTAATTCCAT	GATTCTCTAA	GTATTTAGAT	ATCCCATTTG	CTCCTATCGT	3840
AGTATTTACA	TACTGGTCGA	AAATCGTTCT	TATTGCAACT	GCCTCTTCCT	CATTTATAAA	3900
CAGCTTGCCG	TCTTCAAGTT	TATATCCATA	CGGAGCAAAG	CCACCATTCC	ATTTTCCTTC	3960
CCCTGCTTTT	TGAATGCGAC	CTTCCATTGT	TTGAATACTG	ATGTTTTCTC	TTTCTATTTT	4020
AGCCACAGCT	GATAAAACAG	AAATCATTAG	TTTCCCAGCA	TCTTTAGATG	AATCAATGCC	4080
ATCTTCAACG	CAGATAAGAT	TAACCTCATA	ATCCTGCATT	ATATGAAGTG	TAGAAAGAAC	4140
ATCAGCGGCA	TTTCTTGCAA	ATCTTGATAA	CTTAAACACA	AGAACAAAAG	ATACTCCATC	4200
TTTTCCAGAT	TTTATATCTT	CCATCATTCG	ATTGAACTGT	ATTCTACCTT	CAATAGACTT	4260
GTCAGACTTC	CCGGCATCTT	CATACTCTCC	AACAATTTCA	TAATCGTTGT	AAATAGCAAA	4320
AGCTTTCATT	CGTGATTTTT	GTGCCTCTAA	CGAATACCCC	TCTATCTGTA	TTGACGTAGA	4380
TACTCGTGTA	TAGAGGTATA	CTTTTATTTT	TTCTTTTGAC	ATAGTATTAA	CCTCAATATA	4440
ATTTTCTCTAT	ATCATATATA	ATTTTTTTTAA	TTTAAGTTTG	GACTATCATT	TCAAGTATAT	4500
TATAACACTT	TTATTAGTCC	GTCTCAATTT	GTGTTTTTGC	CATGTCAAAA	CTATTTTTCA	4560
TCTCTTGATT	TTTTGCTGGC	GTTGGATCGG	GTAGATTATC	TAAATCTAAA	GCACCAGCAT	4620
ATTTTGCAAT	CAGATTTGCT	ATTAAATCAG	CCAATCCATT	CCAGTCATTG	TCCAATATAT	4680
ACCTCCTCTA	AAGTTTTATA	TCTAATAATT	ATTTGTTTAA	TTAAGTTTTT	TGACATTGAC	4740
AAGTGCTTTG	GATTAGCAAC	ATAGGAATCT	CACTTCCGCC	TCTATTCGGG	ATGAGCCGGC	4800
TTCAACCTTA	GAAGTATCAT	TACCCTCATT	TTCTTCATAG	CGGATAGGGT	ATCCCTCCCT	4860

1009

ATATTCAAAC TCTTACTTAT CGCTCACTTT CTTTTTGCTT AGCAGAACTT TTTTGGCCGA	4920
ATTATTCAGC CGAAAGATCT TGACGGATAG GTTATTACGC TCCAAAAATA ATTAACGTCT	4980
TGTCTTGGTC TATTCAATTG TTAAGGTTCA AAATTTATCG AGAGTTATTA ATCTTTTAA	5040
AATTGACCA TCAGAAAATA TTTATCTTGA TGTAACAAAA TTCTATAAAT TACCCTCTTA	5100
TACTTAACAG TGAAAAGAAG TCTTCTTGG TAACCAATTT TGAAATAGAA TTTGCTTATA	5160
TAAAAAGGTC CAATCCCCAC TGCATAAATA GCAGTGAAAA TTAGACCCTC TTGGTAACTG	5220
TCATCTAAAA GTCTTCTA	5238

(2) INFORMATION FOR SEQ ID NO: 151:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

GACGATTTAC GAAGAATCGA ACAAGAACCT GTCCTATCA ATTCCCAACC TCTATCTCTA	60
AAATCTTGCA GTTCATGCTT ATACTTTTTT AAGAAATCTA GAATCATAGA TACGGTAGAT	120
GACATCGTCT GGTGACATT GGTCAAATA GAACAAACCA AACGACTCG TTCTATACCT	180
CCAACCTTTC AAATGCATCT CATGTAAATG TTCTTCTTCC TTGTCCAAAT CAACAATGGT	240
GAAAATCCGA AATTCTACTC TGCTATTCAT TGTCTTACCC CAAAATTAGA AAACATGCCT	300
GGCGTTATTT ATTAGATAAT TCTTCCACT TTTGACTCAA TCTCCAAAAA ATATAAGAAA	360
TCTGAATCGC AAAAATATC AATAAAACCC AATCTATTAT GAAAATCAAA AACACTTTCC	420
AACTGAAAGA ACTACCTCCA GTGACAAACT TTGAGAAAAA CGGTAGTAGA GCTAAAAAGA	480
GAAATAAAAT AGGAAGCATC CGCATGTGTA AAATCCGTTT GGCATAAAAA AATCTTTATT	540
TAAACGAAAA TATTATGGCA AAATTTACGC CAGTTTTTGA ACGGCTGATG TAGATATTTT	600
ATACTTTCAA AATGTTTAAA TGTGATTATT TATTTTTGAA AAATAGATCA CCAGCCCGAC	660
TGAAAGTGCT TATAGAATGA TAATAAGTCG CCTGCCGAAA ACAGCGAAAA ATAGCGGTGT	720
TATGCGGAGA TAATCTGACG CGATGCGAAA GTATATTGCA TACTTATTTT CAACAATTTA	780
GCAGAGTATT TTTATAAGTG TGATATAATA GAAGTATAAT TTGTTCTGAT AGTTTATTTT	840
ATGGAGAAGT AGATTTTTAG AATGCGGAGG GTTCAATATG GTTGAGTTTA TAAAGTCTAA	900
GAAAGAAATG AGTGAGGAGG ATATTAAAGC AAATTCATC ACTCCTGCTA TTGTATCCAA	960

1010

AGGATGGAAA	AATGGTGAGC	ATATCGCTTA	CGAAGAATAC	TTCAC TGATG	GTCGAATTGA	1020
AGTTAGAGGA	GATAAGGCTC	GTCGTAAAGA	AGGAAAAAAA	TCAGACTATT	CACTGTATTA	1080
CCAATTTGGA	ACTCGAATTG	CAATTGTTGA	GGCAAAGGAT	AATAAACACA	GCGTTCGAGC	1140
AGGATTACAA	CAAGCTATTG	AATATGGAGA	GATTTTAGAT	GTTCCATTG	TTTATTCTTC	1200
GAATGGTGAT	GGCTTTATTG	AACACGACCG	TATCACGAGA	GAAGAACGTG	AGCTGGAGTT	1260
AGACGAATTC	CCTACTCGTG	AAGAATTATT	TTCTCGTATG	ACGAAGGAAA	AAGGATTGAC	1320
GTACGAAATT	ACAGAAGCTA	TCTCAACTCC	ATACTATACA	GACGCCTTCT	CAATGAAAAC	1380
GCCACGCTAT	TATCAGCAAA	TAGCTATCAA	CCGTACTATT	GAAACAGTTG	CCAGAGGACA	1440
AAAACGAGTA	ATGTTTGTGA	TGGCAACAGG	AACGGGGAAA	ACGTTTCATGG	CTTTTCAAAT	1500
TATTCATCGC	CTTCGAAAAG	CTGGTTTGGC	TAAACGAGTT	TTATTCTTAG	CAGATAGAAA	1560
CATCTTAGTA	GACCAAACGA	TGGCTGAAGA	CTTTAGGCCA	TCGAAAAGG	TAATGACGAA	1620
AATTACACCA	AACTTTTGA	CTGCTCCTGA	AAAATTAAAT	TCTTTTGAAA	TTTATCTAGG	1680
GCTTTATCAG	CAACTAACTG	GTGAAGATGG	AACTGAAACA	CATTATCAAA	AATTTGACAA	1740
AGACTTCTTT	GATTTAATCG	TAATTGATGA	AGCGCACCGT	GGTTCAGCTA	AGGAAAACAG	1800
TAAGTGGCGT	AAGGTAATTG	ATTATTTTCA	TTCTGCGACA	CAGATTGGGA	TGACCGCTAC	1860
TCTTAAAGAA	ACCAAGAATG	CTTCCAATAC	GGAATACTTT	GGTGAGCCAA	TCTATACTTA	1920
TAGTTTAAAA	CAGGGAATCG	AGGATGGTTT	TTTGGCTCCA	TATCGTGTTA	TGAGGGTTAA	1980
TTTAGATGTG	GATGTGGATG	GTTATCGTCC	AGAACTGGA	AAAGTTGATG	CTAACGGACA	2040
ATTAATAGAA	GATAGGTACT	ACGGCAGGAA	AGATTTTGAT	AAAACCATTG	TCATTGATGA	2100
TAGAACGCAA	AGAGTTGCCA	AGTTTGTTTC	TGATTATATG	AAGCAAAACA	ATGCACGATT	2160
TGATAAAACA	ATTGTTTTTT	GTGTTGATAT	TGACCATGCC	GAGCGAATGC	GTGCTGCACT	2220
TGTAAAAGAG	AATCTAGACT	TAGTCCAAGA	AGACTATCGT	TATGTCATGC	AAGTAACTGG	2280
TGACAACGCT	GAAGGAAAAG	CTCAACTGGA	TAAC TTTATG	GATGTCAATT	CTAATTTTCC	2340
CGCTATTGTA	ACAACGTCTA	AATTATTAAC	GACAGGAGTT	AATGCTAAAA	CATGTCGTTT	2400
GATTGTTTTA	GACTCTAATA	TCCAATCCAT	GACTGAATTT	AAACAAATTA	TTGGTCGTGG	2460
CACACGTCTT	TATCCTCAAA	AGGGGAAAGA	ATTTTTTACG	ATTATTGATT	TCGAAATGT	2520
TACCAATTTG	TTTGCTGACC	CTGATTTTGA	TGGTGATCCA	GTGAAGGTGC	TAGAAACAGG	2580
TGCGAAAACA	GTCAGTGGTT	CTACGCCCGG	TTTCGTAGAT	GAGGAAGGTG	ACCCAGTAGA	2640
AAAATATATC	GTTACAGACA	AGCAGGTTAC	CATTCTTAAT	TCTACTGTTC	AAGTATTGGA	2700
TGAAAACGGG	AACTGATTA	CCGAAAGCCT	GACCGACTAC	ACTCGAAAGA	ATATCTTAGG	2760

1011

TAGCTACGCC	ACTTTGAACG	ATTTTATCAC	AGTTTGGCAT	ACGGCAGATA	AGAAGAAGCT	2820
TATCTTAGAC	GAAC TTATA	AAAAAGGAGT	TTATCTAGAT	GCTATTTCGAG	AGTCGGAGGG	2880
AATATCAGAA	CAAGAAATCG	ATGATTTTGA	TTTACTCCTA	AAACTTGCCT	ATGGTCAAAA	2940
AGAATTAACC	AAAACGGAAC	GTATCAATAA	ACTCAAACAA	AGCGGATATT	TATATAAATA	3000
TAGTGAGGAA	GCGCGTGCTG	TTTTGGAAAT	TTTACTGAAC	AAATACATGG	ATAAAGGTAT	3060
TGGAGAACTC	GAAAGCATTG	AAACATTAAA	ACTTCCAGAA	TTTCAGATAT	ATGGTGGAAC	3120
CTTCAAAATC	ATCAATACTT	ATTTTGGAGA	TAAAAAACGA	TATTTACAAG	CAATTAAAGA	3180
ATTGGAGCAA	GAGCTATTTA	CAGTAGCTTA	ATGAAAGGAA	AGTATGTCAA	TTACATCATT	3240
TGTAAAAAGA	ATTCAAGATA	TCACTCGAAA	CGATGCTGGT	GTTAATGGTG	ATGCTCAACG	3300
TATTGAGCAA	ATGTCTTGGT	TATTATTCCT	AAAAATTTAT	GATAGCCGTG	AAATGGTTTG	3360
GGAATTAGAA	GAAGACGAGT	ATGAGTCAAT	TATCCCAGAG	GAATTAAAAA	GGCGAAATTG	3420
GGCTCATGCT	CAAATGGGG	AACGGGTATT	GACAGGCGAT	GAATTACTTG	ATTTTGTCAA	3480
TAACAAGTTA	TTCAAAGAGT	TGAAAGAGCT	TGAAATAACT	TCAAATATGC	CTATTTCGAAA	3540
AACGATTGTT	AAATCAGCTT	TTGAAGATGC	GAACAACTAT	ATGAAAAATG	GCGTCTTGTT	3600
ACGCCAAGTC	ATCAATGTTA	TTGATGAAGT	TGATTTCAAT	AGCCCTGAAG	ATCGTCATTC	3660
GTTTAATGAT	ATTTACGAAA	AAATTCTTAA	AGATATTCAA	AATGCTGGGA	ACTCAGGAGA	3720
ATTTTATACG	CCACGTGCAG	CGACTGATTT	TATTGCCGAA	GTTCTTGACC	CAAACTTG	3780
AGAATCAATG	GCAGACCTTG	CTTGCGGAAC	AGGAGGCTTC	TTGACTTCGA	CTCTGAACCG	3840
TTTAAGTAGT	CAACGTAAAA	CTAGTGAAGA	TACCAAAAAA	TATAATACAG	CTGTTTTTGG	3900
TATTGAAAAG	AAAGCATTTT	CTCATCTTTT	AGCAGTTACA	AATCTGTTTC	TTACGAAAT	3960
TGATGACCCT	AAAATTGTTT	ATGGAAATAC	TTTGGAGAAA	AATGTTTCGTG	AATATACGGA	4020
TGATGAAAAA	TTTGACATTA	TTATGATGAA	TCCACCTTTT	GGAGGGTCAG	AATTAGAAAC	4080
AATAAAAAAT	AAC TTTCCAG	CAGAATTACG	GAGTTCTGAA	ACAGCTGATT	TATTTATGGC	4140
TGTCATTATG	TATCGTTTGA	AAGAAAATGG	TCGTGTTGGA	GTTATTTTAC	CTGATGGTTT	4200
TCTATTTGGT	GAAGGTGTAA	AAACTCGCTT	GAAACAAAAA	CTGGTAGATG	AGTTCAACTT	4260
GCATACGATT	ATTAGGTTGC	CTCATAGTGT	CTTTGCACCG	TATACAGGAA	TCCATACGAA	4320
CATTCTTTTC	TTTGATAAAA	CAAAGAAAAC	AGAAGAAACT	TGGTTTTATC	GTTTAGATAT	4380
GCCAGATGGT	TATAAAAATT	TCTCGAAAAC	TAAGCCGATG	AAGTCAGAAC	ACTTCAATCC	4440
TGTTCTGTGAC	TGGTGGGAAA	ATCGTGAAGA	GATTCTGGAA	GGTAAGTTCT	ACAAATCTAA	4500

1012

ATCATTTACA	CCTAGTGAAT	TGGCTGAGTT	GAATTATAAT	TTAGACCAGT	GTGACTTTCC	4560
AAAAGAGGAA	GAGGAAATCT	TAAATCCCTT	TGAGTTGATT	CAGAATTATC	AAGCGGAAAG	4620
AGCAACTTTA	AATCATAAGA	TTGATAATGT	ATTAGCTGAT	ATTTTGCAGT	TGTTGGAGGA	4680
CAAATAATGA	CACCAGAACA	ACTTAAAGCA	AGTATTCTCC	AAAGAGCGAT	GGAAGGGAAA	4740
TTAGTGCCGC	AAAATCCCAA	TGACGAACCT	GCAAGTGAAT	TATTAAAGAG	AATTAAAGCT	4800
GAAAAAGAAA	AACTTATCAG	TGAAGGAAAA	ATCAAACGAG	ATAAAAAGGA	AACTGAGATA	4860
TTTCGTGGTG	ATGATGGGAA	ACATTATGGG	AAGTTTGCTG	ATGGAAGCAC	TCAAGAAATT	4920
GATGTTCCCT	ATGATATTCC	TGATACTTGG	GAGTGGGTGA	GGTTTTCTAC	ATTGGTTGAA	4980
ATTGTCAGAG	GTGGCTCTCC	ACGACCAATC	AAaGATTATC	TTACTTCTGA	AGTAGATGGA	5040
ATAAATTGGA	TAAAAATAGG	TGATACTGAA	AAGGGTGAAA	AGTATATAAA	TAATGTTAAA	5100
GAAAAAATCA	AAAAATCAGG	GCTTAACAAA	ACTAGATTTG	TAAAAAAAGG	TACATTTTGT	5160
TTAACTAATT	CTATGAGTTT	TGGTAGACCT	TATATTTTGA	ATGTTGATGG	TGCAATACAC	5220
GATGGATGGT	TGGCTATTTT	GAACATGAA	AACTCATTA	ATAAAGATTA	CCTATTCTAT	5280
ATTCTTTTCAT	CAAATGTAGT	TTATTCTCAA	TTTCTATCTC	TAATTAGTGG	AGCTGTTGTG	5340
AAAAACTTGA	ATAGTGATAA	AGTTGCTTCT	ATTCTTATCC	CTCTCCCCCC	ACTATCCGAA	5400
CAACAACGAA	TAGTAGAAGC	AATCGAATCA	GCTTTAGAAA	AAGTAGATGA	ATATGCTGAA	5460
AGTTATAATA	GACTAGAACA	GCTAGATAAA	GAATTTCCAG	ATAAACTAAA	AAAATCTATT	5520
CTTCAATATG	CTATGCAAGG	AAAATTAGTT	GAACAAGACC	CAAATGATGA	ATCAGTCGAA	5580
GTTTTACTTG	AAAAAATACG	AGCAGAAAAA	CAAAAACCTCT	TTGAAGAAGG	CAAGATTAAA	5640
AAGAAAGATT	TGGACATTTT	TATTGTTTCC	CAAGGAGATG	ATAACTCTTA	TTATGGGAAT	5700
ATACCTATGA	ATTGGGTGTT	TATAAAAATA	AAAGATATTT	TTTCAATAAA	TACAGGTCTT	5760
TCTTACAAGA	AGGGCGATTT	AAGCATTAAT	AATAAAGGTG	TTAGAATTAT	ACGTGGTGGT	5820
AATATTAAGC	CTTTAGAATT	TTCTCTGTTG	GATAATGATT	ACTACATTGA	TACACAATTC	5880
ATCTCCTCTG	AGCAAGTTTA	TTTAAAACAT	AATCAGCTAA	TAACACCTGT	ATCAACCTCT	5940
TTAGAACATA	TTGGAAAGTT	TGCAAGAATC	GATAAAGACT	ATGATGGTGT	TGTGGCTGGT	6000
GGATTTATTT	TCCAATTAAC	ACCATTCGAA	AGTTCAGAGA	TTATTTCAAA	ATTTCTATTA	6060
TTTAACTTGT	CCTCTCCGTT	ATTTTATAAA	CAATTGAAAG	CAATAACTAA	ACTATCAGGT	6120
CAAGCTTTAT	ATAATATTCC	TAAAACTACA	CTGAGCGAGC	TATTAATTCC	GTTAGCTCCT	6180
TTTGAGGAAC	AGGAACCTAT	TACTCAAAAA	GTTGAGAAAC	TTTTTGAAAA	AGTAAATCAA	6240
CTTTGAAAAT	GATTCTTTTC	ATCTCTTCAT	GATTAGAAAT	AGGGATTAAT	AATTCGGAGA	6300

1013

TACTGGTACT	ATTTAATGTT	TTCCCTTTGA	TAGCATCTTT	TGAATCACCT	AAAGTAGAGA	6360
TAAGTGGCAA	AAATATCATT	AAGTAATCTC	TGATAATATT	TTCTTTATTA	GCATAGGGGA	6420
ATATCGATAT	AATGGCTTCA	TTATGAGTGG	CAGGAATATC	CAATATGGCA	ACTTTTCCAA	6480
TAGATAATTT	AAAACTCATT	AATAAAGTTC	CTTTAGGTGA	AATGTCTATT	TTCTTTGATT	6540
TTAATGCTAA	TTTAGAAATA	GATTCTCTCG	CATTAGTTAC	ATAACCAGAT	ATAGGCATAT	6600
CTGATATAGA	TACCCAAGGT	ATTTTCAGTTC	CCCAAAAAGT	AGCTTCACTG	CGTGGAGGAG	6660
TTTTTCCTAT	TCTGAAGTTA	ACTAGGCTAG	CAAATTTAAT	ATATCTCCAT	GCTTCTGGGA	6720
TTTCATATAT	AGGATAAGAG	GTTGTTTCGT	CTTTGTTCCC	ATAATAAGAG	CCATAATCAC	6780
AAAAATAGCA	GGTAGTCAGT	TTGACCACCT	GTTATTTTTT	ACCAATTAAC	AATTTTATCT	6840
ACAATATTTT	GTTGTTTCAGT	AGCTGTTTTT	CTTAGATAAA	TTCGAGTAGT	TTCTATACTT	6900
TCGTGTCCCA	TCAAATCTGC	AAGCAAGGCA	ATATCATTTAT	ACTTCGCTAA	AAAATTCTTA	6960
GCAAATAAAT	GCCTAAAAGA	ATGAGGGTAA	ATTACGTTAG	GATTCATTTT	GTATTTATCA	7020
GCATAATTTT	TTAACTGTTG	AGCAACTCCT	CTTGCTGTAA	TTGGTTCGTT	AAATTTATTC	7080
AAAAATAAAT	AACCACTTCG	GCGATTTTCT	GATTCTAACC	AACTAAGACA	ACTATTTCTT	7140
AATTTTTTTAG	GAATGTACAG	TCTACGAATT	TTACCACCTT	TTGAGTAAAT	GTCAAAATAA	7200
CCGATTTCTA	CATGCTCTAC	TTTTAGTTTA	ATAAGTTCAC	TTACACGAGC	CCCAGTTGCA	7260
CCTAAAAACC	AAACGACAAA	ATGCCATTTT	AAAATACCAT	CTTTTTTTCAA	ACTACGTTTA	7320
AGAAAAAGGT	AATCAGCATG	GCTAATGACA	TCTTCTAAAA	ACGGTTTTTG	CTGTACTTTG	7380
ACAAATTTTA	ATTTCAAATC	ATCATGACCA	ATAAAAGCCA	GATATTTTAT	TACTCCTTGT	7440
AGTCGCAAAT	TGACAGTTTT	AGGTTTAAAA	TTGTCTAATA	AATATCCTTT	GTATTCAAAT	7500
AAATCTTCCA	TTTTGAGTTC	GTAATTCTCC	AAGAAAAATC	GAACACCATA	AAGGTACGAA	7560
CGCACAGTAT	TTTCAGCTAA	ACCAGCTTTC	TTCAAATGTA	ATTCAAAATC	TTTCAACGTA	7620
AAACTCCTAT	CTTATGTTTG	ATAGAAATTC	CACCGCACGT	AAAAC TATTA	TACTAAATTA	7680
GTGCGTCAAT	ATGGGCGAAA	AATTGTTTCGA	TTTTATCAAC	GATTCTGGAT	TGTTCAGGAA	7740
GGGGTGGGAG	GGGGATTAAA	TATTCCTTTA	TAGTTTTTCGT	TAATAATTCT	TTTTGTTTTG	7800
TACTACCCGA	CGCTTTTTCT	TCAATAACTG	ACTGAACAAT	AGGAGAGGAA	AGAAAATTAT	7860
AGATGAAATG	GCAATTAATA	ACCCCGATA	AGACTCTTAT	AACTGTAACA	TGGCTATCTG	7920
CAACAGCCCA	GCCATAAGGA	TTTTTATTTT	CATGGTAAAT	AGCTAATCGT	CCTAACGTAC	7980
CTAGACCTGT	TGAATTCCAC	ATTAAATCAC	CATCTCTTAG	TAATCTTTCT	TTCTGGTAAC	8040

1014

TATGAACTGT	TTCGGGATCA	ATAAATCTTG	CTAAGTCAAT	AGAAAAGCCA	GACCATTGAT	8100
TACATTTCTG	AGCAATCACA	GGGTATATAG	GAATATTTGA	ATATTTTGGA	GACTTCCCTC	8160
TTTGAATGTA	GGAGGTTATA	TCGTTTAACC	TCACCCATTC	CCAACCTTCT	GGTATTTTAC	8220
AAGGTACTTC	CTCATAATAA	GAGTTATCAT	CTCCTTGGGA	AACAATAGAA	ATGTCCAAAT	8280
CTTTCTTTTT	AATCTTGCCT	TCTTCAAAGA	GTTTTTGTTT	TTCTGCTCGT	ATTTTTTCAA	8340
GTAAACTTTC	GACTGATTCA	TCATTTGGGT	CTTGTTCAAC	TAATTTTCCT	TGCATAGCAT	8400
ATTGAAGAAT	AGATTTTTTT	AGTTTATCTG	GAAATTCCTT	ATCTAGCTGT	TCTAGTCTAT	8460
TATAACTTTC	AGCATATTCA	TCTACTTTTT	CTAAAGCTGA	TTCGATTGCT	TCTACTATTC	8520
GTTGTTGTTC	GGATAGTGGG	GGGAGAGCAA	TTAATAATAG	ATTAAAATTA	TAATCATTGA	8580
TTGCAGGATA	ACTTGTTCCA	GTAGATTTAT	TATTAACACG	ATTGATAAAA	TTATCTGATA	8640
ATAAATAATA	TTTCAAATAT	GTTTCGTAA	GTAAAGTATC	CAAAACAATA	AATGCTGTAC	8700
TAGCTATCAA	ATACTCTTTA	AGTTCCTCTA	CTACAGCAAT	ATTTTTTAGA	TATGGTCTAA	8760
CTGTTGAAAA	TAAGACACTA	TTCTGCGAAA	CTAATTTTCT	AGCACGGGAA	GGCGCTTGTT	8820
CAGGTGAAAG	ATATTGTAGA	TTTTTGTAGT	TGATTATGTT	CTTTTTTCTA	TCAATACTAG	8880
ACGTATCTAT	ATACCTAAAG	GATTTCTCTG	GCTTATTTTG	CCCAAATTC	CAATAAATTG	8940
ATTTTATCCT	CACCCACTCC	CAAGTATCAG	GAATATCATA	AGGAACATCA	ATTTCTTGAG	9000
TGCTTCCATC	AGCAAACCTC	CCATAATGTT	TCTTATGTGC	TTCAAGTATA	TAAAAAGGCG	9060
TAAAAATACG	CCTATAGATA	ATGGGGTTGA	AATAGGTTTA	TTGTTGATGA	GATTGTAGAT	9120
AATTCAATTT	TTTACTTCCA	ATCGAATATT	CAAATCCTCC	ACCTTTTCTG	CCTGTAATTG	9180
TTCATCATAA	AATTCAATAT	CTTCAGGATT	TTCCCTTGG	CAACCTCGGC	AGAAATATTC	9240
TTCCGCTCGA	TCAGGATTCA	AAAATCGACA	AGCACAAACA	AAACAGTCGC	CATCATCATT	9300
TATTGAGATA	ATATAGTAGA	TTGAAATAAG	ATGTAAACAA	ATCGATTAGG	AAAGTTAAAT	9360
TAGTTTCTAG	AAATTTTTAG	CAGATGTAGT	GTACTATTCT	AGTCTCAATT	TACTATGGCT	9420
TCAAATATAT	CTTTCGAAAA	AATATTTACA	GATGTGTAAT	TTTGAAGCTT	GCAAAAGTTA	9480
GTAAACTTGT	AGATTTTCGAT	TTGAAGTAAC	TTGTTTTCTT	GCCCGATATT	GTTTTTGAAA	9540
TTGAATTTTT	CCATAGTGAC	TCCTTAATTT	TCTTCTACAC	GTCTGATGAT	AAATCTAATT	9600
CGCAAAAGAG	TCAAGAGGAT	TTTTTCGAAA	ATAAATAGCG	ACCGAAATCG	CTATTTTAAG	9660
GGTTATAGGT	ATTTGATGGC	TTAGACTGCT	GTGTGACTGT	TTACCCACAG	GCAATCTTTC	9720
TTCTATATTA	GTATTAGTAA	AGGTCTAAAT	AATTATCAAT	TTCCCATTTG	GAAACGAAGG	9780
TTGCATAACT	TGCCCATTCT	ATTCGTTTGG	CTTCAAGGAA	GCTAGTATAG	ATGTGATCTC	9840

1015

CGAGAGCAGC	TTTAACCACT	TCATCTTCTG	TCAAAGCTTT	CAAAGCGTTG	TGAAGAGTTG	9900
ATGGAAGGTC	TGTAATACCA	GCTTCCTTGC	GCTCTTCTGC	TGTCATGATG	TAGATATTTT	9960
CTTCGATAGG	AGCTGGTGCT	TCGATTTTAT	TTTCAATACC	ATACAAACCA	ACTTCCAAAA	10020
GAACAGCCAT	AGCAACGTAA	GGGTTCGCCA	TTGGATCCAC	TGAACGCAAC	TCAAGACGAG	10080
TTCCCATACC	ACGTGAAGCA	GGTACGCGCA	CAAGTGGCGA	ACGGTTACGA	CCAGCCCAAG	10140
CAATGTAAAC	AGGCGCTTCA	TAACCTGGAA	CCAAACGTTT	GTATGAGTTA	ACTGTTGGGT	10200
TCATGATGGC	AGTATAGTTG	TAAGCATGCT	TGATCAAACC	GCCTAGGAAA	TGGTAAGCTG	10260
TTTCTGACAA	CTGCATTCCCT	TTTGGATCAT	TTGGATCAAA	GAAGGCGTTA	TTTCCTTCTG	10320
CATCAAACAA	GGACATATTA	CAGTGCATAC	CTGATCCAGC	AATACCAAAT	TTTGGCTTCG	10380
CCATAAATGT	TGCGTAAAGT	CCGTGTTTGC	GAGCAATGGT	TTTAACAACA	AGCTTAAAGA	10440
TTTGAATCTT	ATCACAAGCA	CGGAGAACTT	CATCGTACTT	AAAGTCAATC	TCATGCTGTC	10500
CAACCGCAAC	CTCGTGGTGA	CTCGCTTCTA	CTTCAAATCC	CATTTTGGTC	AAGACATTCA	10560
CAATCTCACG	ACGTGTGTTG	TCCGCAAGGT	CAGTAGGTGC	CAAGTCAAAG	TAGCCACCCT	10620
TGTCATTAC	TTCAAGTGTT	GGGTCCCCAT	TTTCATCCAA	CTTAAATAGG	AAGAATTCTG	10680
GCTCTGGACC	AAGGTGAAG	GATTTGAATC	CAACTTCTTC	CATGTGACGA	AGAGCTCGTT	10740
TCAAATTACC	ACGAGGGTCA	CCCGCAAATG	GTTACCTTC	TGTTGTATAG	ACATCACAGA	10800
TCAGACCTGC	AACACTTCCA	TTTTCATCTC	CCCAAGGGAA	GACTGTCCAT	GTATCCAAGT	10860
CCGGGTACAA	GTACATATCC	GACTCATTGA	TACGTACAAA	ACCTTCAATA	GAAGATCCAT	10920
CAAACATAAC	CTTGTTTCGAC	AAGACCTTAT	CTAACTGTTC	ATCTGTAGCA	GGAATTTCTGA	10980
CGTTTTTCAT	GGTCCCAAA	ATATCTGAGA	ACATAAGACG	AATAAAGGTA	ACATTTTTTTT	11040
CCTTGACTTC	ACGACGAATA	TCTGCAGCTG	TGATTGGCAT	AAGTTTTCTC	CTTAATCTAT	11100
GACTACTTGC	GGTTGCCTAA	CCGCGACCAA	AAGGTGACTG	TACTGAAGCA	AAACGCCCCCT	11160
GTTGGAGGAG	TTCAATTGTGA	AGTGCACGAC	GTACTTCAGT	CTGACTAACC	GCTTCTTGG	11220
ATTTTCGCTTC	ACGTTTCAGCA	TATTTTTTCT	TAATGGCAGC	GATATTATAA	CCTTCAGAGA	11280
TATAATCTTT	GATTTCAAGC	AGACGATCCA	TGTCATTCAA	GGAATACATG	CGACGATTTT	11340
CTTCGTTTCG	ATCGGGCTTG	ATCAACTCTT	GATCTTCATA	ATAACGAATC	TGACGCGCCG	11400
ATAGATCGGT	CAACTTCATA	ACACTGCCGA	TAGGAAAAAC	AGCCATATTT	CGGCGAAATT	11460
CTTTTTCTT	CATTTACAAT	TTCTTCTTT	CTGTCTATTA	TAGTCTAAAA	AAAGACAAAC	11520
GTCAATTGAT	AATGTTATAA	AATGTAACAT	TATTTTTCTT	TTTTCTCTAA	AAAGAGACGA	11580

1016

ATACGATCAA	TATCGTAATT	TACGATAATT	GCGACAAAAA	CTCCCATAAA	CGTTTCTAAT	11640
ACACGCACAA	ACACGTACAA	AATTGTCTCA	CCACTTGGAA	TTGATAGGGT	AATGATTAAC	11700
ATAGCTGCTA	CACCACCAAT	AACCCCTGCT	TTGTTATTCA	TGGCTACATT	TGTCATAATG	11760
GTTAACATGG	TGCAGATTGG	AACAAC TACC	AAGGTCACCC	AAAAGGCTTC	GTGGAAAAAG	11820
GTATTTAATA	AGAAGAAGAC	CAAGGCATAG	AGTCCACCGA	TACTATTTCC	TAGAATACGC	11880
GAAGTCCCAA	AATGAACACT	CTCATCAAAA	CTCTCCCTCA	GGCTAAAAAC	GGCTGTCAAA	11940
GCACCAATTT	GAAGACCTTT	CCAGCCAAAA	AAGCCAAAAA	TCAAGAGAAC	TAGAAAAACA	12000
GCAATACCTG	TTTTAAAGGT	TCGCATACCA	AGTTTGAAC T	GGGATTTATC	GAATTTATAT	12060
TTTTTAAAAT	AACTCATAAT	CTCAACTTTC	TATTTCCATT	TTATCATAAA	TCGGTGATTT	12120
TTATGAGTAA	TAGTTGAGAG	GAAGCGTTTT	TATTTTAAGC	AAAAGAAAAG	AGGAACTTTC	12180
ATCCCTCTCT	TCTTTGATTT	ATTTATAAAA	TCTTATTTTT	CTGTCAAGGC	TGCAAGTCCT	12240
GGAAGAACCT	TACCTTCAAG	AAGTTCCATT	GATGCTCCAC	CACCCGTACT	AATCCATGAG	12300
AACTTGCTCTG	CACGGCCAAG	GTTAATCGCT	GCGGCAGCTG	AGTCACCACC	ACCGATGATT	12360
GATTTAACTC	CTGGTTGTTT	CACGATAGCG	TCCATCACAC	CGATTGTACC	AGCTTGAAAA	12420
TCTGGGTTTT	CAAATACACC	CATAGGTCCG	TTCCATACGA	CTGTTTTTGGC	ACCAGTCAAA	12480
GCTTCGTCAA	ATTTGGCGAT	AGATTTTGG A	CCGATGTCAA	GACCAAGGAA	GCCTTCAGAA	12540
ACTGCTTCAC	CTTCAGTGTC	ACGCACTTCA	GTGTAACCAG	CAAATGCGTT	AGCTTCTTTT	12600
GAGTCAACTG	GCAAGATCAA	TTTACCATTT	GCTTTTTTCAA	GAAGAGCTTT	CGCAACATCC	12660
AATTTGTCTT	CTTCTACAAG	TGAGTTACCG	ATTTGATAC	CTTGTGCTTT	GTAGAATGTG	12720
TAAGTCATCC	CACCACCGAT	AAGGACGTTA	TCAGCTTTTT	CAAGCAAGTT	TTCGATAACA	12780
CCGATCTTGT	CTGAAACTTT	TGAACCACCA	AGGATAGCCA	CGAATGGACG	TTCTGGAGTT	12840
TCAACTGCTT	CTTGATGTA	GGCAATTTCTG	TTTTCAAGAA	GGAAACCAGC	AACTGCTTTT	12900
TCAACGTTTG	CTGAGATACC	AACGTTAGAT	GCGTGTGCAC	GGTGAGCTGT	ACCGAATGCA	12960
TCGTTTACGA	AGATACCATC	TCCAAGTGAT	GCCCAGTATT	TACCAAGTTC	AGGATCGTTT	13020
TTAGATTCTT	TCTTGCCGTC	AACATCTTCTG	TAACGAGTGT	TTTCAACCAA	GAGAACTTGT	13080
CCATCTTCAA	GAGCGTTGAT	TGCCGCTTCT	AATTCAGCAC	CACGAGTGAC	ACCTGGGAAA	13140
ACAACATCTT	GACCAAGTTT	TGCTGCCAAG	TCAGCTGCTA	CAGGAGCAAG	TGATTTACCA	13200
GCTTTATCAG	CTTCTTCTTT	CACACGTCCA	AGGTGAGAGA	AAAGAATTGC	ACGTCCACCT	13260
TGTTCGATGA	TGTACTTAAT	AGTTGGAAGA	GCTGCTGTGA	TACGGTTATC	GTTAGTGATT	13320
ACGCCATCTT	TCAATGGTAC	GTTGAAGTCA	ACACGAACGA	GGA CTTTTTT	ACCTTTCAAG	13380

1017

TCAACGTCTT TAACAGTAAG TTTTGCCATG TTACAAAAAC TCCGG

13425

(2) INFORMATION FOR SEQ ID NO: 152:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 905 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

GATTTATCCT ACCGGnGAAT TTCCGGAGGG GTTCTAGCAG CAATCTTAGG AATCTATGAA	60
CGAATGATTG GCTTTCTGGC CCATCCCTTT AAAGACTTTA AAGAAAATGT TTTGTACTTT	120
ATTCCAGTTG CCATCGGTAT GCTTCTGGGA ATCGGCTTAT TTTCTACCC GATTGAATAC	180
CTGCTTGAAA ATTATCAGGT TTTTGTATTA TGGAGCTTTG CGGGAGCTAT TATCGGTACA	240
GTTCTAGCC TCCTCAAAGA ATCAACTCGA GAATCTGACC GAGACAAGAT TGATTTAGCT	300
TGGTTATGGA CAACCTTTAT CATTTCTGGA TTAGGACTCT ATGCCTTAAA TTTTGTCGTT	360
GGAACCTTAA GCGCCAGCTT TCTTAACTTC GTCCTAGCAG GCGCACTATT GGCCCTTGGC	420
GTCTTGGTTC CTGGCCTCAG CCCATCAAAT TACTTTTGA TTTTGGGACT CTATGCTCCT	480
ATGTTGACTG GTTTTAAAAC TTTTGATTTC TTGGGAACCT TCTTTCCGAT TGGAATTGGT	540
GCAGGTGCAA CTCTCATCGT TTTTTCAAAA TTGATAGATT ATGCCTTAAA CAACTACCAC	600
TCACGCGTCT ATCATTTTAT CATCGGTATC GTCCTATCAA GTACCCTTTT GATCTTAATT	660
CCAAATGCAG GAAACGCTGA AAGTATCCAA TACACAGGAC TTTCACCTGT CGGTTATGTC	720
ATCATCGCCT TCTTCTTTC GCTGGGAATC TGGCTTGGTA TTTGGATGAG TCAATTGGAG	780
GATAAATATA AATAATGGCA AAAAAAGTTA AAATCAAAAA AACATTGGTG GAACAAATCC	840
TATCTAAAGC AGCTATCCCT CATCAGGGGA TTCAAATCAA TGCCCTAGAA GGAGAGCTTC	900
CTCAA	905

(2) INFORMATION FOR SEQ ID NO: 153:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

1018

CTTGAATTAA ATAAAAAACG TCATGCGACT AAGCATTTTA CTGATAAGCT TGTGATCCC	60
AAAGATGTGC GTACGGCTAT CGAAATTGCA ACCTTAGCGC CAAGCGCCCA CAACAGCCAG	120
CCTTGGAAT TTGTGGTGGT ACGTGAGAAA AATGCTGAAC TGGCAAAGTT AGCTTATGGT	180
TCCAATTTTG AACAGGTATC ATCAGCGCCT GTAACCATTG CCTTGTTTAC AGATACGGAC	240
TTAGCCAAAC GTGCTCGTAA GATTGCCCCG GTTGGTGGTG CTAATAACTT TTCTGAAGAG	300
CAACTTCAAT ATTTTATGAA AAATCTGCCA GCTGAGTTTG CCCGTTACAG TGAGCAACAA	360
GTCAGCGACT ACCTAGCTCT CAATGCAGGT TTGGTTGCCA TGAAGTTGGT TCTTGCATTG	420
ACAGACCAAG GAATTGGTTC TAACATTATT CTTGGTTTTG ACAAATCAAA AGTTAATGAA	480
GTTTTGGAAA TCGAAGACCG TTTCCGCCCA GAACTCTTGA TCACAGTGGG TTATACAGAC	540
GAAAAATTGG AACCAAGCTA CCGCTTGCCA GTAGATGAAA TCATCGAGAA AAGATAGAAA	600
GAAGAAAAAA TGACAGCAAT TGATTTTACA GCAGAAGTAG AAAAACGCAA AGAAGACCTC	660
TTGGCTGACT TGTTTAGCCT TTTGGAAATC AATTCAGAAC GTGATGACAG CAAGGCTGAT	720
GCCCAGCATC CATTTGGGCC TGGTCCAGTA AAAGCCTTGG AGAAATTCCT TGAAATCGCA	780
GACCGCGATG GCTACCCAAC TAAGAATGTT GATAACTATG CAGGACATTT TGAGTTTGGT	840
GATGGAGAAG AAGTTCTCGG AATCTTTGCC CATATGGATG TGGTGCCTGC TGGTAGCGGT	900
TGGGACACAG ACCCTTACAC ACCAACTATC AAAGATGGTC GCCTTTATGC GCGCGGGGCT	960
TCGGACGATA AGGGTCCTAC AACAGCTTGT TACTATGGTT TGAAAATCAT CAAAGAATTG	1020
GGTCTTCCAA CTTCTAAGAA AGTTCGCTTC ATCGTTGGAA CAGACGAAGA ATCAGGCTGG	1080
GCAGACATGG ACTACTACTT TGAGCACGTA GGACTTGCCA AACCAGATTT CGGTTTCTCA	1140
CCAGATGCTG AATTTCCAAT CATCAATGGT GAAAAAGGAA ATATCACGGA ATACCTCCAC	1200
TTTGCAGGAG AAAATACAGG TGTGCCCCGT CTTACAGCT TTACAGGTGG TTTACGTGAA	1260
AATATGGTAC CAGAATCAGC AACAGCAGTC GTTTCAGGTG ACTTGGCTGA CTTGCAAGCT	1320
AAACTAGATG CCTTTGTTGC AGAACACAAA CTTAGAGGAG AACTCCAAGA AGAAGCTGGC	1380
AAATACAAGG TGACGATCAT TGGTAAATCA GCCCACGGTG CTATGCCTGC TTCAGGTGTC	1440
AATGGCGCAA CTTACCTTGC CCTCTTCCTC AGCCAGTTTG GCTTTGCTGG TCCAGCCAAA	1500
GACTACCTTG ACATCGCAGG TAAAATTCTC TTGAACGATC ATGAGGGTGA AAATCTTAAG	1560
ATTGCTCATG TGGATGAAAA GATGGGTGCT CTTTCTATGA ATGCCGGCGT CTTCCACTTC	1620
GATGAAACAA GTGCTGATAA TACCATTGCC CTCAACATCC GCTATCCAAA AGGAACAAGT	1680
CCAGAACAAA TCAAGTCAAT CCTTGAAAAC TTGCCAGTTG TTTCTGTTAG CCTGTCTGAA	1740
CACGGTCACA CGCCTCACTA TGTGCCAATG GAAGATCCAC TTGTGCAAAC CTTGTTGAAT	1800

1019

ATCTATGAAA AACAAACTGG CTTTAAAGGT CATGAACAAG TCATCGGTGG TGGAACCTTT	1860
GGTCGCTTGC TAGAACGCGG AGTTGCCTAC GGTGCTATGT TCCCAGACTC GATTGATACC	1920
ATGCACCAAG CCAATGAATT TATCGCCTTG GATGATCTTT TCCGAGCAGC AGCAATTTAT	1980
GCCGAAGCTA TTTACGAATT GATCAAATAA AACGATAGAA GTCTGAGATC TTATGCTTGG	2040
ACTTCTTTTT GGAGGGAAAAG TAGATGTCTC AAATCGAAAAG AATCAAACAG GCTATCATGG	2100
CGGATTCGCA GAATGCCAGC TATACAGAGC GTGGCATTGA GCCTCTCTTT GCAGCGCCAA	2160
AAACTGCTCG CATCAATATC ATCGGTCAGG CTCCGGGACT TAAAACTCAA GAAGCAGGCC	2220
TTTACTGGAA AGATAAAAGT GGTGACCGCT TGCGGGACTG GCTAGGTGTG GATGAAGATA	2280
CCTTTTACAA TTCAGGTTAT TTTGCTGTTT TGCCTATGGA TTTCTACTTT CCAGGACATG	2340
GCAAGTCGGG TGATCTTCCG CCTCGTACAG GTTTTGCAAG AAAATGGCAT CCGCAGGTCT	2400
TACAGGAATT GCCTGATATT CAGTTAACCC TCTTGATTGG GCAATATGCC CAAGCCTACT	2460
ATTTACAGGA GAAAATCAGT GGAAGGTAA CGGAGAGGGT GAAACACTAT AAAGACTATC	2520
TGCCAGCCTA TTTTCCGCTA GTTCACCCAT CACCACGAAA TCAAATCTGG ATGGCCAAAA	2580
ATCCTTG GTT TGAGGCAGAA GTAGTGCCAG ATTTGAAAAA AAGAATTAAA ACCATTTTAT	2640
AGTCAATGAA AATCAAAGAG CAAACTAGGA AGCTAGTCGT AGGCTGCTCA AAGTACAGCT	2700
TTGAAGTTGC AGATAAAACT GACGAAGTCG GTAACATACG CACGGTAAGG CGACGCTGAC	2760
GTGGTTTGAA GAGATTTTCG AAGAGTATTA GAAGAAAAAG AATGAAAGAA ATAGCCTTTG	2820
ACGCATTTTA CCAGCTTTAC CAAAACGACC AGCTTTCTTT AGTGGATGTG AGAGAAGTGG	2880
ATGAGTTTGC AGCTCTTCAT TTAGAAGGTG CCCACAACCT ACCGCTTAGT CAATTGGCTG	2940
ATAGTTATGA TTAATTGGAC AAAGATCGCT TGCATTATAT TATTTGCAAA TCTGGAATGA	3000
GATCGGCGCG TGCTTGCCAA TTCCTATTAG AACAAGGTTA TAATGTTATC AATGTCCAGG	3060
GTGGCATGTT AGCCTTTGAA GAACTTTAAA ATTTTGCAAT TCTCCTACTT GGTGTGGACT	3120
GGGTAGGAGA GTTTTATTTT TAGATAATTC TTATTTTAA GAAAATTGAA AACATTTAAT	3180
ATTTGCCTCG TGATGCTTTT TTCAGACTCC TAATCGTGGT ATACTAGGTC AGTATTTTAT	3240
AAATATGAAG GAGATTTTTA TGGCTAAAAA AGGTACCCTA ACAGGTTTGC TCCTGTTTGG	3300
AATATTTTTT GGTGCGGGGA ACTTGATTTT TCCGCCTTCT CTAGGTGCTC TATCTGGAGA	3360
ACATTTTCTT CCTGCCATCG CAGGTTTTGT CTTTTCAGGC GTTGGTATCG CCGTCTTGAC	3420
CCTTATTATT GGAACGCTAA ATCCTAAAGG ATATATCTAC GAGATTTCAA CGAAGATAGC	3480
GCCTTG GTT GCGACTCTTT ACCTCTCAGT TCTTTACTTG TCAATCGGTC CATTCTTTGC	3540

1020

TACCCACGT ACTGCTACAA CAGCTTACGA AGTAGGGATT AGCCCCCTTT TGTCGGATGC	3600
AAATAAAGGA CTTGGCTTGA TTGTATTTAC GGTCTGTAT TTTGCGGCAG CCTATTTGAT	3660
TTGCTTAAT CCATCAAAAA TCTTAGACCG CATTGGACGT ATTTTAACGC CAGTCTTTGC	3720
AATTTTGATT GTTATCTTGG TCGTCTGGG AGCTATCAAA TATGGTGGA CAAGTCCTCA	3780
AGCTGCTTCA CTGCTTATCA AGCTTCTGCC TTTGGTACAG GTTTCCTAGA AGGTACAAT	3840
ACCTTGGACG CCCTTGCCTC AGTGGCCTTT AGCGTAATCG CAGTTCAAAC CTTGAAACAA	3900
CTTGGATTTT CAAGTAAGAA AGAATACATT TCAACTATTT GGGTTGTTGG TATCGTTGTT	3960
GCCCTTGCCT TCAGCGCTCT TTACATCGGT TTAGGTTTTT TGGAAATCA TTTCCCAGTA	4020
CCAGCTGAAG CGATGAAGGG TGGAAACACCA GGTGTTTACA TCTTGTCA CAAGCACTCAA	4080
GAAATCTTTG GCTCAACAGC TCAACTCTTC CTTGCAGCTA TGGTTACCGT AACCTGCTTC	4140
ACAACGACTG TTGGTTTGAT TGTGTCAACA GCTGAGTTCT TTAATGAGCG CTTCCCACAA	4200
ATCAGCTACA AGGTTTATGC GACAGCCTTT ACCTTGATTG GATTGCTAT TGCCAATTTG	4260
GGTCTTGATG CGATTATC	4278

(2) INFORMATION FOR SEQ ID NO: 154:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1953 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

ACCCGATCAA ATGACAAAAG CTAACCTTGG TGTCGTAGGT ATGGCCGTAA TGGGTCGTAA	60
CCTTGCCCTT AATATTGAAT CTCGTGGTTA CACAGTTGCT ATCTACAACC GTAGTAAAGA	120
AAAAACGGAA GATGTGATTG CTTGCCATCC TGAAAAGAAC TTTGTACCAA GCTATGACGT	180
TGAAAGTTTT GTAAACTCAA TCGAAAACC TCGTCGTATC ATGCTGATGG TTCAAGCTGG	240
ACCTGGTACA GATGCTACTA TCCAAGCCCT TCTTCCACAC CTTGACAAGG GTGATATCTT	300
GATTGACGGA GGAAATACTT TCTACAAAGA TACCATCCGT CGTAATGAAG AATTGGCAAA	360
CTCTGGTATC AACTTTATCG GTACTGGGGT TTCTGGTGGT GAAAAAGGTG CCCTTGAAGG	420
TCCTTCTATC ATGCCTGGTG GACAAAAGA AGCCTACGAA TTGGTTGCGG ATGTTCTTGA	480
AGAAATCTCA GCTAAAGCAC CAGAAGATGG CAAACCATGT GTGACTTACA TCGGTCCTGA	540
TGGAGCTGGT CACTATGTGA AAATGGTTCA CAATGGTATT GAGTACGGTG ATATGCAATT	600
GATCGCAGAA AGCTATGACT TGATGCAACA CTTGCTAGGC CTTTCTGCAG AAGATATGGC	660

1021

TGAAATCTTT ACTGAGTGGA ACAAGGGTGA ATTAGACAGC TACTTGATTG AAATCACAGC 720
TGATATCTTG AGCCGTAAAG ACGATGAAGG CCAAGATGGA CCAATCGTAG ACTACATCCT 780
TGATGCTGCA GGTAACAAGG GAACTGGTAA ATGGACTAGC CAATCATCTC TTGACCTTGG 840
TGTACCATTG TCACTGATTA CTGAGTCAGT GTTTGCACGC TACATTTCAA CTTACAAAGA 900
AGAACGTGTA CATGCTAGCA AGGTGCTTCC AAAACCAGCT GCCTTCAACT TTGAAGGAGA 960
CAAGGCTGAA TTGATTGAAA AGATCCGTCA AGCCCTTTAC TTCTCAAAAA TCATTTTCATA 1020
CGCACAAGGA TTTGCTCAAT TGCCTGTAGC CTCTAAAGAA AACAACTGGA ACTTGCCATT 1080
TGCAGATATC GCATCTATCT GGCCTGATGG CTGTATCATC CGTTCTCGTT TCTTGCAAAA 1140
GATTACAGAT GCTTACAACC GCGATGCAGA TCTTGCCAAC CTTCTTTTGG ACGAGTACTT 1200
CTTGGATGTT ACTGCTAAGT ACCAACAAGC AGTACGTGAT ATCGTAGCTC TTGCGGTTCA 1260
AGCAGGTGTG CCAGTGCCAA CTTTCTCAGC AGCTATTACT TACTTTGATA GCTACCGTTC 1320
AGCTGACCTT CCAGCTAACT TGATCCAAGC ACAACGTGAC TACTTTGGTG CTCACACTTA 1380
CCAACGTAAA GACAAAGAAG GAACCTTCCA CTACTCTTGG TATGACGAAA AATAAGTAGG 1440
TCAGCCATGG GGAAACGGAT TTTATTACTT GAGAAAGAAC GAAATCTAGC TCATTTTTTA 1500
AGTTTGGAAC TCCAGAAAGA GCAGTATCGG GTTGATCTGG TAGAGGAGGG GCAAAAAGCC 1560
CTCTCCATGG CTCTTCAGAC AGACTATGAT TTGATGTTAT TGAACGTAA TCTGGGAGAT 1620
ATGATGGCTC AGGATTTTGC AGAAAAATTG AGCCGAACTA AACCTGCCTC AGTCATCATG 1680
ATTTTAGATC ATTGGGAAGA CTTGCAAGAA GAGCTGGAAG TTGTTCAGCG TTTTGCAGTT 1740
TCATACATCT ATAAGCCAGT CCTTATCGAA AATCTGGTAG CGCGTATTTT GCGATCTTC 1800
CGAGGTCGGG ACTTCATTGA TCAACACTGC AGTCTGATGA AAGTTCCAAG GACCTACCGC 1860
AATCTTAGGA TAGATGTTGA ACATCACACG GTTTATCGTG GTGAAGAGAT GATTGCTCTG 1920
ACACGCCGTG AGTATGACCT TTTGGCGACA CGG 1953

(2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6474 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

CCGGCAGTAC ACGAGCTTGG GGAACAGCCA CTGGAACGAT GAGGTGTGAG CTCAAAATAT 60

1022

CCTCCAGTTA	TGTTTTTCCT	AATAGTATAC	CGGAAGAGTG	AAAGGATTTT	ATAATGGAGC	120
GGTTACAAAG	AACCTACTTT	CTATTAAACA	GTATACTATG	AAAATGTGAA	AATTTAACAT	180
TTTTTTGTAC	AAATTTTATA	AATTATTGCC	TTTTTAATAT	CAATAGTTAA	TCTCTTATCC	240
AGATCCCCCT	TGTGTAAACT	TTATCTTTAT	AAGCTTCAAG	GCCCCTATCC	CATCTATTTG	300
CAACAATTAG	ATCACTTTGT	TTTGTAATA	GTTCAAAATT	CTTTTCAATA	ATTACGTTAT	360
CTATACTAAC	GTTTAAATTT	GGTTCATATA	CTAAAATTTT	TATACCGACA	ATCAATAGTT	420
CATTAATTAT	ACTTAAAATA	GCTGACTCTT	TGTAATTATC	TGAATTATAT	TTCATCCCCA	480
ATTTATATAT	TCCTACTATC	TTTGGCTTTC	GTTCCAATAT	TTGTTTAACT	ATGAACTGTT	540
TTCTATTTGT	GTTTGAAATA	TCAATCGCTT	CTATCACTGG	GGCATTTATT	TCTATAAATT	600
CTTTTTTTAA	TTGTTTAGTA	TCTTTGGGAA	GACAATATCC	TCCAAATCCA	AAAGAAGGAT	660
TATTATAAAA	ATTTCCAATT	CTTGGATCTA	AACAAACACC	TTTTATTACA	ACTTCAGCAT	720
TTAAGCTTCT	CCTCTCAGCA	AAAGAATCTA	GTTCAATAAA	AAAGCAACAC	GGAGAGCTAA	780
GAATGTGTTA	GAAAAAAGCT	TAATTGCTTC	TGCTTCAGTA	GGAGAAACTA	ACATAACATT	840
TTTAATATTG	GCAGTACTAT	GAGTACTAAT	CGAAAGGAAC	AACTCTGCAA	TTTTTCTTCC	900
TTCAACTGTC	TCATCTCCAA	CAACTATGCG	ACTTGGATAT	AAATTATCAT	ATATAGAACA	960
ACCTTCTCTC	AAAAATTCAG	GGACAAAAAT	GATATTTTTT	GTATCAAACA	GCCTTTTTTAA	1020
TTTGTTTGAA	AAGCCGATCG	GAAGTGTGA	CTTTAAATA	ATCTTTCCAT	TAGGTTTTTAC	1080
CCTCAGAATC	TTCGATACCG	TTTGTTGAT	TTCATATGTA	TTAAAACTAC	CAATTTTCTC	1140
ATCATAATCT	GTCGGAAGCG	CAATAATATA	ATAATCAATA	TTATTTTTTAA	TTTCAGAAAA	1200
TGTATCAAAA	AAAGTAATAT	TTAAGTTATT	CTCGCAAAAA	AACTTCATAA	GCTCTTCATT	1260
TTTAGATGGA	AGAATGCCCT	TTTTTAAATT	ATTTATTTTT	ACAGAATCTA	TATCATATGC	1320
AACAACTTTA	TATTTAGATG	CAAATAGTAA	CGCGTAGGCC	AGCCCAACAT	GCCCCAAACC	1380
AATTACTGCT	ATATTCATAA	AACTACTTCC	TTATTTCTTA	ATCCAAAATC	TAATAGAAAT	1440
AGCTGCCCCA	TTCTTAAAT	ACAACCTTTT	AATATTGTTT	AAAAGTTTTT	CAACTGATTT	1500
CCAGATTATC	AAAATCTGAG	ATTTATAGCA	CAATATTGAT	GATATTCTAT	CAATATAATT	1560
TTTTTCATCA	AGTTCCTCTT	GATACATTTT	TAATTCTTTA	GTTTTTCCCA	TATAACTAAC	1620
CATACTACTA	TCACTTACAT	ATGGGAAGTC	CTCATAATAT	ATTACTTTAT	AACGCATAAA	1680
TTCAAGCGCC	CTTCCAATAC	TATTCACAAA	AACATGAGCA	ACATGGTCAC	CAAGTGAAAG	1740
CGGACAATAT	ACGACACATT	TGTCGTCTAA	ATGCATTAAC	AGCTCTTTTA	TGATATCATT	1800
CTTTAATGTG	TCCTCATTTT	TTAATTCACT	ATAGATATGA	CGGTATAGAA	AATTGCCATT	1860

1023

TCTATCTTTC	CTATAGAGAC	ATTCATAGTA	CGATAAGTGT	CTAAAATCAC	ATTGTAGACG	1920
TTCACAAGCT	AACCTGTCTT	CTTTCTTCCT	TTCTTCAATC	GGATATTTCC	CAAGGTTACA	1980
CAACTTATGA	AATTGCTTAG	CAGAGGGCTG	TAGCTGTTGG	CTCAAAGGGT	AACCAGAAAA	2040
TATAGTAATA	ACAAGTACAA	TTTCTCCTTC	TGAAGTTAAT	TTTGAAATAT	AATCACCACA	2100
GGAAAAAATT	GCGTCATCTA	AATGTGGAGA	TAAAAAGATA	TACTTAGTAT	TGTTACTCAT	2160
AACCATTCCC	TCTACAATTT	ATCTAAAAAC	TCACTAAGTG	TCTGATTAAA	TTCCACATCA	2220
TCAAAAAAAT	TCACCTTATT	CTTAATAATG	AATATTTTCG	TAAATAAACA	TATATATAAA	2280
TATTTCAATA	TCCTTTCAAT	ATCATCCTCT	AAATTCTCCT	CAATATTTTG	TATCAGCCCA	2340
TTTACAATCT	TATTAAAAAA	GATAAGCTCT	TTATCTCTAA	AATTAAATAT	TTTCATACAA	2400
CTGTTGTATC	GAAAAATATA	TAAAATAATT	TTTACTAATG	TTTGAATATT	TAAACAACCTA	2460
AATAAATGAG	TTGTACCCGG	GACACTATTT	ATGTTATCAA	GAACACTATC	TTGAAACCTC	2520
AACTCACAGT	TCTTTTTGTG	AAATTCTTTT	TTATCGTTTA	GATCTGATAT	TTTTTTAGAC	2580
ATTTCAACAA	TCTCAGACAT	TTTATATGGA	TATCTAGGAT	GAATGCCAAA	ACTATGCAAA	2640
ATGAACTGCA	CCCCAAAAGT	TAGACAGAAT	AAATCTAACT	TTTGGGGTGC	AGTTCATAAG	2700
ATTGGGATAT	TTTTTTTTAG	CTAGAAGTAG	TAGAAATATA	TAGTCAAATA	ACAGATACCT	2760
TAAGGGTTTC	TCATCTACAT	AAAAAAATGA	TACTTTTTTC	TCTTCAGTAA	TTACCTCATA	2820
AGCTTCACAA	TAGAATCTCA	TGTTCCTC	CCCTATATTC	TTAAATAAAA	TCCTTTGGAA	2880
ATTGATATAT	CTTAGTAAAA	TATTGTTTAA	GTTCCGGATG	CGGAGCATGG	GTAACAATAA	2940
TGACAGTCAA	ATCCTCTCTA	TCTAATATCT	TACGTTCAAT	CGCTAACGAA	GTTCTCCTAT	3000
CGATAGCAGA	AGTTCCTCG	TCAATTAATA	CTATTTTCTT	ATTTCTAATT	AGCCCTCTAG	3060
CTAAAGTAAT	TTTTGTTC	TGCCCTCCTG	ACAGTAATCT	CCCATCATCA	CCAACATAAT	3120
AATCTAAAAT	GTTATTAGGA	AAATCTTTTA	CACTCAAACC	AACTTGCTCT	AAAGACTGTA	3180
GTATTTCTTC	ATCAGTATAA	TTTTCTTCCA	ATAAAAATAT	ATCTCTAATC	GTACCTTCAA	3240
ACAAATAAGC	TTTTGTATCT	ACATATAGAA	CATTCGAAAC	CATATTTAAA	TAGGAGGTTT	3300
TTTTATATC	ATCCCCGCAG	AATCGCAATT	CTCCACTATA	ATCTCTCAAA	AAGCCATTCA	3360
ATAATTTTAA	TAATGTAGAT	TTCCCGCTTC	CACTTTCACC	TAAAATTAAA	TACTTTTCAT	3420
TACGTTGAAA	AAAAAAATTT	AAGTTTTTTA	ATATTTCTTT	ATCTCCATAC	TTATAGCAAA	3480
TATTTTTTGC	TTCATATAAC	GGAAAATCTC	TATTCACCTC	ATTTGGTTCG	ATATCATTCA	3540
TTTTATTTGA	CTCAATTGGA	TTAATTGAAT	ACAATTTTAA	AAAAAATAGG	TTCGTACCAA	3600

1024

TAATAGAGGA	TAATTGACCT	CCTAATTCAC	CTAGCGCTGT	AAAAATAACA	CCTGTTAGTG	3660
CTCCTATTGC	TTCAATAGTA	CCAATTTTCA	CTATTCCTTT	TATTGCAAGA	TAGCCTGTTA	3720
AAAAAACGAG	AGATATCTGA	AAAAAATAT	TGAGAAAGAA	GCTAATAGCG	CCTGCTAACG	3780
TTTCTACAGT	TGTCTTCTT	TGTATAACCA	TCTTTAATAA	AATTCCTGCT	TCTTTAATTT	3840
TCTTAGGCAA	TACATATAAA	AGATTCAAGG	ACGCTAACAC	ATCAAATCCA	TTCAATATAG	3900
TCTCACTAGA	TTTTAAAAAA	GCTTCATTTT	GGTTAGTTAA	ATTTAGACTA	ACTTCTCGCA	3960
TTTTTCGATGC	AAAGATTTTT	GGTACAAGTA	GCATAATCAT	TAATGAAAAC	AAGGTGGCTA	4020
CAGTCAATGA	CCAATGATAG	TGATTAAGAG	TCACAACTGC	AAATATAGTA	CCAGAAATTC	4080
CTTTTATTAC	TAAAAAAAGT	TGTTTAAACG	CCTGATCATT	TAAAGTCTGA	ACATCATTAT	4140
TTAGCCACGA	AAGATATGTT	CCTGATGATT	TACTATGAAA	TTCTTGATAG	GTAGAGTTAG	4200
AGATGTCTGT	GGCAACTCTA	TTTCGAATCT	CTAGATTAAA	CTCTTGGATC	ACTTCAACCT	4260
GATAATTTTT	CACTACCCAG	TCAAGGAATA	TTATCCCACA	CCAGACAATC	ATTTGGTAGA	4320
TTGACAATTT	CAAAAACCGC	TCTAAATTCA	TCGCAATTAA	TTCATTCAAC	ACCAGAGCAT	4380
TAATAGTTGC	TGCATAAATT	AGCAATAATT	GACCAGCAAC	AATAAATATC	GTTAATAAAC	4440
TAAATTTTTT	TATATTTGAT	TTTATAATAG	TATACACAAT	AGTTTCTCAC	TTTCTAAATT	4500
TTAATTGAAC	ATAGTTTTC	TATATACAAT	AGAAAAAACC	AAAATGATAT	AATAACATAT	4560
ATTTCAAAAA	AGAAATTCGT	TAAAAATTTT	TTCTTCTCTT	GCCTTCTTGA	TTACTTTTAA	4620
AGCCTTGCA	TTGTCTCCTA	TTAATAGTAA	CCGCTTTATG	TTTAAAGAAT	AATATTTCTT	4680
TGTAACCAAT	ATTCTCTCGT	TGAAACTCAA	TAAATTAAAA	TATTTCCCTAC	AGTAATTATA	4740
ATATTCTTCA	TCTGCATTAA	TTGTTTTTTG	TGTCACTCCA	GTGATACCGT	TTTCTTTACT	4800
GTGAGCGTAG	TAATTCACCA	AGAATTCTCG	CACTATATCA	ATTTGGTATC	CTTGAACAAG	4860
TAGTTTTAAT	AAAACAACAC	CGTCCTGATG	TGAATCTATT	TTCTCAAAAC	CATTAATTAA	4920
TTCTAGCACC	TCTTTTTTAC	ACAACCAAAA	TGACGTACCT	GCTATATTGT	GAACCATTTG	4980
AACAAACAAG	GGATTTCCAA	CAAAATCGGT	CTTCTCCTCT	TCTCGTGTAC	CATTTGGATA	5040
AATTATTATT	CCATAACTAC	AACTAAAGC	TAAATTCTTC	ATTCTACTCT	TTTTAAAACA	5100
AGCCATCAAC	TTTAAAATTC	GATCTGGCAT	ATATTCATCA	TCATCGTCTA	AAAATGATAT	5160
ATACTTACCT	CTAGAATTTT	TGATACCTAT	GTTTCTGGCA	TTAGTTGCAC	CTAAATCTTC	5220
ATTACTTAAA	ATTAACCTAA	TTCTATGATT	GGTATAGCCA	AATTGATGGA	TAATTTTATT	5280
TCTTAAATTT	ACATTACTAT	AATTATCATC	AATAATTATA	ACTTCGATAT	TTTTATAACT	5340
TTGATGTAAA	CAACTTTTCA	CAGCTCTAAT	CAGAGATTCA	TACCTATTAT	GTGTTGGTAT	5400

1025

TATAATACTT ACTAATTCTT GATCTATATT CCTATCCATG ACTACTCTTC TCTAATAATT	5460
CATCATATAC TCTCATGGTT TCTACAAACA TTTTTTGCAC AGAAAAATGT TTTCTTATTT	5520
TTGATTACT ATTCTCACCT ATATATTTCA AATACTCAGA ATCATTGAGT AAAAAATTAG	5580
CACAAGCACA CACTCCCTCA ACATCTTCCT TCTCAAATAA AAATCCATCA ACCCTATGTT	5640
CAATAATTTT ACTTAACCCG CCAACATTAC TAGCTAAAAC CGGAGTTCCT TGTGACATTG	5700
ACTCTAAAAC ACACATAGGT ATTCCTTCTG TATCAGAAGG AATATACAAT AAATCCGATA	5760
TTTGGTAAAC TATAGTAGCT GGATAGATTT CACCAAGTAA CCTGAAATTA TCTCTACATT	5820
TCAAATGGCA AATTTTTTCT TTCAAAGCAG CCCACATACT ACCATTTCCA GCCATAATAA	5880
AAATCACATC TTCTCTGACT AAAAATAATT TTTCTGCAAA TTCAAGGAAT CTATCCGGCC	5940
TTTTTTCTGG ATCCAACCTT CCAACATAAC AAATGATTTT TTGTTATTTG GAATACAAAA	6000
TTCTTTTTTA AAGTCTTGAA CACCTACTAC ATCTAAATCG CTATTTGATA CATTAATTCC	6060
GTTATTTATT GCAACTATCT TCTTATTTTT TATTATACTC TCCAATCTTT TTTTTCATAG	6120
TTTCAGATAC ACAAATAAAA GCATCTCCCA TAGAATATGT CCAAAAATCA AAATAAGTCA	6180
AGAATTTCTT TTTTAAGTTA TATTCAACCC ATCCATGGCA TGTTATCACT GTCTTAACCT	6240
TTCCAAATCC ATTCTTGTC AAGTTTTTTT ACATATATAA AAAATAATTA GTTGAGTAGC	6300
CATGACAGTG TATAAGTTGG ATTTTAAATA ATTTTAAAAT ATTTTAAACG TGTAAGGCAG	6360
TTTCAAATTT ATTTGAACAT TGAGTACAAT CAACATAGGC AATATCTAAA TTTTATAAT	6420
CATCAATAAC CTTTGAATCT CTAGATACAA TTATCAAAAT AGGGAATAGA GACA	6474

(2) INFORMATION FOR SEQ ID NO: 156:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4792 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

TATTTAACGA TTTTTTTCAT GTCATTTTCCT CAAAATAGA ATACCTTATA ATCTTAACAG	60
AAAAAGAGCA TTTACGCCAT TATATGATAT CTATCTCTGT GATAAGTTTT TTTTATGGGT	120
AATTTAAAAG ACCAAACGCA AGATGGCAAT CAAGACCACT CCAAAGAGAA CTGTTCCGAC	180
TAGATTGCGG TAGCGAAAGG CTACCCAAGC TGTTGGAAAG ACGGCTAAGA AGTCCAGTCA	240
TTTGATTGGA GGAAGACTGC CAACCTTACC TGTCCTACG CTTGAAAGAA TCAGGGCAAA	300

1026

GATAATGGAA	ACAGGCAAAA	ACTTCAAAAA	ACGCTCAACA	ATCGCAGGCA	GGCCCTTATA	360
CTTGACCAAG	ATGAAGGGAA	TCATACGGGG	AATCCAAGTC	ACCAAGCCAG	AGAAAATAAC	420
TGCTAATAAA	AGATACTTAC	TGACCATCTA	AAACCACCCC	CATGCTACAA	CCAAGTAGCG	480
TCGCAAACAG	AACAGCTAGT	GACTGAGACA	TCACTGTCAA	GAGCAAAAAG	AAGGACACCG	540
CAACAACCTGC	TAGGATAATG	AGCAGATTGC	GGACAGGAAT	CCGTCTTTGC	ATAATCTGAA	600
ATTGCGAAGC	AAAATACCAA	TAAACATCCC	AACCAGGGCA	AAATCCAAGC	CAAAGATTTC	660
TGGATTTGGT	AGCAGGCCAC	CCAGAGCCGT	TCCGACTACT	GTCCCCACAA	ACCAAGCCAC	720
ATAGCTGTTA	AGATTGTTTC	CGTGCAATCA	CATAGGATTT	ACCTTGTCTG	TATGGGCCAA	780
TTCACCCATC	AAAACGCCAT	AGGTCTCATC	TGTCAAGATA	CTAGACATAC	CGATATTGTA	840
CCAAAGACTG	GTATGACGGA	AATAAGTCGA	TGCGTGTAAG	CTCAACAAAA	AGAGACGCAA	900
GTTGATTAGA	AAAACCGTCA	TAGCAATAGC	TGCCACAGGA	GCTTGAACCA	CAATCAGTGC	960
CAACATGGCA	AACTGGGCAC	TCCCAGCATA	AACAAAGAGA	CTCATCAAGC	CCATCTCAAC	1020
AGGTGTCACA	TAGGGCGCAC	CGATAATTCC	ACAGGCCAGG	CCGATACTGA	CATAGCCAAG	1080
AGCCGTTGGC	ATGGCTGCCT	GCGCCCCCTC	CTAAAATCCT	TTTTCTTTCA	TCTTTCTCCT	1140
CATATTGTCT	TAATAATACT	CAATGAAAAT	CAAAGAGCAA	ACTAGGAAAC	TAGCCGCAGG	1200
TTGCTCAAAA	CACTGTTTTG	AGGTTGCAGA	TAGAACTGAT	GAAGTCAGCT	CAAACACTG	1260
TTTTGAGGTT	GTGGATAGAA	CTGACGAAGT	CAGCTCAAAA	CACCGTTTTG	AGGTTGTGGA	1320
TAGAACTGAC	GAAGTCAGTA	ACCATACCTA	CGGCAAAGTG	AAGCTGACGT	GGTTTGAAGA	1380
GAGTTTCGAA	GAGTACAAGT	AGGCTGAAAA	GAATCCAACC	ACAGCATGGA	CTATTATATA	1440
GCAGATTGAA	ATAAGATGAG	AACAAATCGA	TTGGGAAAGT	AAAATTAATT	TCTATAAATG	1500
TTTTAGCAAT	TGTTTCGTAC	TATTTTAGAT	TCAGTCTATT	ATAACACATT	CAGAAAAGAG	1560
AAAAAAGTCT	GTTGATTTTG	ACCATCATAA	AAAGACTGGC	AATCCAGTCT	CAAACATATA	1620
TTATAGAAAT	TCTCCACTAA	ATACTTTCAC	GAATATTCAG	AAGCATAACA	AAGGCAACTA	1680
GAAGAAATAG	CAATAAAACA	AAGCTAACTG	CCAGAGTTCC	AAAGCTAGTA	GCAATGGTTA	1740
CCAAAGCTAT	TGTAAATAAG	CTAGGTAAAA	CAACCGTAAT	GGCACCGATA	GAGGATTGAA	1800
CTGCTCCCAT	TGACTCCTCA	GGTATTTGTT	TAAAAACGAG	TTCTTGCAAT	CTAGGAGAGA	1860
GAACACCTGC	GAAAAAGGCA	TCCAAGGTAC	TAAAGATGAG	AATCCAGTCA	AAACGAACTG	1920
TGGCAAATCC	TACTAGAAGA	AGCAACTGGA	TGACAAGTGA	GGCATAGAGA	GCTGTTTTTA	1980
TGGAAATGGT	ATGTTGCAGA	TAGCCACTTA	CAAGGCTTCC	GACAATCAGG	GCTGATAATT	2040
CTAGTGTGGC	TAACAAGGCA	AGAGATTGAC	CAGTTTGTA	ATTCAAAAAG	GGCTGGTTCC	2100

1027

TTAAAAATAG	AGTGGAATA	GGAACCGTAA	CATTTATCAC	TGCTTGACTA	GTAGAGATAA	2160
TAAACAAAAC	CAAGAGCACC	TTATTCATAT	TCCATATCAA	TTTCGATGAT	TGGAGCAAAT	2220
GCTGGCAAAA	GGATTTTACA	GAGAGTCCTT	CTTGATAGCT	AATCGTTTTT	TCTACTTTCA	2280
AGAGGTCAGT	TTTTATGAAG	AGGATACCTA	AAAATGCGAT	TAAAAAGGTA	AGAGCGTTCA	2340
GTAAGGAAAT	AAACTGGATG	GATAGAATGC	CTAGTAAGAC	TCCTCCTAGG	ATATTACTGA	2400
TTGTTTTTAC	TAAACTAACA	GTTGACTGTT	TAAAGCCAAT	AGCTTCTGCC	AGATGGTCTT	2460
GCCCAATAAT	TCTAATGAAA	ATCGGAGTGA	GCATGGCGCC	TGAAAAATAA	CTCAATGTGT	2520
CAGACAAGAG	GTTAATCAGA	CAAATAAATG	CTACTAGCAA	CAAGGAGAAA	GACTGCCCTG	2580
AAAGTGATAA	AGACACTATA	GAGTAAAGCA	AAAATTTTGC	AAAATAATG	ACTGTGTATT	2640
TCAAGACACG	ATGATGTTGA	AAATCCGCCA	AAACTCCCAG	AAAGATTTGT	AGAACTTGGG	2700
GCAGGGTTTC	TGAAATCGTG	ATGAGTAAAA	TCGCCAAAGG	GGCAAAAGAT	GCATCTGCCA	2760
CATAATTCAG	GAAGGCCAGA	TAAAAAATCG	TATCCCCAAG	CGTTGAAATC	CACTGGTTGA	2820
TAGTTAATTG	CCTAAAATCT	CTATTTTGAA	GAAATACTTT	CATCACAACT	CCTTCTTAAG	2880
TTCAAATGGG	AATCTTTCCC	CAAGGATAGA	CCGCGATACT	ACTAACAACC	AAAATTACAG	2940
TAACATCAAA	AGCTGACCAA	TGCCATTGTA	GACTATATGC	AGTCCAATAG	GCCAATAAAT	3000
TGACTTTGTC	ATTCTAAATA	AGACTGCAAA	TATAAGACCT	CCACCCATAT	AGAAGACAAA	3060
GTCTGTCAAG	ACCCAACCGT	GATTACTAAT	GTGCGAGACC	CCAAATAAAA	CAGCGGAACC	3120
AAGTACATCT	AGCCCCCAT	TCTTTCCTTT	TTCCAGAGCA	GTCATCACTA	ATCCACGATA	3180
AATCATGTCT	TCAAAAATGG	GACCTGCAAT	CACAGGATAA	AAAAAATACA	TCAAAAATGC	3240
TGTAGCCCC	GTAAAAGTCG	GAGCAGCATG	TTGATAAGAA	ATTTCAATTC	GAGTAGGTGG	3300
GAAAAGAAAA	AAGGTAACGA	AATTCCAAAC	AACAAAAGCA	AGCAGAGCTA	GGAAGGAATA	3360
GAAAAGATAG	GATCCTTTAA	ACTTTCTACT	ATTGATTTTC	TGCCATTTCC	CCGACCAAAT	3420
CATAGCAATA	AGAGCAAATA	AAACCACAAG	AAAATTCAAC	ATCATATCCG	ACAGATAATA	3480
GGCAAAGTCA	GATAGCCCAG	TAACAAGGTC	GCTGCGTAAA	ACTAGAACAC	TGAAGTTCTG	3540
GTCAGCAATA	ACTAGTAGAA	AACTATAAT	AAAGTAGCGG	TGTGAGATTA	TCTTTTTCAT	3600
ATATCACCTT	TCTAATATCC	AAATACCAAT	AAAGTAACAA	TGAGTAAGAA	ACTATTCCAT	3660
GAAGCATGCA	GAGCTATAGC	CCAATAGATG	GATCGGGTGT	AGCGAAACAT	CATACAAAAT	3720
ATCAAGCCCA	TTCCAAAATA	CTTTATGAAA	TCTGTCGTTA	TCCAACCATA	CTGCAAAACA	3780
TGCATAGCGC	CAAATATGGC	AGCGGAAACA	AGAACATCAA	GATAGTATCT	CTTAAGTTTA	3840

1028

GATAAACTTG TCATCAAAAG ACCACGACAA ACAACCTCTT CTGATACAGG TCGGATAATA	3900
CTAGTATAAA GTATTCGCGT AACAAAATAG CTAATTCCTG TTAAATTGGT GGCTACTTCT	3960
ACGACTGTAC TTCCATTCTG GGTACGAGGA AAGATATAGG TTGTTAGATT TGCCCACACG	4020
AACAATAAGA AAAAAGAAAG AAGGAAAACA CCCAGGTAAG ACCAACGAAA CTGGAAACGA	4080
CCACACTCTT TCCAATGTTT ACTTTTGACA AAAGCAATTG TAGCTATAGT TCCCAGAATA	4140
AGTACCAATA AACTTGGAA CACATAGTAC ATATTATCAG ACAAAGCAAC CATAAAATCT	4200
AAGTCTGATG TGACATTAAA AATGAGGTAA TAAGTCAAAA TCAACAAGCC AGTTGCTAGG	4260
TGAAATTTCA CTTCTTTCAT TTTCTTCATC CTATTATCTC CTATAAGAGC CTATCTTCTA	4320
CGGCGGCCAA ACAATCCATC TGCTAAATCT ATAGTCCAAT CAAAAGCTCC ACGATTAGGA	4380
CTCATCCCTT GATTGCCCCA ACCAGGGTAA ATTCCTGGGA CGCCCCAACC AGATATACCA	4440
CTTCTTCCAC CACCTCCCAT AGAATTACG AGGTGCTCTC CTCTAACATC TTGCAACTCA	4500
GCTTCTGTCA ATTCCATTGT TTCTGCAAAT TGTAATTTA ACATCTTTTA CACTCCTTCA	4560
ATTATCTTCA TTTGTAAACC ACTTCTGCGA CCTAGGATTT GCTTCAAGTG CTTTACAAGT	4620
ACAGTATAAC ACGAACATTG GCTTATTTTA GAAAATCGCA TATTTGATAT TTTTCTTAT	4680
AGAAATTTCA GATTTGCGAT TTTGGTGAAT TTGATTACTT CTCTGGTATA ATAAAGTTAC	4740
TACTAATGAG GAGTGGAGAA ATATGAAGAA ACAAATTTTA ACATTATTGA AA	4792

(2) INFORMATION FOR SEQ ID NO: 157:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

CCGTTCTCGG CGACGGCCAT CTGATGAAGC TATTTATGAG GGAAACTGGC AAGCTGGAGA	60
GTCAGAGTAT CTAGTCTTTC ACCGATTGCT GTGGCAGCAG ATGTGCAGGG AAAAGGAGTT	120
GCTCAAACCT TCTTAGAGGG CTTGATTGAA GGTTTTGATT ATCTTGATTT TCGCTCAGAT	180
ACGCATGCTG AAAACAAGGT TATGCAACAT ATTTTGTAAA AACTTGCTTT TAAACAAGTC	240
GGTAAGATGC CAGTAGATGG CGAACGCTTG GCCTATCAAG AATTAAAGAA ATAATGCAAA	300
AGAAGTATGT AAAAATCCTC TACTCCTCAC CAATTGGTAT TCTATCACTT GTAGCTGATG	360
ACCATTTATT GTATGGAATT TGGGTTTCAGG AGCAGAAGCA TTTTGAGAGG GGACTAGGAG	420
ATGAAACGAT AGAAGAAGTT GTTAGTCATC CTATTTTAGA CCCAGTTATT GCTTGCTTAG	480

1029

ATGATTACTT TAAAGGCAAG CCTCAGGATT TATCCAACTT GCTCTTGGCG CCAATCGGAA	540
CGAATTTTGA AAAGAGAGTT TGGGACTATT TACAGGGCAT TCCTTATGGT CAGACAGTGA	600
CCTATGGACA AATTGCTCAA GACCTGCAAG TGGCTTCTGC TCAAGCAATT GGTGGAGCAG	660
TGGGACGCAA TCCTTGGTCT ATCCTAGTAC CTTGTCATCG TGTGTTGGGA GCAGGCAAGC	720
GTCTGACAGG TTATGCTGCA GGAGTGGAAA AGAAAGCTTG GCTCTTGGAG CATGAAGGAG	780
TAGATTTTAA AGATAGAAGC AATAGAAGGA GAAGCACATG TTAGAATTTA TCGAATACCC	840
CAATGTTCA ACTTGTAATA AAGCAAAACA AGAATTAAAT CAATTAGGTG TGGACTATAA	900
AGCCGTCCAT ATCGTGGAAG AAACACCTAG CCAAGAAGTC ATTTTGAATT GGCTAGAAAC	960
CTCAGGATTT GAATTGAAGC AATTTTTCOA CACCAGTGGT ATCAAATACC GTGAATTAGG	1020
GCTAAAAGAT AAGGTAGGAA GTTTGTCAAA CCAAGAAGCG GCTGAGTTGC TAGCAAGTGA	1080
CGGTATGTTG TTAAAACGGC CCATTTTAGT AGAAAATGGA ACTGTTAAGC AAATCGGTTA	1140
TCGAAAATCT TATGAGGAAC TGGGACTGAA ATAGTTTTTA TCTATCTCTT TGATAGATAA	1200
AATATATAAC TTCCCTGTTT CAAAGTATGA TAAACTAGTA GGTAGACAAA GTCTGTATCT	1260
GACCGTAGCA AATAATTTCA TTGACGGCAG AAGCATGGTA GCATGAATCA TTATCAGAAG	1320
AGGATGTTTT TATGAATGTT ACAACGATTT TAGCATCAGA TTGGTACCAA AACTTGATGC	1380
AATTGATTCC GGATGGCAAG CTGTTTAGCC TACGTTCCGT CTTTGATGGA ATCCCTAGAA	1440
TTGTCCAACA ACTTCCAACA ACAATTATGT TGACAATTGG TGGTGCCCTT TTTGGCTTGG	1500
TTTTGGCGCT TCTTTTGGCC ATTGTGAAGA TCAATCGTGT CAAGATTTTA TATCCCTTGC	1560
AGGCCTTCTT TGTTAGTTTC TTAAAAGGGA CACCGATTTT GGTGCAACTC ATGTTGACCT	1620
ACTACGGAAT CCCTTTGGCT TTGAAAGCCC TCAATCAGCA ATGGGGAACT GGTCTCAATA	1680
TCAATGCGAT TCCAGCTGCA GCTTTTGCGA TTGTCGCCTT TGCCTTTAAT GAGGCAGCTT	1740
ATGCTAGTGA AACCATTTCGT GCAGCCATTC TCTCAGTTAA TCCTGGTGAG ATTGAGGCGG	1800
CACGCAGTCT GGGTATGACC CGAGCGCAAG TTTATCGACG AGTGATTATT CCTAATGCAG	1860
CGGTGGTAGC TACTCCAACC TTGATTAATT CCCTCATCGG TTTGACCAAG GGAACATCTC	1920
TAGCTTTTAG TCGGGGTGTT GTGGAAGTCT TTGCCCCAAG TCAGATTCTA GGTGGAGCTG	1980
ATTATCGCTA TTTTGAACGC TTCATCTCCG TTGCCCTTGT TTATTGGGTA GTCAATATCG	2040
GAATTGAAAG CCTCGGTCGT TTCATCGAGA GAAAAATGGC TATTTCTGCA CCTGATACAG	2100
TGCAACAGAT GTGAAAGGAG ACCTTCGTTA ATGATTAAGA TTTCGAATTT AAGCAA	2156

(2) INFORMATION FOR SEQ ID NO: 158:

1030

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

GTATCTCTAC ACATGTCTTC AATCGATTTT GTTGTCCTCC AATTTAATTC CTTATATGCT	60
TTGTCTGCAT TTGCATAACA AGTTGCAACG TCTCCTGAAC GTCTTGGAAC TATTTTATAA	120
GGAATAGGGA TCTTATTAAC ACTTTCAAAT GTATTTACAA GTTGTAATAC ACTAGTGCCT	180
TCTCCCGAGC CTAGGTTATA GATATAAACA TCTGTTTTTT CAGATACTTT TTCTAAAGCT	240
TTTATATGTC CTATTGCTAA ATCTACTACA TGGATATAAT CACGCACACC AGTACCATCA	300
AGCGTATCAT AATCATTTCC GAACACACTT AGCTCTGATA GCTTACCTAC CGCTACTTGT	360
GCAATATAAG GCATCAAGTT GTTAGGAATT CCTGAGGGAT CTTCCCCAAT CAAACCAGAC	420
TCATGAGCAC CAATTGGATT GAAATAACGA AGCAACGCAA TACTCCATTC TGAATCTGCC	480
ACATGAACAT CTTTTAAAAT TTGCTCAAGC ATCACTTTCG TATACCCATA AGGATTTGTC	540
GCACTTGTTT GCATCGTCTC AATTAGAGGT GACTGATTGT TAATTCCATA TACAGTCGCA	600
CTTGAAGAAA AGACAATCTT TTAAACATTA AATTCTGACA TCACTTCAAC AAGTGCCAAT	660
GTACTCATAA TATTATTTTT GTAGTACATC ACAGGCTTTT GCACGGATTC TCCGACAGCT	720
TTATAACCTG CAAAATGAAT TGCAGCATCA ATCGATTCTT GTTCAAATAC CTTTCTCAAT	780
GCTTGTTTAT CACAAACATC TAATTCGTAA AACACGGGAC GTATTCCTGT AATTGCTTCA	840
ATACGGTCTA GCACCAAGAT GCTAGAGTTC GAAAGGTTGT CGACAATGAT AACTTCCTTT	900
CCTAAATTTA GTAATTCTAC TACGGTATGG CTACCAATAT AACCAGCTCC GCCTGTTACC	960
AATATTGCCA TCTGGGTTTC CTCCTAATTA ATTCCAACCG ACTTAACAAA TCTCATAAAC	1020
GCTTCATGCC CAGACGGTGT ATTCTTATAA ACTCCTGCAT CTTCCAGAAC TCTCGCAAAC	1080
ACTTGTCTTG CTTCTGTGTTG AACTACGCTA TTAACCTCTT CTTTATTAAT GCGAGGATAT	1140
TTTTCTTTCA ATTGGTCGGC CCATTCTAAA TGATAATCCG CAATTGCATT ATCCTCTCCT	1200
AAAAGATATT TTCCAACCTC TTCTAACTCT GGTTTCAAAC GAGGTGGTAA TATCGCAAGT	1260
CCCATCACTT CGATTAACCC GATATTTTCC TTTTAAATAT GTTGTAATAC AATATCTAAT	1320
TGGAAAACAC CATCTGGGTA TTGTTTCACTA GTATGATTAT CTCTTAGAAC AATATCTAAT	1380
TCGTATCTCC CGTCCACTTT ACGAGCAATA GGAGTCACCG TATGGTGTGG GACATCTTCA	1440
GTCATAGCAA TGATGTCTAC TTCTAAATCT GAATATTCTC TCCACTTATT TAGAATTTTA	1500

1031

GTAGCTAAAT CTAACAAGCG ATTTTTATTT TCACTTTGTA ACCTAATTAC TGACATTGGC	1560
CATTTTACAA TACCAGCATT AACATCCTCA AAGTCTTTAA AACAAAATTC ACTCTCAAAT	1620
TTTGCTTTTT CCATTGGGAA AATATGTTTC CCTCCCTGGT AGTGGTTATG ACTAAGAATG	1680
GAGCCTCCTG AGATAGGAAG ATCAGAATTT GAACCAGCAA AATATCCTGG CAAAATATCA	1740
ACAATCTCCA ATAATTGTTT AAATGTTTTA GAGGTAATAG CCATTGGTAC ATGTTGACTA	1800
TTCAAAAATA TCGCATGCTC ATTAAAGTAT GAGTAGGGAG AATACTGGAA TCCCCATACT	1860
TCGTCACCAA GTTTC AACCG AATAATTCTA TGATTCTGAAC GTGCTGGATA ATTTATTCTG	1920
CCCTGATATC CTTCAATTTT CATACATAGT AAACATTTGG GATAATTAGT TGCTTTTACT	1980
AATTTTTCAG CAGCAATTGT TTTTGGATCT TTTTCGGGTT TTGACAAATT TATCGTAATC	2040
TCTAGCTCTC CGTATTTAGT TGATGCTCGA AACTCAATAT TCTTAGCAAT AGCAGAAGTT	2100
TTAATATAAT CACTATCTTT ACTTAACTTA TAAAACTCTT CAACTGCTTC TTGAGGTGAT	2160
ATATCATATG AACTCCAAAA AATATCATTT AATCGACTAG GTAAAGGAAC TATGAAATTC	2220
ATTAACCTCTG CTCCTAAACA TTCCTTTTCC TCGATTAAAT CTTTAATTTT ACCGTTTTTT	2280
AAGGCGATTT CCACTAAGTA ATCTTTTATT TGTTTCAGGT CATTTTCATC GGAAATGCGA	2340
TCAATTCCTT CCTCACCTAT TAACGCTAGT ACTCTATTTT TCACATATAT TTTGTCAATT	2400
TCATTATACA TTCCGTATTC AATTACTCTA TCAACAAAAT TATCAATAAT TGTTTTTATA	2460
TATTTTCTT TCTAATTTAT GTTCCCATAT TTTCTATACA TTATCCATTT ATAAATTGCT	2520
TGCGTAGTAT GAGCAATTTT ATCAAGGTGA TGAATAATAT CTAAAGCACT AATTACTTCA	2580
GAAACGTTCC CATCATCTTC AAATATGTAA TTCATTATTT TCTTTTCCAT ATTTATACTA	2640
AGCTCTTCTA TCTCATCTG TTTTGTATA ACAACCATAT CTAAACATCC AGATTGTTCC	2700
TCTCTATAAC AAGATATAGC CCTATTCATA TGCAGTCCGA TAACTTCATG AAGTATTTTT	2760
ATTTTGTAAA TAATTTTCTT CAAAATTTCA TTATTTTGAA GAATCTGTAG ATTTTTTAAA	2820
ATTTCAACAA TTCTATCCCC AATACGTTCA ATGTCAGTTG ATATTTTAT TACACTAATA	2880
ATTCTTCTTA AGTCATATGA AACAGGATGT TGTAACAAA TTAACTCATA TCCTTTTTTA	2940
TCAATATTTA GAACTGACTC ATTTATGATT AAATCTTCTT TAATCAATTC TACTCGTTCT	3000
TCATTTGATA AATATTCAA TAACTTCTCA TATTTATCAA GCACAGATAC CCAAATGGTC	3060
TCTAAATTAT TTGATAATTC TATAATTTCA TTTTCTAAAT ATAACCTTAA CATTTAGGTA	3120
CCTCTTCTTA ACAAAGTTCTG	3140

(2) INFORMATION FOR SEQ ID NO: 159:

1032

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9048 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

CCGGATGATT TCCTGGTCAG ATAGGGGGAA AGTGA CTTC TCAGCAATCG CGCGTAGAGT	60
AGGATTCCCT TCACGGATAA TATCGTTCAT ATCAATTAAG TGAGCAGCTT TTGTAATACG	120
TTCTATTGCA GACATTTTCT CTCCTTATAT TATGTTTAGT GCAGTTAGCT ACTGCCAAAG	180
CCCAAGTGGT A TACTTGGA TAAGCCACTG TGGATTAGTT CATTTTCTTT CATTACCTCT	240
ACATGATATC ACAAATGAC AAGAATTGAA AGCATTATGG CATTTAGGAT TTATAGAAAA	300
TAGATAGGAA GTTCAATTCA ATTGTGAAAG AAATACTTAT CTGTGATATA ATAAAAAGAA	360
AAGGCTTGCA TAAGAAAGTA GGGAGAACGA AGATACAAAG AAGACAAAAT CGAAATCAGG	420
GTGGTTTAGC TTTTCGTTTT ATGAAGGGCT TGGTAACTT TTTAGGAGTT ATCGCAAGTG	480
GAGCAATAAG GGATTTGTGG CGATACTCTT GCTAGCAGTT GGT TTATCAA TGGGCTTGGT	540
CTTGTTGTTT GAAAGCTTCC AAGGAATCCC TTGACTAGTC AAAAACGAGA TACTATTTCT	600
CAAGAGGGGA CTAAGCAAAA GTCTCAGGAG TAGGAAGAGG AAAAACTGC CAGAATTATG	660
GCCCACGGGG ATTTGCTCTA CCACGATGGA CTTTCTTTT CAGCTAAAAA AGAAGACGGT	720
ACCTATGACT TTCATGAAAA TTTTGAGTAT GTGACTCCTT GGCTCAAGCA AGGGGACTAA	780
GCAGCAGATT TAGCTATTGG TGATTTTGAA GGAACCATTA ATAAGGATCA TTATTTAGCG	840
GGTTATCTTC TCTTTAATGC TCCTGTTGAA GTTATGGATG CTATTAAGGA GGCAGGTTAT	900
CATGTGCTGG ATTTAGCTCA TAATCATATT TTGGATTTCG AAATTGAGGG AGTTATTTCA	960
ACGGCCGATA TTATTGAGAA AGCTGGAATC ACTCCAATCG GAGTTTATAC GCACGAACCA	1020
CGTGATCAGG CTCCGCTGGT CATTAAGGAA GTGAATGGTA TCAAGGTTGC ATTGTTAGCC	1080
TATTCCTATG GTTTC AATGG AATTGAGCAG TATATTTCTC AGGAAGACTA TAATCGTTAT	1140
CTTTCAGATT TAAACGAAGA TAAGATGAAG GTTGAAATTG AACGGGCAGA GAAGGAAGCA	1200
GATATCACCA TTATCATGCT TCAGATGGGT GTTGAGTATC GATTGGAACC AACTGAAGAA	1260
CAAAAAGCTC TTTATCACAA GATGATCGAT TTGGGAGCGG ATATTATCTT TGGAGGGCAT	1320
CCTCACGTTG TTGAACCATC TGAAACGGTT GAAAAAGATG GAGATAAGAA ACTCATTATC	1380
TATTAAATGG GGAAC TTCAT TTCCAATCAA CGAATTGAAT CTATGGGAGA TGAAGAGAAT	1440
GCTAAGTGGA CTGAACGTGG TGTTCCTCATG GATGTCACCA TCAAGAAGAA GGATGGAAAA	1500

1033

ACAACTATCG	GAACAGCTAA	AGCTCATCCT	ACTTGGGTCA	ATCGAACACC	AAAGGGAACC	1560
TTTTCAACCAG	AAGGATATCC	CTTGTATCAT	TACCAAACCTT	ATATTTTGGA	AGATTTTATA	1620
GAGGATGGCA	GTCATCGTGA	CCAGTTAGAT	GAAGCGACTA	AGGAACGAAT	TGATACAGCC	1680
TATAAAGAAA	TGAATGAACA	TGTGGGATTG	AAGTGGTATT	AGCTTGAATC	CAGAGGAAAG	1740
TAAATGATGA	TTAAGGTAAT	TGCGACAGAT	ATGGATGGGA	CCTTGCTGGA	TGCTAGAGGT	1800
CAGCTTGATC	TCCCACGATT	GGAAAAGATT	TTAGATCAGT	TGGATCAAAG	GGGCATTTCGT	1860
TTTGTCATTG	CGACGGGCAA	TGAAATTCAC	CGCATGAGAC	AACTACTGAG	TCCCTTGGTG	1920
GATCGAGTGG	TTCTGGTTGT	TGCTAATGGC	GCTCGTATTT	TTGAAAACAA	TGAATTGATT	1980
CAGGCTCAGA	CATGGGATGA	CGCCATTGTC	AACAAGGCTT	TGACTCATTT	CAAGGGTCGA	2040
GCGTGTCAAG	ACCAGTTTGT	TGTAACGGGG	ATGAAGGGTG	ATTTTGTCAA	GGAAGGTACG	2100
ATTTTACAG	ATCTTGAAAG	TTTTATGACT	CCAGAAATGA	TTGAAAAATT	CTACCAACGG	2160
ATGCAATTTG	TGGATGAATT	AACATCTGAC	CTCTTTGGTG	GTGTGCTCAA	GATGAGCATG	2220
GTTGTTGGTG	AGGAACGTTT	GAGTTCGGTT	TTGGAAGAAA	TCAATGCTCT	CTTTGATGGC	2280
CGTGTCCGAG	CTGTATCCAG	TGGCTATGGT	TGCATTGATA	TCCTCCAAGC	TGGGATTCAT	2340
AAAGCATGGG	GCTTGGAGGA	ATTACTCAAG	CGCTGGGACT	TGAAATCCCA	AGAAATCATG	2400
GCTTTTGGTG	ATAGTGAAAA	TGATGTTGAA	ATGCTTGAAA	TGGCTGGAAT	TGCCTATGCG	2460
ATGGAAAAATG	CTGATGAGAA	AGCCAAAGCT	GTGGCGACTG	CTCTAGCACC	AGCCAACAGC	2520
CAAGGAGGAG	TTTATCAAGT	CTTGGAAC	TGGTTAGAAA	AAGGAGAATG	AAGTGGCAGT	2580
ACAGTTATTA	GAAAATTGGC	TCCTAAAGGA	ACAAGAAAAA	ATTCAAACCTA	AGTATCGTCA	2640
CCTAAATCAC	ATTTCTGTTG	TAGAACCAAA	CATTCTTTTT	ATTGGGGATT	CCATTGTCGA	2700
GTATTATCCT	CTACAGGAGC	TATTTGGGAC	TTCAAAGACG	ATTGTCAATC	GAGGAATTCG	2760
TGGCTATCAG	ACAGGACTGT	TACTAGAGAA	CCTTGATGCT	CATCTATATG	GTGGAGCAGT	2820
AGATAAAATT	TTTCTTCTGA	TTGGGACAAA	TGATATCGGA	AAGGATGTTT	CTGTGAATGA	2880
GGCTCTCAAT	AATCTCGAAG	CTATCATTTCA	ATCCGTTGCT	CGCGATTATC	CATTGACAGA	2940
GATTAAATTG	CTTTCCATTT	TGCCTGTCAA	TGAGAGAGAG	GAGTACCAGC	AGGCAGTCTA	3000
TATCCGCTCG	AATGAAAAA	TTCAGAACTG	GAATCAAGCC	TATCAAGAGC	TTGCATCTGC	3060
CTATATGCAG	GTGGAATTTG	TGCCAGTATT	TGATTGTTTG	ACAGACCAAG	CAGGCCAACT	3120
CAAAAAAGAA	TATACAACTG	ATGGACTGCA	CCTCAGTATT	GCTGGTTATC	AGGCTTTGTC	3180
AAAATCCTTG	AAAGACTATC	TTTACTAAAT	AGCTAAATAA	TGTTAAATTT	GAGCATAATA	3240

1034

TCTTGTA AAA	AATTCTA AAA	TCCTTTA AAA	TAAAAAGTGA	CGGAGGAATT	TATGAATGTA	3300
AATCAGATTG	TACGGATTAT	TCCTACTTTA	AAAGCTAATA	ATAGAAAATT	AAATGAAACA	3360
TTTTATATTG	AAACCCTTGG	AATGAAGGCC	TTGTTAGAAG	AATCGGCCTT	TCTGTCACTA	3420
GGTGACCAAA	CGGGTCTTGA	AAAGCTGGTT	TTAGAAGAAG	CTCCCAGTAT	GCGTACTCGT	3480
AAGGTAGAGG	GAAGAAAAAA	ACTAGCTAGA	TTGATTGTCA	AGGTGGAAAA	TCCCTTAGAA	3540
ATTGAAGGAA	TCTTATCTAA	AACAGATTCTG	ATTCATCGAT	TATATAAAGG	TCAAAATGGC	3600
TACGCTTTTG	AAATTTTCTC	ACCAGAAGAT	GATTTGATTT	TGATTCATGC	GGAAGATGAC	3660
ATAGCAAGTC	TAGTAGAAGT	AGGAGAAAAG	CCTGAATTTT	AAACAGATTT	GGCATCAATT	3720
TCTTTAAGTA	AATTTGAGAT	TTCTATGGAA	TTACATCTCC	CAACTGATAT	CGAAAGTTTC	3780
TTGGAATCAT	CTGAAATTGG	GGCATCCCTT	GATTTTATTC	CAGCTCAGGG	GCAGGATTTG	3840
ACTGTGGACA	ATACGGTTAC	CTGGGACTTA	TCTATGCTCA	AGTTCTTGGT	CAATGAATTA	3900
GACATAGCAA	GTCTTCGCCA	GAAGTTTGAG	TCTACTGAAT	ATTTTATTCC	TAAGTCTGAA	3960
AAATTCCTCC	TTGGTAAAGA	TAGAAATAAT	GTTGAATTGT	GGTTTGAAGA	AGTATGAAGT	4020
GGACCAAGAT	TATTAAAAAA	ATAGAAGAAC	AAATCGAGGC	AGGGATTTAT	CCCGGAGCCT	4080
CTTTTGCGTA	TTTTAAGGAC	AATCAATGGA	CAGAGTTCTA	TTTAGGCCAG	AGTGACCCAG	4140
AGCATGGCTT	GCAGACTGAG	GCAGGACTAG	TTTATGACCT	AGCTAGTGTC	AGCAAGGTTG	4200
TTGGGGTTGG	CACAGTTTGT	ACCTTCTTGT	GGGAAATAGG	TCAATTAGAT	ATTGATAGAC	4260
TGGTAATAGA	TTTTTTACCT	GAGAGTGATT	ATCCAGACAT	CACTATTCGC	CAGCTCTTGA	4320
CTCATGCAAC	AGACCTTGAT	CCTTTTATTC	CTAATCGTGA	TCTTTTAACA	GCCCCTGAAT	4380
TAAAGGAAGC	GATGTTTCAT	CTCAACAGAC	GAAGTCAGCC	AGCCTTTCTT	TATTCGGATG	4440
TCCATTTTTT	GCTGTTGGGC	TTTATTTTGG	AAAGAATTTT	TAATCAAGAT	TTGGATGTGA	4500
TTTTAAAGGA	TCAAGTCTGG	AAACCTTGGG	GAATGACGGA	AACTAAGTTT	GGGCCAGTTG	4560
AGCTTGCTGT	TCCAACAGTT	AGAGGTGTAG	AGGCAGGCAT	AGTGCATGAT	CCCAAGGCTC	4620
GTCTCCTGGG	TAGACATGCT	GGGAGTGCTG	GTTTATTTTC	GACTATAAAG	GATTTACAAA	4680
TCTTTTTTAGA	ACACTATTTA	GCAGATGATT	TTGCAAGAGA	CTTAAATCAA	AATTTTCTC	4740
CTTTGGATGA	CAAGGAACGT	TCTTTAGCAT	GGAATTTGGA	AGGAGATTGG	CTAGACCATA	4800
CGGGCTATAC	AGGTACCTTT	ATCATGTGGA	ATCGTCAGAA	GCAAGAAGCC	ACTATTTTCC	4860
TATCGAATCG	TACCTATGAA	AAGGACGAGA	GAGCTCAATG	GATATTAGAC	CGCAATCAAG	4920
TGATGAACCT	GATTCGCAAA	GAAGAGTAAG	GAGAGACATG	TCAAATAGTT	TAAAAGGGAC	4980
TTTACTAACA	GTTGTGGCTG	GTATTGCTTG	GGGGTTGTCA	GGAACGAGTG	GCCAATACCT	5040

1035

AATGGCACAC	GGAATTTTCGG	CTCTGGTCTT	GACTAACTTG	CGTCTTTTAA	TCGCTGGTGG	5100
AATTCTCATG	CTCTTGGCTT	ATGCTACTGC	AAAGGATAAA	ATACTGGTCT	TTTTAAAGGA	5160
TAGAAAGAGT	TTGCTGTCTC	TTCTTATTTT	TGCTCTGATT	GGTCTTTTTT	TCAACCAATT	5220
CGCCTATCTG	TCTGCTATTC	AGGAGACCAA	TGCGGGAACA	GCGACGGTGC	TTCAGTATGT	5280
TTGTCCTGTC	GGAATTTTAA	TTTATAGCTG	TATCAAGGAT	AGGGTGGCAC	CGACACTGGG	5340
AGAGATAGTT	TCCATCATAT	TCGCCATCGG	AGGAACCTTC	CTGATCGCAA	CACATGGGCA	5400
GTTGGACCAG	TTATCCATGA	CACCTGCTGG	TCTGTTCTGG	GGTCTCTTTT	CTGCCTTGAC	5460
TTATGCTCTG	TATATCATTT	TACCCATAGC	CTTGATTAAA	AAGTGGGGGA	GCAGCTTGGT	5520
CATTGGTGTG	GGAATGGTCA	TAGCAGGTTT	GGTCGCCCTT	CCTTTTACAG	GGGTTCTACA	5580
GGCCGATATC	CCGACTAGTC	TTGATTTTCT	CCTTGCGTTT	GCAGGCATTA	TCCTTATCGG	5640
GACTGTCTTT	GCCTATACAG	CTTTCCTTAA	AGGAGCCAGT	CTGATAGGAC	CGGTCAAGTC	5700
AAGCTTGTTG	GCTTCAATTG	AGCCAATATC	GGCGATTTTC	TTTGCCTTCT	TAATAATGAA	5760
TGAACAATTT	TATCCCATTG	ATTTTCTTGG	TATGGCAATG	ATATTGTTTG	CTGTAACTTT	5820
GATTTCTTTG	AAAGATTTAT	TCTTAGAAAA	ATAAAAAAGA	CTCTTTGTCC	GTGACAGAGA	5880
GTTTTTGCGT	GGTAATCTAA	TTATTTTCAA	GATAAAATTC	AAAGCGTTCG	CCTACATATT	5940
GACTTTTTAC	GTATTCAAAA	GCAGTACCAT	CTTCTAGGTA	GGAAACCTGG	GTCAATCCAA	6000
GAATAGCATG	TCCTTTTTCA	ACTTCCAAAT	AGTGGGCAAT	CTTTTCTTTA	GCAAGGCGAG	6060
CATAGATGGT	CTGTTGAGAT	TTGCCGATAC	GATAGCCATG	TTTTTGCAAG	GTTTGGAAGA	6120
AATGACTGGT	GATTTCTTCT	TTTTTTAAAGT	CCTTAATGAA	TTTTTCAGGA	ATAGAAGCAA	6180
CTTCATAAAC	TAGGGGAACT	TGGTCGGCAT	AGCGGACCCG	CTCCATTCGG	ATAATATTGT	6240
CCGTTGGAAA	AATTCCTAGC	TTGGCAACTT	CTTGCTCATT	GGGAATGGTT	TTTTTGTAGG	6300
AAATGAGCTG	GCTAGAGGGA	ACTTTACCTT	GGGATTTGAC	AATTTCAAGT	AAACTGGTTG	6360
TCCCTCGCAT	CTTTTCTTGT	ACTCGAGTAC	TGGAAACAAA	GGTGCCGCTT	CCTACACGGC	6420
GCTCTAAGAC	GCCTTCTTCG	ACTAATAGAG	ATACGGCTTG	GCGGAGGGTC	ATGCGACTGA	6480
CCGCAAACTG	CTCAGCTAAA	TCTCTTTCAC	TGGGAAGCCT	CTCACCAATA	GCCCAACGGT	6540
ACTCGTCAAT	ATCCTTTTTT	ATCTGATCAT	GGATTTTTAT	ATAAGCAGGT	AGCATATTTT	6600
TCACTTCATT	TCTATCTTTT	CTCTATTGTA	CCCCAATAAA	CTAGAAAAAG	TCAAACTTCG	6660
CCTTGTTTAG	TTGGTAATTC	GCCCTTATTT	GTGATAGAAT	ATTGAGAAAA	GATATTTCTT	6720
TTGAGAAAGG	AAAAAGATGA	GCAACATTTT	AACTGATTTG	CAAGATGTAG	AAAAAATCAT	6780

1036

CGTATTGGAC	TATGGTAGCC	AGTACAACCA	GCTGATTTCA	CGCCGTATCC	GTGAGATTGG	6840
TGTTTTTTCA	GAAGTAAAAA	GCCATAAAAT	TTCAGCTGCT	GAAGTTCGTG	AAGTCAATCC	6900
TGTAGGAATT	ATTCTATCAG	GTGGTCCAAA	TTCTGTATAT	GAAGATGGTT	CATTTGATAT	6960
TGACCCAGAA	ATCTTCGAAC	TCGGAATTCC	AATTTTGGGA	ATCTGTTATG	GTATGCAGTT	7020
ATTGACCCAT	AAACTTGGAG	GAAAAGTTGT	TCCTGCAGGT	GATGCTGGAA	ATCGTGAATA	7080
CGGTCAATCA	ACCCTAACTC	ACACACCATC	AGCGCTTTTT	GAATCAACAC	CTGATGAACA	7140
GACTGTTTTG	ATGAGCCATG	GTGATGCGGT	TACTGAGATT	CCTGCTGACT	TTGTTTCGTAC	7200
AGGTACATCA	GCTGACTGCC	CATACGCAGC	CATCGAAAAC	CCAGATAAAC	ACATTTACGG	7260
TATCCAATTC	CACCCAGAAG	TTCGTCATTC	TGTATACGGA	AATGATATCC	TTCGTAACTT	7320
TGCCCTTAAC	ATTTGTAAGG	CTAAAGGTGA	CTGGTCAATG	GATAATTTCA	TTGACATGCA	7380
GATCAAAAAA	ATTCGTGAAA	CCGTCGGTGA	TAAACGTGTC	CTTCTTGGTC	TATCAGGTGG	7440
TGTTGACTCA	TCTGTCGTTG	GGGTTCTTCT	CCAAAAAGCG	ATTGGCGATC	AATTGATCTG	7500
TATCTTCGTA	GACCACGGTC	TTCTTCGTAA	AGGCGAAGCT	GATCAAGTTA	TGGACATGCT	7560
CGGTGGTAAG	TTTGGTTTGA	ATATCGTCAA	AGCAGACGCT	GCTAAACGTT	TCCTTGACAA	7620
ACTTGCTGGC	GTTTCTGACC	CTGAACAAAA	ACGTAAAATC	ATCGGTAACG	AGTTTGTCTA	7680
TGTATTCGAT	GACGAAGCAA	GCAAGCTCAA	AGATGTGAAA	TTCCTTGCTC	AAGGTACTTT	7740
ATATACAGAT	GTTATCGAGT	CTGGTACGGA	TACAGCTCAA	ACTATCAAGT	CACACCACAA	7800
CGTGGtGGTC	TTCCAGAAGA	TATGCAGTTT	GAATTGATTG	AACCACTCAA	TACTCTTTAC	7860
AAGGATGAAG	TTCGTGCTCT	TGGTACAGAG	CTTGGTATGC	CAGACCATAT	CGTATGGCGC	7920
CAACCATTC	CAGGACCAGG	ACTTGCTATC	CGTGTCATGG	GTGAAATCAC	TGAAGAGAAA	7980
CTTGAAACCG	TTCGTGAATC	AGACGCTATT	CTTCGTGAAG	AAATCGCTAA	AGCTGGACTT	8040
GACCGCGATA	TTTGGCAATA	CTTCACTGTT	AACACAGGCG	TTCGTTCACT	CGGTGTTATG	8100
GGTGACGGTC	GTACGTATGA	CTACACGATT	GCAATCCGTG	CTATCACTTC	TATCGATGGT	8160
ATGACTGCTG	ATTTTGCCAA	AATTCCATGG	GAAGTACTTC	AAAAAATCTC	AGTACGTATC	8220
GTAAATGAAG	TGGATCATGT	TAACCGTATC	GTCTACGATA	TTACAAGTAA	ACCACCTGCA	8280
ACAGTTGAGT	GGGAATAATC	GCAAAAAAAT	TAAAAGCTTT	GTAAATCAA	CGGTTACAGA	8340
GGATTAAAAA	CTGTAACTGG	GATTAAAACG	GGAACATTTG	CTAAAAAGAA	TAAATTGAAT	8400
AATAGTTCCA	AGTGGTTTAC	ATTTGGACAA	AAAATTAGAC	CGTAGTTTTT	AAGCTGCGGT	8460
CTTTTGATAT	ATATAATGAG	AATTAATGGC	TCTTTGTCAA	CTGTAGTGGG	TTGAAGTCAG	8520
CTAAGCTCGA	GAAAGGACAA	ATTTTGTCTT	TTCTTTTTTT	ATATTCAGAG	CGATAAAAAAT	8580

1037

CCGTTTTTTG AAGTTTTCAA AGTTCCGAAA ACCAAAGGCA TTGCGCTTGA TAAGTTTGAT	8640
GAGATTATTG GTCGCTTCCA ATTTGGCGTT AGAATAGTGT AGTTGAAGGG CGTTGACGAT	8700
TTTCTCTTTG TCCTTTAGAA AGGTTTTTAA GACAGTCTGA AAAAGAGGAT GAACCTGCTT	8760
TAGATTGTCC TCAATGAGTC CGAAAAATTT CTCCGGTTCC TTATTCTGAA AGTGAAACAG	8820
CAAGAGTTGA TAGAGCTGAT AGTGATGTTT CAAGTCTTGT GAATAGCTCA AAAGCTTGTT	8880
TAAAATCTCT TTATTGGTTA AATGCATACG AAAAGTAGGG CGATAAAAAT GTTTATCGCT	8940
GAGTTTACGA CTATCCTGTT GTATGAGCTT CCAGTAGCGC TTGATAGCCT TGTATTCATG	9000
AGACTTTCGA TCCAATTGAT TCATGATTTG AACACGCACA CGACTCGG	9048

(2) INFORMATION FOR SEQ ID NO: 160:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

GTACCTTTAT TGATGAATGG ACTGTTTAAA TCAGTAGCAC GCCAACCAGA TATGCTTTCT	60
GAGTTTCGTA GTTTGATGTT TTTAGGTGTT GCCTTTATTG AAGGAACTTT CTTTGTAAC	120
CTTGTCTTCT CATTTATTAT CAAATAAATA CATGGAACGA GAAGAAAAGG GAGGATTTTA	180
GATGGAAGAA AGTATTAATC CAATCATCTC TATTGGTCCT GTTATCTTCA ATCTGACTAT	240
GTTAGCCATG ACTTTGTTGA TTGTGGGAGT TATTTTTGTC TTTATTTATT GGGCAAGCCG	300
CAATATGACC TTGAAACCCA AAGGAAAGCA AAATGTACTT GAGTATGTCT ATGACTTTGT	360
TATTGGATTT ACAGAACCTA ACATTGGTTC GCGCTACATG AAAGATTACT CACTCTTTT	420
CCTTTGTTTA TTCCTTTTCA TGGTGATTGC CAATAACCTT GGCTTAATGA CAAAGCTTCA	480
AACGATCGAT GGGACTAACT GGTGGAGTTC GCCAACCGCT AATTTACAGT ATGACTTAAC	540
CTTATCTTTT CTTGTCATTT TGTTGACACA TATAGAAAGC GTTCGTCGTC GTGGATTTAA	600
AAAAAGTATA AAATCTTTTA TGAGTCCTGT TTTTGTCTATA CCGATGAATA TCTTGGAAGA	660
ATTTACAAAC TTCTTATCTT TGGCTTTGCG GATTTTTGGG AATATCTTTG CAGGAGAGGT	720
CATGACGAGT TTGTTACTTC TTCTTTCCCA CCAAGCTATT TATTGGTATC CAGTAGCCTT	780
TGGAGCTAAT TTGGCTTGGA CTGCATTTTC TGTCTTTATT TCCTGCATCC AAGCTTATGT	840
TTTTACTCTT TTGACATCTG TGTATTTAGG GAATAAGATT AATATTGAAG AGGAATAGAA	900

1038

AGGAGTAACT	GATGCACGTA	ACAGTAGGTG	AATTAATTGG	TAATTTTATT	TTAATCACTG	960
GCTCTTTTAT	TCTTTTGCTA	GTCTTGATTA	AAAAATTTGC	ATGGTCTAAT	ATTACAGGCA	1020
TTTTCGAAGA	AAGAGCTGAA	AAAATTGCTT	CAGATATTGA	CAGAGCTGAA	GAAGCCCGTC	1080
AAAAAGCAGA	AGTATTGGCT	CAAAAACGCG	AAGATGAATT	GGCTGGTAGC	CGTAAAGAAG	1140
CTAAGACAAT	CATTGAAAAT	GCAAAGGAAA	CAGCTGAGCA	AAGTAAGGCT	AATATCTTAG	1200
CAGATGCTAA	ACTAGAAGCA	GGACACTTAA	AAGAAAAAGC	CAATCAAGAA	ATTGCTCAAA	1260
ATAAAGTAGA	AGCTTTACAG	AGTGTTAAGG	GTGAGGTCGC	AGATTTGACC	ATCAGCTTAG	1320
CTGGTAAAT	CATCTCACAA	AACCTTGACA	GTCATGCCCA	TAAAGCACTC	ATTGATCAGT	1380
ATATCGATCA	GCTAGGAGAA	GCTTAATGGA	CAAGAAAACA	GTAAAGGTAA	TTGAAAAATA	1440
CAGCATGCCT	TTTGTCCAAT	TGGTACTTGA	AAAAGGAGAA	GAAGACCGTA	TCTTTTCAGA	1500
CTTGACTCAA	ATCAAGCAAG	TTGTTGAAAA	AACAGGTCTG	CCTTCTTTTT	TAAAACAAGT	1560
GGCAGTAGAC	GAGTCGGATA	AGGAAAAAAC	AATTGCTTTT	TTCCAAGATT	CTGTGTCGCC	1620
TTTATTACAA	AACTTTATCC	AGGTTCTGGC	CTACAATCAC	AGAGCAAATC	TTTTTTATGA	1680
TGTGCTTGTA	GATTGCTTGA	ACCGACTTGA	AAAAGAAACA	AATCGATTTG	AAGTGACGAT	1740
TACGTCTGCT	CATCCTCTAA	CTGATGAACA	GAAGACTCGT	TTGCTCCCTT	TGATTGAGAA	1800
AAAAATGTCT	CTGAAAGTAA	GGAGTGTAAG	AGAACAAATC	GATGAAAGTC	TCATTGGTGG	1860
TTTTGTCAAT	TTTGCCAATC	ACAAGACAAT	TGATGTGAGT	ATTAAACAAC	AACTTAAAGT	1920
TGTTAAAGAA	AATTTGAAAT	AGAAAGTGGT	GTTCTTTTGG	CAATTAACGC	ACAAGAAATC	1980
AGCGCTTTAA	TTAAGCAACA	AATTGAAAAT	TTCAAACCCA	ATTTTGATGT	GAAGTAAACA	2040
GGTGTGTGTA	CCTATATCGG	GGACGGTATC	GCGCGTGCTC	ACGGCCTTGA	AAATGTCATG	2100
AGTGGAGAGT	TGTTGAATTT	TGAAAACGGC	TCTTATGGTA	TGGCTCAAAA	CTTGGAGTCA	2160
ACAGACGTTG	GTATTATCAT	CCTAGGTGAC	TTTACAGATA	TCCGTGAAGG	CGATACAATC	2220
CGCCGTACAG	GGAAAATCAT	GGAAGTCCCT	GTAGGTGAAA	GTCTGATTGG	TCGTGTTGTG	2280
GATCCGCTTG	GTCGTCCAGT	TGACGGTCTT	GGAGAAATCC	ACACTGATAA	AACTCGTCCA	2340
GTAGAAGCAC	CAGCTCCTGG	TGTTATGCAA	CGTAAGTCTG	TTTCAGAACC	ATTGCAAACCT	2400
GGTTTGAAAG	CTATTGACGC	CCTTGTACCG	ATTGGTCGTG	GTCAACGTGA	GTTGATTATC	2460
GGTGACCGTC	AGACAGGGAA	AACAACCATT	GCGATTGATA	CAATCTTGAA	CCAAAAAGAT	2520
CAAGATATGA	TCTGTATCTA	CGTCGCGATT	GGACAAAAAG	AATCAACAGT	TCGTACGCAA	2580
GTAGAAACAC	TTTCGTCAGTA	CGGTGCCTTG	GAATACACAA	TCGTTGTGAC	AGCCTCTGCT	2640
TCACAACCAT	CTCCATTGCT	CTTCCTAGCT	CCTTATGCTG	GGGTTGCTAT	GGCGGAAGAA	2700

1039

TTTATGTATC	AAGGTAAGCA	TGTTTTGATT	GTATACGATG	ATCTATCAAA	ACAAGCGGTA	2760
GCTTATCGTG	AACTGTCGCT	CTTGCTTCGT	CGTCCTCCAG	GTCGTGAAGC	CTTCCCAGGG	2820
GATGTTTTCT	ATCTCCACAG	CCGTTTGCTT	GAGCGCTCAG	CTAAAGTTTC	TGATGAACTT	2880
GGTGGTGGAT	CAATTACAGC	CCTACCATTT	ATCGAGACAC	AAGCAGGAGA	TATCTCAGCC	2940
TATATCGCAA	CCAACGTGAT	TTCTATCACT	GATGGACAAA	TCTTCCTTGG	CGATGGCCTC	3000
TTCAATGCAG	GTATTCGTCC	AGCCATCGAT	GCGGGTTCAT	CTGTATCTCG	TGTAGGTGGT	3060
TCTGCACAAA	TCAAAGCCAT	GAAGAAGGTT	GCTGGTACAC	TTCGTATCGA	CCTTGCTTCA	3120
TACCGTGAGT	TGGAAGCCTT	TACTAAGTTT	GGTTCTGACT	TGGACGCAGC	AACACAGGCT	3180
AAGTTGAACC	GTGGACGTCG	TACCGTTGAG	GTCTTGAAAC	AACCTGTTCA	CAAACCATTA	3240
CCTGTTGAGA	AACAAGTAAC	CATTCTTTAT	GCTTTGACAC	ATGGTTTCTT	GGATACTGTT	3300
CCAGTAGATG	ATATTGTTCG	TTTCGAGGAA	GAGTTCCATG	CCTTCTTTGA	TGCTCAACAT	3360
CCAGAGATTT	TGGAAACCAT	TCGTGATACA	AAAGACTTGC	CAGAAGAAGC	AGTCTTGGAT	3420
GCTGCGATTA	CAGAGTTTCT	CAATCAATCT	AGCTTCCAAT	AAGAATAGAG	GTGTCAGATG	3480
GCAGTATCTC	TAAATGATAT	TAAAACAAAA	ATCGCCTCAA	CAAAAAATAC	GAGTCAAATC	3540
ACTAATGCCA	TGCAAATGGT	ATCGGCTGCT	AAGCTAGGTC	GTTCTGAAGA	AGCTGCTCGC	3600
AACTTCCAAG	TTTACGCTCA	GAAAGTGCCT	AAACTTTTGA	CAGATATCCT	TCATGGTAAT	3660
GGAGCTGGTG	CTTCAACTAA	TCCGATGTTG	ATTAGCCGTT	CTGTGAAGAA	GACAGGCTAT	3720
ATCGTTATCA	CTTCAGACCG	CGGTTTGCTT	GGAGGTTATA	ATTCCCTCTAT	TTTGAAAGCT	3780
GTTATGGAGT	TGAAAGAAGA	ATACCACCCA	GACGGTAAAG	GTTTTGAAAT	GATCTGTATC	3840
GGTGGGATGG	GAGCTGATTT	CTTTAAGGCT	CGCGGTATTC	AACCACTTTA	TGAATTACGT	3900
GGCTTGTCAG	ACCAACCTAG	CTTTGATCAA	GTTCGTAAGA	TTATTTCAAA	AACTGTTGAA	3960
ATGTACCAAA	ATGAACTCTT	TGATGAGCTT	TATGTTTGCT	ACAACCACCA	TGTCAATACG	4020
CTAACCAGTC	AAATGCGTGT	GGAACAAATG	CTTCCGATTG	TTGACTTGGA	TCCAAATGAA	4080
GCGGATGAAG	AGTACAGCTT	GACTTTTGAA	TTGGAAACCA	GCCGAGAAGA	AATTCTGGAG	4140
CAGTTGTTGC	CTCAGTTTGC	AGAAAGTATG	ATTTACGGTG	CCATTATCGA	TGCCAAGACA	4200
GCTGAGAATG	CTGCGGGCAT	GACAGCCATG	CAAACAGCGA	CAGATAATGC	TAAGAAAGTC	4260
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ACAGAAATCG	TAGCAGGTGC	TAGTGCCTTA	GAATAGGCTC	TAGTCCAGCT	CGTATGAAAA	4380
TGAACTTAGG	ACCTAGTTGA	GCTAGGAACC	GACAGTATCT	TATATAGAAT	AGGAGAAGGA	4440

1040

GATGAGTTCA	GGTAAAATTG	CTCAGGTTAT	CGGTCCCGTT	GTAGACGTTT	TGTTTGCAGC	4500
AGGGGAAAAA	CTTCCTGAGA	TTAACAATGC	ACTTGTCGTC	TACAAAAATG	ACGAAAGAAA	4560
AACAAAAATC	GTCCTTGAAG	TAGCCTTGGA	GTTAGGAGAT	GGTATGGTTC	GTA CTATCGC	4620
CATGGAATCA	ACAGATGGGT	TGACTCGTGG	AATGGAAGTA	TTGGACACAG	GTCGTCCAAT	4680
CTCTGTACCA	GTAGGTAAAG	AAACTTTGGG	ACGTGTCTTC	AACGTTTTTG	GAGATACCAT	4740
TGACTTGGA	GCTCCTTTTA	CAGAAGACGC	AGAGCGTCAG	CCAATTCATA	AAAAAGCTCC	4800
AACTTTTGAT	GAGTTGTCTA	CCTCTTCTGA	AATCCTTGAA	ACAGGGATCA	AGGTTATTGA	4860
CCTTCTTGCC	CCTTACCTTA	AAGGTGGTAA	AGTTGGACTT	TTCGGTGGTG	CCGGAGTTGG	4920
TAAAACTGTC	TTAATCCAAG	AATTGATTCA	CAACATTGCC	CAAGAGCACG	GTGGTATTTT	4980
AGTATTTGCT	GGTGTGGGG	AACGTACTCG	TGAGGGGAAT	GACCTTTACT	GGGAAATGAA	5040
AGAATCAGGC	GTTATCGAGA	AAACAGCCAT	GGTCTTTGGT	CAGATGAATG	AGCCACCAGG	5100
AGCACGTATG	CGTGTTGCCC	TTACTGGTTT	GACAATCGCT	GAATACTTCC	GTGATGTGGA	5160
AGGCCAAGAC	GTGCTTCTCT	TTATCGATAA	TATCTTCCGT	TTCACTCAGG	CTGGTTCAGA	5220
AGTATCTGCC	CTTTTGGGTC	GTATGCCATC	AGCCGTTGGT	TACCAACCAA	CACTTGCTAC	5280
GGAAATGGGT	CAATTGCAAG	AACGTATCAC	ATCAACCAAG	AAGGGTTCTG	TAACCTCTAT	5340
CCAGGCTATC	TATGTGCCAG	CGGATGACTA	TACTGACCCA	GCGCCAGCAA	CAGCCTTCGC	5400
TCACTTGGAT	TCAACAACAA	ACTTGGAACG	TAAGTTGGTA	CAATTGGGTA	TCTACCCAGC	5460
CGTTGACCCA	CTTGCTTCAA	GCTCACGTGC	CTTGGCACCT	GAAATCGTTG	GAGAAGAGCA	5520
CTATGCAGTT	GCTGCTGAAG	TAAAACGTGT	CCTTCAACGT	TACCATGAAT	TGCAAGATAT	5580
CATTGCTATC	CTTGGTATGG	ATGAGCTTTC	TGATGAAGAA	AAGACCTTGG	TTGCTCGCGC	5640
CCGTCGTATC	CAGTTCTTCT	TGTCACAAAA	CTTCAACGTT	GCGGAACAAT	TTACTGGTCA	5700
GCCAGGTTCT	TATGTTCCAG	TTGCTGAAAC	TGTACGTGGC	TTTAAGGAAA	TCCTTGATGG	5760
TAAATACGAC	CACTTGCCAG	AAGATGCCTT	CCGTGGTGTA	GGTCTATCG	AAGATGTGAT	5820
TGCAAAAGCT	GAAAAAATGG	GATTTTAAGA	GGTGATCTAT	GGCTCAGTTA	ACTGTCCAGA	5880
TCGTGACACC	AGATGGTCTC	GTCTATGATC	ACCATGCCAG	CTATGTATCG	GTTGGAACCTC	5940
TGGATGGTGA	GATGGGGATC	TTGCCACGAC	ATGAAAATAT	GATTGCGGTT	TTAGCAGTTG	6000
ATGAAGTAAA	GGTAAAACGT	ATCGATGATA	AAGATCACGT	GAAGTGGATT	GCAGTAAACG	6060
GTGGCGTTAT	TGAAATTGCC	AATGATATGA	TCACAATCGT	CGCTGACTCT	GCAGAACGTG	6120
CTCGTGATAT	CGATATCAGT	CGTGCAGAAC	GTGCCAAACT	TCGTGCAGAA	CGTGCAATTG	6180
AAGAAGCACA	AGACAAACAT	TTGATTGACC	AAGAACGTCG	TGCTAAGATT	GCTTTGCAAC	6240

1041

GTGCTATTAA	CCGTATTAAT	GTCGGAAATA	GACTATAAGA	AAAAATGAAC	TTGAAAATAC	6300
CAAGTTCATT	TTTTATGGTG	TTTAAAGGAG	CAAAACGGAT	GCAGACTGCT	TCGGGAACAT	6360
GGAAGTCGTT	GGAGAGTTCT	GCTAGACGAC	CATTGTCACA	ATTACGTTTA	AAGACAGTTG	6420
CATTGTCAGA	GTCTTGATGG	ACAACAATGA	GAAATTTTGT	GTCGGGTGTC	AAATCAAAAT	6480
CACGTGGAGT	CTGACCATGC	GTTGGAACGA	TTTCTAATAA	CTCTAAGCTA	CCGTCCGCAA	6540
GGATGGTATA	TACTGCGATA	GAATCATGGC	CACGGTTAGA	AGCGTAGAGG	TATTTACCGT	6600
CTTTAGAGAG	ATGAATAGCA	GCGGTTCCAT	TAAAGCCTTC	GTAAGCTTCC	GGTAAAGTTG	6660
AAATGACCTG	CATACGTTCA	AATTCGCCAA	CGCCATCGTA	GATTAAAACT	TCGATAGTAC	6720
TATTGAGTTC	ACAAATGAGA	TAAGCGATTT	TATAGTGGTT	ATGGAAAATG	ATATGGCGTG	6780
AGCCTGCTCC	TGGCTTGCTG	TGATAGGTAT	AGAGCTTAGA	TAATTTTCCT	TCTTGATCGA	6840
GGTCATAGGT	GATGACTTGG	TCAGTTCCCA	AGTCGCAGGT	CACTAGATAG	TGGTCAGGTG	6900
TTAAATCTGT	ATAGTGAACA	TGGGGGGAAG	CTTGATTTTC	ATGTGGACCT	TGGCCACTGT	6960
GTTGATCCAT	ATCACTAAGT	AGAAGACTAC	CATCTTCCTG	GCGTTTATAA	ACAAGGACTT	7020
GTCCCTTGTTG	ATAGTTAGCT	GCGTAAACCA	AATCACGCTT	TTCATCGACA	GCAACATAAC	7080
AGTGGGGAGC	TCCTTCTTCA	ACAACATGAT	TTAACACAGT	CCCGTCAGTT	TGATAGGCTG	7140
CAATTCCCCC	CTTATCGTCT	TGGCTACCAA	CAGTGTATAA	ATGTTGGTGC	TGGTCAAAGG	7200
CAAGGTAGGT	TGGACTTGGC	TCAGCTGCAA	AAAGTTCTAG	ATTTGAAAGC	TGACCAGTTT	7260
CTGTATCAAA	GTCTGCCTTG	TAAATCCCTT	GAGAAGTACG	ACGTGTATAA	GTTCCAAAAT	7320
AAACAGTTTC	TTTCATTACT	ATACCTCTGT	GTAAAGATAA	GACTATTATA	TCACAAAAAC	7380
AAGTAAATTA	AAGATATCCA	ATTAGATGTA	AGCACTTTAA	AAAAGAGTTA	TTTTGTTTCA	7440
AAAATGGTAT	AATGAGAGAA	CAATAGAAAAG	GAAGTATTTA	TGGAGCAAAA	AGAGAAACAT	7500
TTTAGCCTAT	CTTGGTTTTT	CAAGTGGTTT	TTAGATAACA	AGGCAATTAC	GGTATTTTTA	7560
GTAACCTTAT	TATTGGGACT	GAATCTTTTT	ATTTTAAGTA	AGATTAGTTT	TCTATTTTCA	7620
CCTGTTTTAG	ACTTTTTTAGC	AGTTGTGATG	TTGCCAGTCA	TTTTGTCTGG	TTTGTTATAT	7680
TATTTGTTGA	ATCCTATTGT	TGATTGGATG	GAGAAGCATA	AGGTTAATCG	TGTTATAGCT	7740
ATCACTATTG	TCTTTGTTAT	CATCGCTCTC	TTTATCATTT	GGGGCTTGGC	AGTCGCCATT	7800
CCAAATCTGC	AACGTCAGGT	TTTGACCTTT	GCAAGAAACG	TTCTGTTTTA	CTTAGAAGAT	7860
ATAGATAGGA	TTGTTAATGG	ATTGGTAGCC	CAGCACCTGC	CAGATGATTT	CAGACCTCAA	7920
TTAGAGCAAG	TTTTGACCAA	TTTTTCTAGC	CAGGCTACAG	TTTTGGCAAG	TAAGGTTTCA	7980

1042

TCTCAGGCAG	TCAACTGGGT	GAGTGCCTTT	ATTAGCGGGG	CTTCTCAAGT	GATTGTTGCC	8040
TTGATTATCG	TTCCTTTCAT	GCTCTTTTAT	CTCTTGCGTG	ATGGGAAAGG	CTTGCGTAAC	8100
TATTTGACCC	AATTCATTCC	AAGAAAATTG	AAGGAACCTG	TTGGACAAGT	TTTATCAGAT	8160
GTGAATCAAC	AGTTGTCCAA	CTATGTTCGA	GGGCAAGTGA	CAGTGGCTAT	TATTGTAGCA	8220
GTAATGTTTA	TCATCTTCTT	CAAGATTATT	GGTCTACGCT	ATGCGGTTAC	GCTGGGGGTT	8280
ACTGCTGGTA	TTTTAAATCT	GGTCCCCTAT	CTTGGTAGCT	TTCTAGCCAT	GCTTCCTGCT	8340
CTAGTATTGG	GTTTGATTGC	TGGTCCAGTC	ATGCTTTTGA	AAGTAGTGAT	TGTCTTTATC	8400
GTAGAACAAA	CTATTGAAGG	CCGTTTTGTC	TCTCCATTGA	TTTTGGGAAG	TCAATTAAAC	8460
ATCCACCCTA	TTAATGTTCT	CTTTGTTTTG	TTAACTTCAG	GATCTATGTT	TGGTATCTGG	8520
GGAGTTTAC	TTGGTATTCC	GGTTTATGCC	TCTGCTAAGG	TTGTCATTTT	AGCCATTTTC	8580
GAATGGTATA	AGGTAGTCAG	TGGTCTATAT	GAATTAGAGG	GTGAGGAAGT	CAAGAGTGAA	8640
CAATAGTCAA	CAGATGTTAC	AGGCTTTGGA	GGAGCAAGAT	TTAACTAAGG	CTGAGCATTA	8700
TTTCGCCAAA	GCTTTAGAAA	ATGATTCAAG	TGATCTTCTG	TATGAATTGG	CAACTTATCT	8760
TGAAGGGATT	GGTTTCTATC	CTCAGGCCAA	GGAAATTTAC	CTGAAAATTG	TAGAGGATTT	8820
TCCAGAGGTT	CATCTTAATC	TAGCTGCAAT	TGCTAGCGAG	GATGGTCAAA	TAGAAGAAGC	8880
CTTTACCTAT	CTTGAGGAAA	TCCAAGCTGA	CAGTGACTGG	TATGTCTCGT	CTTTGGCTCT	8940
GAAGGCAGAC	CTTTACCAGC	TGGAAGGTTT	GACAGATGTG	GCACGTGAGA	AATTATTGGA	9000
GGCCTTGACC	TACTCAGAGG	ATTCTCTCTT	GATATTGGGT	TTGGCAGAGT	TGGATAGTGA	9060
GTTGGAAAAT	TACCAAGCGG	CTATTCAAGC	CTATGCCCAG	TTAGATAATC	GCTCGATTTA	9120
TGAGCAAACG	GGCATTTCCA	CCTATCAACG	AATTGGCTTT	GCCTATGCTC	AGTTAGGGAA	9180
ATTTGAAACG	GCTACTGAGT	TTTTAGAAAA	AGCCCTGGAG	TTAGAATACG	ATGACTTAAC	9240
AGCTTTTGAG	TTGGCCAGTC	TTTATTTTGA	TCAAGAAGAA	TATCAAAAAG	CCACCCTCTA	9300
CTTTAAGCAG	CTTGATACCA	TTTCTCCTGA	CTTTGAAGGC	TATGAGTATG	GGTACAGTCA	9360
GGCTTTACAT	AAGGAACATC	AAGTTCAAGA	AGCCCTGCGT	ATCGCTAAGC	AAGGATTAGA	9420
GAAAAATCCC	TTTGAAACTC	GCCTCTTGCT	AGCTGCTTCA	CAATTTTCTT	ATGAATTGCA	9480
TGATGCTAGT	GGTGCAGAAA	ATTATCTCCT	TACTGCAAAA	GAAGACGCTG	AGGATACAGA	9540
AGAAATCTTG	CTTCGTTTAG	CCACTATTTA	TCTGGAGCAG	GAGCGTTATG	AGGATATTCT	9600
AGAATTGCAG	AGTGAGGAGC	CAGAAAATCT	TTTGACCAAG	TGGATGATTG	CTCGTTCTTA	9660
TCAAGAAATG	GACGATTTGG	ATACTGCTTA	TGAGTATTAT	CAAGAGTTGA	CAGGAGATTT	9720
GAAGGACAAT	CCAGAATTTT	TGGAACACTA	TATCTATCTC	TTGCGTGAAT	TGGGACATTT	9780

1043

TGAAGAAGCA AAAGTCCATG CTCACACTTA CTTAAAACTG GTTCCAGATG ATGTGCAAAT	9840
GCAAGAAGCTG TTTGAGAGAT TGTAAGAATG TTTAACCCTAA ATCATTCTATA CCTCTCTCAA	9900
CTAGATGTAA CTTACAAAAC CCCTGACCTC ATGAGCCACT TTCTTCCTCC TCATGAGGTC	9960
AGTTTTACTT TCTGCTGTTT CAGTATCGTT TTTCTTCGCT AGATTTCTCTC AAAAGGGCAG	10020
ACTCCTCCCT TGGTGCGTCA CACGATTTTT TCATCTCGAC TGTTCCTTAA TGCATCATTA	10080
ACGACGCTTT TCTTCTAGGT GGTTCATAAG GAACAGGAAG ATTCAGGTTG ACTTTTCTAA	10140
TCCTAGAATA AAGTGCTGAA AACAATTCGG AATAGGCATA GAGACTAGAC AATTTGAGGA	10200
GCTGCTTGCG TCCTGTTCGA ACACATTTTC CCACCACGTG AAGAAAAAGA TGGCGGAAGC	10260
GTTTGATTGT TAAAGTTTGG AAGTCACCTC CAGCTAGATG TTTGAGAAAA AGATAGAGAT	10320
TGTAGGCGAT ACAGCTCATC ATCATACGAA TTCGTTTTTG ATTAAGGTTG AACTATCCGT	10380
TTTATCGCCA AAAAATCGG	10399

(2) INFORMATION FOR SEQ ID NO: 161:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

GATAAGATTA AGTTAGAAAA GAAAGAACTA GGACATATCT ACCAGATTCA GGTTTTTAAT	60
AGCTATGGGC AGGAAGAAAT CTATCGTGTG ATTTTGATGG AGACCAATAT TAGTTCGGTT	120
TCAACCAATA TCAAGTATGC TGCTGTCTTG ATTAATACCA GTCAGTTGGA ACAGGCTAGT	180
CAAAAGCATG AGCAATTGAT TGTGGTCGTG ATGGCTAGTT TCTGGATTTT GTCTTTACTT	240
GCCAGTCTCT ATCTAGCTAG GGTCAGTGTT AGGCCCCCTGC TTGAGAGTAT GCAGAAGCAA	300
CAGTCTTTTG TGGAAAATGC CAGTCATGAG TTACGAACTC CACTCGCAGT TTTGCAAAAT	360
CGCTTAGAGA CCCTTTTTCG TAAGCCAGAA GCTACCATTA TGGATGTGAG CGAAAGCATT	420
GCATCGAGTT TGGAAGAAGT CCGAAATATG CGTTTTTTAA CGACAAGCTT GCTGAACTTA	480
GCTCGGAGAG ATGATGGGAT TAAGCCGGAG CTTGCAGAAG TTCCAACCTAG CTTTTTTAAT	540
ACAACTTTCA CAACTACGA GATGATTGCT TCGGAAAATA ATCGTGTCTT CCGTTTTGAA	600
AATCGTATCC ATCGAACAAT TGTCACAGAT CAGCTTCTTC TGAAACAACT GATGACCATT	660
CTTTTCGATA ATGCCGTCAA GTATACTGAG GAGGATGGTG AAATTGATTT TCTTATCTCG	720

1044						
GCGACCGATC	GCAATCTTTA	TTTACTTGTT	TCTGATAATG	GAATCGGTAT	TTCGACAGAA	780
GATAAAAAGA	AAATTTTGA	CCGTTTTTAT	CGAGTAGACA	AGGCTAGAAC	CCGGCAAAAA	840
GGTGGTTTG	GTTTAGGATT	ATCCCTAGCC	AAGCAAATTG	TAGATGCTCT	AAAAGGAACT	900
GTTACTGTCA	AAGATAATAA	ACCCAAGGGA	ACAATCTTTG	AAGTGAAGAT	TGCCATTCAG	960
ACACCATCTA	AAAAGAAAAA	ATAAAAAATAT	CGCTCCAATT	GGGGCGATAT	TTTGGAATTA	1020
TCTTCTACGT	TTTCGTTTGA	TAATAGACCG	TTGAACTTTT	AAAACAAGTA	AGCTGAATCC	1080
GATTGCTGCG	GCAAAGGCAA	GAGCAGTTGA	TAATTTTAAT	GCTAAAAAGA	TAAAACTAAA	1140
GATAGCAATA	CAGATACAAA	AAACAGCGAT	ATTAATAAAA	AATAGGATTT	CCTTGAGATT	1200
GGCATCAGAT	TGCGCTTCAG	GTGTATAAGC	TTGGTAATGA	GGAAGCTGCT	GGTTTAATTC	1260
TTCTTGATAG	TCTACCTCAT	AGGATTGTAA	TTTTCTTACG	GGCATGATTC	TCTCCTTAAC	1320
AGTACATACC	TATTTTATCA	TTTTTTTCGGC	AGAGAATTAT	TACAGAAAGG	TTACAAAAAG	1380
AATAAAGTCC	CTTTTCATTT	TCAAAGCATG	GCTGATTTTG	GAGAAATGTG	GTATAATTTT	1440
TCTTATGGAA	AAGATTGTCA	TTACAGCAAC	TGCTGAAAGT	ATTGAACAAG	TTGAACAAC	1500
ACTCGAAGCT	GGCGTAGACC	GTATCTATGT	CGGTGAGAAA	GATTTTGGTC	TTCGTCTGCC	1560
AACGACCTTT	AGTTATGACC	AATTACGTGA	AATCGCTAAG	TTGGTTCATG	ATGCTGGTAA	1620
GGAATTGATC	GTTGCGGTCA	ATGCTCTCAT	GCACCAAGAT	ATGATGGACC	GTATCAAGCC	1680
TTTCTTAAAC	TTCTTGGAAG	AAATCAAGAC	AGACTATATT	ACGATTGGGG	ATGCAGGCGT	1740
CTTTTACGTA	GTTAACCGCG	ATGGTTATTC	ATTTAAGACC	ATCTACGATG	CTTCAACCAT	1800
GGTAAC TAGC	AGTCGTCAGA	TTAACTTCTG	GGGACAAAAG	GCTGGCGCAT	CTGAGGCTGT	1860
TTTGGCGCGT	GAAATTCCAT	CAGCTGAACT	TTTCAAAATG	CCAGAGATTT	TGGAAATTCC	1920
TGCTGAAGTT	TTGGTTTACG	GTGCTAGCGT	CATCCATCAT	TCTAAACGTC	CACTCTTGCA	1980
AAACTACTAT	AACTTTACAC	ATATCGATGA	TGAAAAGACG	CATAAACGTG	ACCTCTTCTT	2040
GGCTGAGCCA	AGTGATCCAG	AGAGCCACTA	TTCCATTTTT	GAAGATAATC	ATGGGACCCA	2100
TATCTTTGCC	AACAATGACC	TTGATTTGAT	GATCAAATTA	ACAGAATTGG	TGGAGCATGG	2160
CTTTACTCGC	TGGAAACTAG	AAGGGCTCTA	CACTCCTGGT	CAGAACTTTG	TTGAGATTGC	2220
AAAAC TCTTT	ATCCAAGCGC	GTAGCTTGAT	TCAAGAGGGC	AAC TTTAGTC	ATGCTCAAGC	2280
CTTCTTGCTG	GATGAAGAAG	TTCGTAAACT	TCACCCTAAA	AACCGTTTCC	TTGATACAGG	2340
ATTTTATGAC	TACGATCCTG	ACATGGTTAG	ATAAAATACA	TGATTCGTTG	AGAGAAGGAA	2400
GATGCAAACA	TTTCTTCTCT	CAATTTTTTCG	TATTTCTTCA	CTATTTTACA	AAAATCAGCA	2460
GGCTAGAATG	CTCTATTCTGA	TGGGATTTTT	AAGAAAAGTA	GTGTTCTTGA	GTTTGAAAAT	2520

1045

TATCCTATGT	TTGCAGGTGC	CAAATGGCCC	TTTTTTTGGT	ATAATTTTTT	ATAATGAAAA	2580
CGATTGGTAA	TCGCTATGTT	GTGGTGGATT	TAGAGGCAAC	TAGCACAGGT	AGTAAGGCTA	2640
AAATTATCCA	AGTGGGAATT	GTCGTGATTG	AGGACGGAGA	AATCGTCGAT	CACTATACGA	2700
CGGATGTCAA	TCCACATGAA	CCCTTGGATG	CTCATATCAA	AGAACTGACA	GGATTGACAG	2760
ACCAACGTCT	GGCGCAAGCA	CCTGATTTTT	CGCAAGTTGC	CAGAAAAATA	TTTGACTTGG	2820
TGGAGGATGG	GATTTTTGTA	GCCCATAATG	TTCAGTTTGA	TGCTAATCTC	TTGGCGGAAA	2880
ATTTATTTTT	TGAAGGCTAT	GAGCTAAGAA	ACCCTCGTGT	TGATACGGTC	GAATTGGCCC	2940
AGGTCTTTTT	CCCTGAACTG	GAAAAATATA	GCTTGCCGAT	TTTGTGTCTG	GAATTAGGAA	3000
TTCCTCTTAA	ACACGCACAC	ACAGCCCTTT	CAGATGCCCA	AGCTACAGCA	GAATTACTTC	3060
TTTTTTTACG	GAAAAAGATG	ACCCAGCTTC	CTAAAGGTCT	CTTGGAACGC	TTGCTGGAAA	3120
TGGCTGACGC	TCTCCTATAT	GAGTCCTACC	TGGTTATTGA	GGAAACTTAT	CGCAACCAAT	3180
CTATCCTGAG	TTCTCCAGAC	TTGGTCCAAG	TTCAAGGTCT	ATATTTTAAG	AAAACGGAAG	3240
CTTCTCTGGA	GCCACGAAAA	CTATCTCAAG	ACTTTTCTAA	AAATATTTCT	CTGTTGAACC	3300
TTGAAGTGAG	GGAGGAACAA	GAAAGTTTTG	CTAAAGAGGT	TGGCTTGCTA	TTGAAAGATG	3360
AACCTGTCTC	TCTGATTCAA	GCGCCGACAG	GGATTGGGAA	AACCTATGGC	TATCTCTTAC	3420
CCGCTTTATC	TCAATCCAAA	GAGCGACAAA	TTGTTCTTAG	TGTTCCGACA	AAGATTCTTC	3480
AAAATCAAAT	CATGGAAGAA	GAAGGTAAAC	GCCTCAAGGA	AGTGTTCAT	ACAGATATTC	3540
ATAGCTTAAA	GGGACCACAA	AATTATCTGA	AGTTGGATGC	CTTTTATCAT	TCCTTGCAGG	3600
AAAATGATGA	AAATCGCTTA	TTTAGACGCT	TTAAAATGCA	AGTCTTGGTC	TGGCTTACTG	3660
AGACAGAGAC	AGGAGATTTG	GATGAAATCG	GGCAACTCTA	CCGTTACCAA	CATTTTCTAG	3720
CAGACCTTCG	TCATGATGGG	AATTTATCAT	CCCAGAGCTT	ATTTGTGACG	GAAGATTTTT	3780
GGAAACGTAG	TCAAGAAAGG	GCAGAGACTT	GCAAGCTTTT	AGTGAATAAT	CATGCCTATC	3840
TCGTAACCAG	ACTTGAAGAT	AATCCTGAAT	TTGTCAGTGA	CCGTTTACTG	ATTATTGATG	3900
AAGTCCAAAA	GATTTTGTTA	GCTCTAGAAA	ATCTGCTTCA	AGAGACCTAC	GATATACAAT	3960
CTATTATCGA	TTAATTGAT	AAGGCTTTAG	TAGGAGAAGA	AAACAGGGTT	CAACAACGGA	4020
TACTAGAAAG	TATTCGCTTT	GAGTGTCTCT	ACTTGATAGA	ACAATTTTCA	TCTGGCAAAT	4080
CTAGGAAAAA	TATCTTAGAT	TCTCTGGACA	ATCTCCATCA	GTATTTTTC	GAATTGGAAG	4140
TAGAAGACTT	TGATGAGCTG	GTCGCTATT	TTACAGCTGA	AGGTGATTAC	TGGCTTGAAG	4200
TAACTGAAAC	GAGTCAAAAG	AAAATTCAGA	TTTCTTCTAC	AAAATCAGGC	CGTACTCTTC	4260

1046

TGTCCTCTTT	ACTTCCTGAG	AGTTGCCAAG	TCTTGGGAGT	ATCGGCTACT	CTTGAGATTA	4320
GTCAGAGGGT	TTCTTTGGCA	GACCTTTTAG	GCTATCCTGA	AGCTAAATTT	GTCAAGATTG	4380
AATCTCGGGG	AAAACAGGAA	CAAGAAGTGG	TCATGGTCAA	AGATTTCCCT	CTGGTAACAG	4440
AAACCTCCTT	AGAAGTCTAT	GCCAGAGAGG	TAGCTGCTTT	ACTAGTGGAA	ATTCAAGCTT	4500
TCCAGCAACC	GATTTTGGTT	CTCTTTACCG	CTAAAGACAT	GCTTCTAGCA	GTATCGGATT	4560
TACTTACAGT	TAGCCACTTG	GCCCAGTATA	AAAATGGGGA	TGTTCATCAG	CTAAAGAAAC	4620
GCTTTGAAAA	AGGTGAACAA	CAAATCTTGC	TTGGTGCAGC	AAGTTTCTGG	GAGGGAGTTG	4680
ATTTTTCAAG	CCATCCTTCT	GTGATTCAAG	TTGTACCGAG	GCTTCCTTTC	CAAAATCCTC	4740
AAGAACCCTT	GACGAAAAAG	ATTAATCAAG	AACTGAATCA	AGAAGGGAAA	AATGCCTTTT	4800
ATGATTATCA	ATTGCCAATG	GCCATTATTC	GTTTAAACAA	GGCTTTGGGA	AGAAGTATGA	4860
GACGTGAATA	CCAACGTTCC	TTAACTCTTA	TTTTGGATAG	GAGAATCGTC	GGAAAACGAT	4920
ACGGCAAACA	AATAGTAGCA	TCTCTAGCAG	AAGAAGCGAC	TGTTAAAACC	ATCTCTCGAT	4980
CCGAAGTTGA	CGAGGCTATT	GATAGATTTT	TTAATGAGCT	TTGATAAATA	GTATTGTATG	5040
AAAGTATAAG	GTTAGTATAT	ATGAAACGTT	CTCTCGACTC	AAGAGTCGAT	TACAGTTTGC	5100
TCTTGCCAGT	ATTTTTTCTA	CTGGTCATCG	GTGTGGTGGC	TATCTATATA	GCCGTTAGTC	5160
ATGATTATCC	CAATAATATT	CTGCCCATTT	TAGGGCAGCA	GGTCGCCTGG	ATTGCCTTGG	5220
GGCTTGTGAT	TGGTTTTGTG	GTCATGCTCT	TTAATACAGA	ATTTCTTTGG	AAGGTGACCC	5280
CCTTTCTATA	TATTTTAGGC	TTGGGACTTA	TGATCTTGCC	GATTGTATTT	TATAATCCAA	5340
GCTTAGTTGC	ATCAACGGGT	GCCAAAAACT	GGGTATCAAT	AAATGGAATT	ACCCTATTCC	5400
AACCGTCAGA	ATTTATGAAG	ATATCCTATA	TCCTCATGTT	GGCTCGTGTC	ATTGTCCAAT	5460
TTACAAAGAA	ACATAAGGAA	TGGAGACGCA	CGGTTCCGCT	GGACTTTTTG	TTAATTTTCT	5520
GGATGATTCT	CTTTACCATT	CCAGTCCTAG	TTCTTTTAGC	ACTTCAAAGT	GACTTGGGGA	5580
CGGCTTTGGT	TTTTGTAGCC	ATTTTCTCAG	GAATCGTTTT	ATTATCAGGG	GTTTCTTGGA	5640
AAATTATTAT	CCCAGTATTT	GTGACTGCTG	TAACAGGAGT	TGCTGGTTTC	TTAGCTATCT	5700
TTATTAGCAA	GGACGGACGA	GCTTTTCTTC	ACCAGATTGG	AATGCCGACC	TACCAAATTA	5760
ATCGGATTTT	GGCTTGGCTC	AATCCCTTTG	AGTTTGCCCA	AACAACGACT	TACCAGCAGG	5820
CTCAAGGGCA	GATTGCCATT	GGGAGTGGTG	GCTTATTTGG	TCAGGGATTT	AATGCTTCGA	5880
ATCTGCTTAT	CCCAGTTCGA	GAGTCAGATA	TGATTTTTAC	GGTATTGCA	GAAGATTTTG	5940
GCTTTATTGG	CTCTGTCCTG	GTTATTGCCC	TCTATCTCAT	GTTGATTTAC	CGTATGTTGA	6000
AGATTACTCT	TAAATCAAAT	AACCAGTTCT	ACACTTATAT	TTCCACAGGT	TTGATTATGA	6060

1047

TGTTGCTCTT	CCACATCTTT	GAGAATATCG	GTGCTGTGAC	TGGACTACTT	CCTTTGACGG	6120
GGATTCCCTT	GCCTTTCATT	TCGCAAGGGG	GATCAGCTAT	TATCAGTAAT	CTGATTGGTG	6180
TTGGTTTGCT	TTTATCGATG	AGTTACCAGA	CTAATCTAGC	TGAAGAAAAG	AGCGGAAAAG	6240
TCCCATTCAA	ACGGAAAAAG	GTTGTATTAA	AACAAATTAA	ATAAGGAGAA	AATCATGGTA	6300
AAAGTAGCAG	TTATATTAGC	TCAGGGCTTT	GAAGAAATTG	AAGCCTTGAC	AGTTGTAGAT	6360
GTCTTGCGTC	GAGCCAATAT	CACATGTGAT	ATGGTTGGTT	TTGAAGAGCA	AGTAACGGGT	6420
TCGCATGCAA	TCCAAGTAAG	AGCAGATCAT	GTCTTTGATG	GAGATTTATC	AGACTATGAT	6480
ATGATTGTTC	TTCCTGGAGG	TATGCCTGGT	TCTGCACATT	TACGTGATAA	TCAGACCTTG	6540
ATTCAAGAAT	TGCAAAGCTT	CGAGCAAGAA	GGGAAGAAAC	TAGCAGCCAT	TTGTGCGGCA	6600
CCAATTGCCC	TCAATCAAGC	AGAGATATTG	AAAAATAAGC	GATACACTTG	TTATGACGGC	6660
GTTCAAGAGC	AAATCCTTGA	TGGTCACTAC	GTCAAGGAAA	CAGTAGTGGT	AGATGGTCAG	6720
TTGACAACCA	GTCGGGGTCC	TTCAACAGCC	CTTGCCTTTG	CCTACGAGTT	GGTGGAGCAA	6780
CTAGGAGGGG	ACGCAGAGAG	TTTACGAACA	GGAATGCTCT	ATCGAGATGT	CTTTGGTAAA	6840
AATCAGTAAA	ACGGGAGTTA	TTCTCTCGTT	TTTTATGTGG	AAACTCAGG	GAAATCATCG	6900
CTTTTTTTCAT	AAAAAATGC	TATAATGAAG	GGTATGAAAT	ATCACGATTA	CATCTGGGAT	6960
TTAGGTGGAA	CTTTACTGGA	TAATTATGAA	ACTTCAACAG	CTGCATTTGT	TGAAACATTG	7020
GCACTGTATG	GTATCACACA	AGACCATGAC	AGTGTCTATC	AAGCTTTAAA	GGTTTCTACT	7080
CCTTTTGCGA	TTGAGACATT	CGCTCCCAAT	TTAGAGAATT	TTTTAGAAAA	GTACAAGGAA	7140
AATGAAGCCA	GAGAGCTTGA	ACACCCGATT	TTATTTGAAG	GAGTTTCTGA	CCTATTGGAA	7200
GACATTTCAA	ATCAAGGTGG	CCGTCATTTT	TTGGTCTCTC	ATCGAAATGA	TCAGGTTTTG	7260
GAAATTTTAG	AAAAAACCTC	TATAGCAGCT	TATTTTACAG	AAGTGGTGAC	TTCTAGCTCA	7320
GGCTTTAAGA	GAAAGCCAAA	TCCCGAATCC	ATGCTTTATT	TAAGAGAAAA	GTATCAGATT	7380
AGCTCTGGTC	TTGTCATTGG	TGATCGGCCG	ATTGATATCG	AAGCAGGTCA	AGCTGCAGGA	7440
CTTGATACCC	ACTTGTTTAC	CAGTATCGTG	AATTTAAGAC	AAGTATTAGA	CATATAAGAA	7500
AAAGGAATAA	GATGACAGAA	GAAATCAAAA	ATCTGCAGGC	ACAGGATTAT	GATGCCAGTC	7560
AAATTCAAGT	TTTAGAGGGC	TTAGAGGCTG	TTCGTATGCG	TCCAGGGATG	TACATTGGAT	7620
CAACCTCAAA	AGAAGGTCTT	CACCATCTAG	TCTGGGAAAT	TGTTGATAAC	TCAATTGACG	7680
AGGCCTTGCC	AGGATTTGCC	AGCCATATTC	AAGTTTTTAT	TGAGCCAGAT	GATTCGATTA	7740
CTGTTGTGGA	TGATGGGCGT	GGTATCCCAG	TCGATATTCA	GGAAAAACA	GGCCGTCCTG	7800

1048

CTGTTGAGAC CGTCTTTACA GTCCTTCACG CTGGAGGAAA GTTCGGCGGT GGTGGATACA	7860
AGGTTTCAGG TGGTCTTCAC GGGGTGGGGT CGTCAGTAGT TAATGCCCTT TCCACTCAAT	7920
TAGACGTTCA TGTTACACAA AATGGTAAGA TTCATTACCA AGAATACCGT CGTGGTCATG	7980
TTGTGCGAGA TCTTGAAATA GTTGGAGATA CGGATAAAAC AGGAACAAC TTTCACTTCA	8040
CACCGGACCC AAAAATCTTC ACTGAAACAA CAATCTTTGA TTTTGATAAA TTAAATAAAC	8100
GGATTCAAGA GTTGGCCTTT CTAAATCGCG GTCTTCAAAT TTCAATTACA GATAAGCGCC	8160
AAGGTTTGGA ACAAACCAAG CATTATCATT ATGAAGGTGG GATTGCTAGT TACGTTGAAT	8220
ATATCAACGA GAACAAGGAT GTAATCTTTG ATACACCAAT CTATACAGAC GGTGAGATGG	8280
ATGATATCAC AGTTGAGGTA GCCATGCAGT ACACAAC TGG TTACCATGAA AATGTCATGA	8340
GTTTCGCCAA TAATATTCAT ACCCATGAAG GTGGAACACA TGAACAAGGT TTCCGTACAG	8400
CCTTGACACG TGTTATCAAC GATTATGCTC GTAAAAATAA GTTACTGAAA GACAATGAAG	8460
ATAATTTAAC AGGGGAAGAT GTTCGCGAAG GCTTAACTGC AGTTATCTCA GTTAAACACC	8520
CAAATCCACA GTTTGAAGGA CAAACCAAGA CCAAATTGGG AAATAGCGAA GTGGTCAAGA	8580
TTACCAATCG CCTCTTCAGT GAAGCTTTCT CCGATTTCCT CATGGAAAAT CCACAGATTG	8640
CCAAACGTAT CGTAGAAAAA GGAATTTTGG CTGCCAAGGC TCGTGTGGCT GCCAAGCGTG	8700
CGCGTGAAGT CACACGTAAA AAATCTGGTT TGGAAATTTT CAACCTTCCA GGGAAACTAG	8760
CAGACTGTTC TTCTAATAAC CCTGCTGAAA CAGAACTCTT CATCGTCGAA GGAGACTCAG	8820
CTGGTGGATC AGCCAAATCT GGTGCTAACC GTGAGTTTCA GGCTATCCTT CCAATTCGCG	8880
GTAAGATTTT GAACGTTGAA AAAGCAAGTA TGGATAAGAT TCTAGCCAAC GAAGAAATTC	8940
GTAGTCTTTT CACAGCCATG GGAACAGGAT TTGGCGCAGA ATTTGATGTT TCGAAAGCCC	9000
GTTACCAAAA ACTCGTTTTG ATGACCGATG CCGATGTCGA TGGAGCCCAC ATTCTGTACCC	9060
TTCTTTTAAC CTTGATTTAT CGTTATATGA AACCAATCCT AGAAGCTGGT TATGTTTATA	9120
TTGCCCAACC ACCAATCTAT GGTGTCAAGG TTGGAAGCGA GATTAAAGAA TATATCCAGC	9180
CGGGTGCAGA TCAAGAAATC AAATCCAAG AAGCTTTAGC CCGTTATAGT GAAGGTCGTA	9240
CCAAACCGAC TATTCAGCGT TATAAGGGGC TAGGTGAAAT GGACGATCAT CAGCTGTGGG	9300
AAACAACCAT GGATCCCGAA CATCGCTTGA TGGCTAGAGT TTCTGTAGAT GATGTGCAGA	9360
AGCAGATAAA ATCTTTGATA TGTTGATGGG GATCGAGTTG TCCTCGTCG	9409

(2) INFORMATION FOR SEQ ID NO: 162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6415 base pairs
 - (B) TYPE: nucleic acid

1049

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

CCTGGGAAAG TCTTGAAAAT TATGATAGAA TGGTGGAAGG AAAAATTCAG GAGAGTAGTA	60
GTGACTCAAA ATGTTGAAAG TCTTCTCGTA TCCATTGTAA TCAGTGCATA CAATGAAGAA	120
AAATATCTGC CTGGTCTAAT TGAAGACTTA AAAAATCAAA CCTATCCTAA AGAGGATATT	180
GAAATTCTAT TTATAAATGC TATGTCCACA GATGGGACCA CAGCTATCAT TCAGCAATTT	240
ATAAAGGAAG ATACAGAGTT TAACTCAATT AGATTGTATA ACAATCCTAA GAAAAATCAA	300
GCTAGTGGTT TTAACCTGGG AGTTAAACAT TCTGTAGGGG ACCTTATTTT AAAAATTGAT	360
GCTCATTCAA AAGTTACTGA GACTTTTGTA ATGAACAATG TGGCTATTAT TCAACAAGGT	420
GAATTTGTCT GTGGGGGGCC TAGACCGACG ATTGTCTGAAG GAAAAGGAAA ATGGGCAGAG	480
ACCTTGCATC TTGTTGAGGA AAATATGTTT GGCAGTAGCA TTGCCAATTA TCGAAATAGT	540
TCTGAGGATA GATATGTTTC TTCTATTTTT CATGGAATGT ATAAACGAGA GGTTTTCCAG	600
AAGGTTGGTT TAGTAAATGA GCAACTTGGC CGAACTGAAG ATAATGATAT TCATTATAGA	660
ATTCGAGAAT ATGGTTATAA AATCCGCTAT AGCCCAAGTA TTCTATCTTA TCAGTATATT	720
CGACCAACAT TCAAGAAAAT GCTGCATCAA AAGTATTCAA ATGGTTTGTTG GATTGGCTTG	780
ACAAGTCATG TTCAGTTTAA GTGTTTATCA TTATTTCACT ATGTTTCCTG TTTATTTGTT	840
TTGAGTCTTG TGTTTAGTCT AGCATTGTTA CCGATCACAT TCGTATTCAT AACTTTACTA	900
TTAGGTGCCT ATTTTCTACT TTTGTCATTA CTCACTTTGC TGACTTTATT AAAACATAAA	960
AATGGATTTT TAATTGTGAT GCCCTTTATT TTATTTTCCA TTCACTTTGC TTATGGCCTT	1020
GGGACGATTG TAGGTTTAAT TAGAGGATTT AAATGGAAGA AGGAGTACAA GAGAACAATA	1080
ATTTATTTGG ATAAAATAAG CCAAATAAAT CAAAATATGC TATAATAACA ATATAGTAAA	1140
ACTCTTTTAA GGAGGAGTAG ATTTCTATGA ATAAAAAAT AACAGATTAT GTGATTGATC	1200
TGGTGGAAT TTAAATAAAA CAACAAAAGC AGGTTTCTTG GGGAATATTT GATATTTTCA	1260
GTATGGTGGT TTCCATCATT GTATCTTATA TTTTATTTTA TGGGCTGATT AATCCAGCAC	1320
CTGTTGACTA CATTATCTAT ACGAGTTTGG CCTTCCTGTT CTATCAATTG ATGATTGGTT	1380
TTTGGGGGTT GAACGCGAGC ATTAGTCGTT ACAGCAAGAT TACGGATTTT ATGAAAATCT	1440
TTTTTGGTGT GACTGCTAGC AGTGTCTTGT CATATAGTAT CTGTTATGCC TTCTTGCCAC	1500
TCTTCTCCAT CCGTTTCATC ATTCTCTTTA TCTTGTTGAG TACCTTCTTG ATTTTATTGC	1560

1050

CACGGATTAC	TTGGCAGTTA	ATCTACTCCA	GACGCAAAAA	AGGTAGTGGT	GATGGAGAAC	1620
ACCGTCGGAC	CTTCTTGATT	GGTGCCGGTG	ATGGTGGGGC	TCTTTTATG	GATAGTTACC	1680
AACATCCAAC	CAGTGAATTA	GAAGTGGTCG	GTATTTTGGA	TAAGGATTCT	AAGAAAAAGG	1740
GTCAAAAAC	TGGTGGTATT	CCTGTTTTGG	GCTCTTATGA	CAATCTGCCT	GAATTAGCCA	1800
AACGCCATCA	AATCGAGCGT	GTCATCGTTG	CGATTCCGTC	GCTGGATCCG	TCAGAATATG	1860
AGCGTATCTT	GCAGATGTGT	AATAAGCTGG	GTGTCAAATG	TTACAAGATG	CCTAAGGTTG	1920
AAACTGTTGT	TCAGGGCCTT	CACCAAGCAG	GTAAGTGGCTT	CCAAAAAATT	GATATTACGG	1980
ACCTTTTGGG	TCGTCAGGAA	ATCCGTCTTG	ACGAATCGCG	TCTGGGTGCA	GAAGTACAG	2040
GTAAGACCAT	CTTAGTCACA	GGAGCTGGAG	GTTCAATCGG	TTCTGAAATC	TGTCGTCAAG	2100
TTAGTCGCTT	CAATCCTGAA	CGCATTTGTCT	TGCTCGGTCA	TGGGGAAAAAC	TCAATCTACC	2160
TTGTTTATCA	TGAATTGATT	CGTAAGTTCC	AAGGGATTGA	TTATGTACCT	GTGATTGCGG	2220
ACATTCAAGA	CTATGATCGT	TTGTTGCAAG	TCTTTGAGCA	GTACAAACCT	GCTATTGTTT	2280
ATCATGCGGC	AGCCCAACAAG	CATGTTCTTA	TGATGGAGCG	CAATCCAAAA	GAAGCCTTCA	2340
AAAACAATAT	CCGTGGAACT	TACAATGTTG	CTAAGGCTGT	TGATGAAGCT	AAAGTGTCTA	2400
AGATGGTTAT	GATTTTCGACA	GATAAGGCAG	TCAATCCACC	AAATGTTATG	GGAGCAACCA	2460
AGCGCGTGGC	GGAGTTGATT	GTCAGTGGCT	TTAACCAACG	TAGCCAATCA	ACCTACTGTG	2520
CAGTTCGTTT	TGGGAATGTT	CTTGGTAGCC	GTGGTAGTGT	CATTCCAGTC	TTGAACGTC	2580
AGATTGCTGA	AGGTGGGCCT	GTAACGGTGA	CAGACTTCCG	TATGACCCGT	TACTTTATGA	2640
CCATTCCAGA	AGCTAGCCGT	CTGGTTATCC	ATGCTGGTGC	TTATGCCAAA	GATGGGGAAG	2700
TCTTTATCCT	TGATATGGGC	AAACCAGTCA	AGATTTATGA	CTTGGCCAAG	AAGATGGTGC	2760
TTCTAAGTGG	CCACACTGAA	AGTGAAATTC	CAATCGTTGA	AGTTGGAATC	CGCCCAGGTG	2820
AAAAACTCTA	CGAAGAACTC	TTGGTATCAA	CCGAACTCGT	TGATAATCAA	GTTATGGATA	2880
AGATTTTCGT	TGGTAAGGTT	AATGTCATGC	CTTTAGAATC	CATCAATCAA	AAGATTGGAG	2940
AGTTCCGCAC	TCTCAGTGGA	GATGAGTTGA	AGCAAGCTAT	TATCGCCTTT	GCTAATCAAA	3000
CAACCCACAT	TGAATAAAAA	AGAAAAACGC	ATAGTATCAA	GTTACACAAC	CTTGGTAATA	3060
TGCGTTTTAT	TATGTAGAGA	CTTATACTCT	TCGAAAATCT	CTTCAAACCA	CGTCAACGTC	3120
GCCTTGCCGT	ATATGGTTAC	TGACTtCGTC	AGTTCTATCC	ACAACCTCAA	AACAGTGTTT	3180
TGAGytGACT	TCGTCAGTTC	TATCCACAAC	CTCAAAACAG	TGTTTTGAGc	TGACTtCGTC	3240
AGTTCTATCC	ACAACCTCAA	AACAGTGTTT	TGAGCTGAcT	TCGTCAGTTC	CATCCACAAC	3300
CTTAAAACAG	TGTTTTGAGy	TGACnTTCGT	CAGTTCCATC	TACAACCTTA	AAACAGTGTT	3360

1051

TTGAGCTGCC	CGCAGCTAGT	TTCCTAGTTT	GCTCTTTGAT	TTTCATTGAG	TATTACTTCA	3420
TTTTCTTCTG	AAATGGAATT	GTTACCCAGT	CTATGCTATT	GAAAATACGC	CAAAACTTCT	3480
AAGGGTTTGT	GAGCGATATA	ATCAGGTTGA	TAGTTTAGTA	GATCTGCTTG	CTCTCCAAAT	3540
CCCCAAGTGA	TGGCCAATTT	CTGAATACCT	GTTTCTCGAG	CTCCCAGCAT	ATCAAACCTG	3600
GTATCTCCGA	TGATGATGGC	TTGTTCTGGT	GCTAGTTGAT	GTGTCTGCAA	GGCTTGGTGA	3660
ATGACATCTG	CCTTATGGGG	TGCTTCAGGG	CTAGAACCAT	AAATGCCATC	AAAGAAATGA	3720
TGGATTTCCA	AGTTTTTTGC	CATGTCTTGA	GCAGTAGATG	TATCCTTTGT	CGTGGTGATG	3780
TAGAGTGGAT	AACTGCTCGA	TAACCTCTCA	AGCAAGTCTA	TAATCTGAGG	AAAGAGTTGA	3840
GCTTCATAGA	TGCCTTTTGC	CTTATAGTAA	GAACGATATA	TCTGCACGGC	TTCAGAAATT	3900
TGGTCTTTGG	ACAGGCAGGT	CGCAAAACTA	CTTTCGAGAG	GTGGTCCCAT	AAAACCACGA	3960
ATAGTTTTTG	CATCAGGGCT	AGGCACCCCC	AGCTCTTTAA	AGGTATAGGT	AAAGGCATTG	4020
TGAATCCCGA	TAGAACTATC	AACGAGGGTT	CCATCCAAAT	CGAAAAAAAT	CGCTGTGATA	4080
GAGGTCATGG	TTTCTCCTAT	TTGATAAGCT	TATTCTCCGA	AAATTTCTTT	TTGGAGGCGA	4140
CGACCAGTAG	GGGTGGTAGC	GAGTCCACCT	TCAGCTGTTT	CACGAAAGGC	AGTTGGCATG	4200
CTTGCTCCTA	CTTGGTACAT	GGCATCGATC	ACTTCATCCA	CAGGGATTTT	AGATTCGATA	4260
CCTGCCAAGG	CCATGTCTGC	TGCGATGAAA	GCAAAGCTAG	CTCCCATGGC	ATTACGTTTG	4320
ACACAGGGAA	CTTCGACCAA	ACCTGCAACA	GGGTCACAGA	TGAGGCCTAG	CATATTTTTA	4380
ATGACAAAGG	CAATAGCTTG	ACTGGCCTGA	TAAGGTGTTC	CACCTGCAGC	CAGAGTCAAG	4440
GCGGCAGCAC	TCATAGCAGA	GGCTGAACCA	ACTTCAGCTT	GACACCCACC	CTCAGCACCT	4500
GAGATGGAGG	CATTGTTTGC	GATGACTAGT	CCAAAGGCAC	CAGCAGCAAA	GAGGAAATCC	4560
AATTGTTGCT	CGTGGCTGAG	GTCTAATTTT	TCAATAGCAG	CAGTGAGAAC	GGATGGCAGA	4620
CAGCCAGCAC	TTCCAGCGGT	TGGAGTGGCA	CAGACCAAGC	CCATTTTGGC	ATTGTGTTCA	4680
TTGACTGCGA	TGGCATTTCG	GGCAGCCGAG	AGAATCGTAT	AATCTGACAG	AGTTTTTCCG	4740
TTTTTCGATGT	AGTGATCCAA	TTTGGCAGCA	TCTCCACCTG	TCAGGCCACT	ACGAGATTTA	4800
TTTTTCATTGA	GGCCAAGTTG	GACAGAGGCT	TTCATAACTT	CCAGATTGCG	TTCCATGAGA	4860
AGGAAGACTT	CTTCACGTTC	GCGACCGGTC	AATTCAAACCT	CTGTTGTAAT	CATGAGTTCT	4920
GCGACATTTT	CTTGAAAGTC	CAGATCTGCT	TGCTCGACCA	ATTCTTTGAT	AGAATAAAAC	4980
ATGCTTCCTC	CTATTTAAAG	AAATTGACAT	TGTGGAGATG	AGGGATTTTT	CGAATTTCTT	5040
CGATAGCCTC	ATCACAGTTG	CGACTGTCAA	CTTCGATAAT	CATAATGGCT	TTTTCACCAG	5100

1052

CTTTTTCACG AGTGACATTC ATCTGGGCGA TATTGATACC ATAGCGGGAA AGCGCCTCTG	5160
TAACAAGGGC AATCATACCT GGAATATCTT GATGAACGAT GATGATAGTC GGTGTATTCA	5220
TATTGAGAGA GACGGCAAAA CCATTGAGTT CGGTTACCTG AATATTTCCCT CCACCGATAG	5280
AAATACCAGT CACGCTGATG GTCTTGTGGG CATTTTAAAC AGTAATTTTA GTGGTGTAG	5340
GGTGAGGGGC ATTGCTGTCT TTCTGAATGG TCCAGACAAT CTTGATACCA CGCTTGTGGG	5400
CAATTTCCAG ACTATTTGGA ATTTCAAGGAT CATCTGTATC CATTCCTAAA ATACCTGCAA	5460
CAAGGGCTAG GTCTGTTCCG TGACCACGAT AGGTCTTGGC AAATGAGTTA AAAAGTTGGA	5520
ATTCAACTTC TGTCGGAGTA TCATCAAAAA TGAAGAGAC AATCTTCCCA ATACGAACAG	5580
CACCAGCGGT ATGGCTACTA GATGGGCCAA TCATAACTGG TCCGATGATA TCAAAGACAG	5640
ATTGAAAACG AAGTGATTTT ATCAGTTTCC CCTTATAAAA ATTCTTATCT CTATTATATC	5700
AAAGAATGAG GGGCTTGGCT TTAATTGTGG ATGAAAACCT TTCTAATACC TCAAATAGCA	5760
TAAAAATAGT ATCTTTTATG ACAAAAAACA CCTTATTTAG GGAAATAAAA AATAATTTTG	5820
TAATATTTCT ACATAAAAGT GTCAAGAAAC GGTAATATTT AAAGGGTATG ATAGAACTAT	5880
AGAAAGAAGG AGAATTTTCG AATATGAAAT CAATAACTAA AAAGATTAAA GCAACTCTTG	5940
CAGGAGTAGC TGCCTTGTTT GCAGTATTTG CTCCATCATT TGTATCTGCT CAAGAATCAT	6000
CAACTTACAC TGTTAAAGAA GGTGATACAC TTTCAGAAAT CGCTGAAACT CACAACACAA	6060
CAGTTGAAAA ATTGGCAGAA AACAACCACA TTGATAACAT TCATTTGATT TATGTTGATC	6120
AAGAGTTGGT TATCGATGGC CCTGTAGCGC CTGTTGCAAC ACCAGCGCCA GCTACTTATG	6180
CGGCACCAGC CGCTCAAGAT GAAACTGTTT CAGCTCCAGT AGCAGAAACT CCAGTAGTAA	6240
GTGAAACAGT TGTTTCAACT GTAAGCGGAT CTGAAGCAGA AGCCAAAGAA TGGATCGCTC	6300
AAAAAGAATC AGGTGGTAGT ATACAGCTAC AAATGGACGT TATATCGGAC GTTACCAATT	6360
AACAGATTCA TACCTGAACG GTGACTACTC AGCTGAAAAC CAAGAACGGG TACCG	6415

(2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

TACCCCTTTC GAATTTTGGC AAAAATTCGG TAAGGCTTTG ATGGTAGTTA TCGCGGTTAT	60
GCCGGCTGCT GGTTTGATGA TTTCAATCGG TAAGTCTATC GTGATGATTA ACCCAACCTT	120

1053

TGCACCACTT	GTCATCACAG	GTGGAATTCT	TGAGCAAATC	GGTTGGGGGG	TTATCGGTAA	180
CCTTCACATT	TTGTTTGCCC	TAGCCATTGG	AGGAAGCTGG	GCTAAAGAAC	GTGCTGGTGG	240
TGCTTTCGCC	GCTGGTCTTG	CCTTCATCTT	GATTAACCGT	ATCACTGGTA	CAATCTTTGG	300
TGTATCAGGC	GATATGTTGA	AAAATCCAGA	TGCTATGGTA	ACTACTTTCT	TTGGTGGTTC	360
AATCAAAGTT	GCTGATTACT	TTATCAGTGT	TCTTGAAGCT	CCAGCCTTGA	ACATGGGGGT	420
ATTCGTAGGG	ATTATCTCAG	GTTTTGTAGG	GGCAACTGCT	TACAACAAAT	ACTACAACCT	480
CCGTAAACTT	CCTGATGCAC	TTTCATTCTT	CAACGGGAAA	CGTTTCGTAC	CATTTGTAGT	540
TATTCCTTCGT	TCAGCAATCG	CTGCAATTCT	ACTTGCTGCT	TTCTGGCCAG	TAGTTCAAAC	600
AGGTATCAAT	AACTTCGGTA	TCTGGATTGC	CAACTCACAA	GAAACTGCTC	CAATTCTTGC	660
ACCATTCCTTG	TATGGTACTT	TGGAACGTTT	GCTCTTGCCA	TTTGGTCTTC	ACCACATGTT	720
GACTATCCCA	ATGAACTACA	CAGCTCTTGG	TGGTACTTAT	GACATTTTAA	CTGGTGCAGC	780
TAAAGGTACT	CAAGTATTCG	GTCAAGACCC	ACTATGGCTT	GCATGGGTAA	CAGACCTTGT	840
AAACCTTAAA	GGTACTGATG	CTAGTCAATA	TCAACACTTG	TTAGATACAG	TACATCCAGC	900
TCGTTTCAAA	GTTGGACAAA	TGATCGGTTT	ATTCGGTATC	TTGATGGGTG	TGATTGTTGC	960
TATCTACCGT	AATGTTGATG	CTGACAAGAA	ACATAAATAC	AAAGGTATGA	TGATTGCAAC	1020
AGCTCTTGCA	ACATTCTTGA	CAGGGGTTAC	TGAACCAATC	GAATACATGT	TCATGTTTAT	1080
CGCAACACCT	ATGTATCTTG	TTTACTCACT	TGTTCAAGGT	GCTGCCTTCG	CTATGGCTGA	1140
CGTCGTAAAC	CTACGTATGC	ACTCATTCGG	TTCAATCGAG	TTCTTGACTC	GTACACCTAT	1200
TGCAATCAGT	GCTGGTATTG	GTATGGATAT	CGTTAACTTC	GTTTGGGTAA	CTGTTCTCTT	1260
TGCTGTAATC	ATGTACTTTA	TCGCAAACCT	CATGATTCAA	AAATTCAACT	ACGCAACTCC	1320
AGGGCGCAAC	GGAAACTACG	AAACTGCTGA	AGGTTCAAGG	GAAACCAGCA	GCGAAGTGAA	1380
AGTTGCAGCA	GGCTCTCAAG	CTGTAAACAT	TATCAACCTT	CTTGGTGGAC	GTGTAAACAT	1440
CGTTGATGTT	GATGCATGTA	TGACTCGTCT	TCGTGTAACT	GTTAAAGATG	CAGATAAAGT	1500
AGGAAATGCA	GAGCAATGGA	AAGCAGAAGG	AGCTATGGGT	CTTGTCATGA	AAGGACAAGG	1560
GGTTCAAGCT	ATCTACGGTC	CAAAAGCTGA	CATTTTGAAA	TCTGATATCC	AAGATATCCT	1620
TGATTCAGGT	GAAATCATTC	CTGAAACTCT	TCCAAGCCAA	ATGACTGAAG	CACAACAAAA	1680
CACTGTTCAc	TTCAAAGATC	TTACTGAGGA	AGTTTACTCA	GTAGCAGACG	GTCAAGTTGT	1740
TGCTTTGGAA	CAAGTAAAGG	ATCCAGTATT	TGCTCAAAAA	ATGATGGGTG	ATGGATTTGC	1800
AGTAGAACCT	GCAAATGGAA	ACATTGTATC	TCCAGTTTCA	GGTACTGTGT	CAAGCATCTT	1860

1054

CCCAACAAAA	CATGCTTTTG	GTATTGTGAC	GGAAGCAGGT	CTTGAAGTAT	TGGTTCACAT	1920
TGGTTTGGAC	ACAGTAAGTC	TTGAAGGTAA	ACCATTTACA	GTTTCATGTTG	CTGAAGGACA	1980
AAAAGTTGCA	GCAGGAGATC	TCCTTGTCAC	AGCTGACTTG	GATGCTATCC	GTGCAGCAGG	2040
ACGTGAAACT	TCAACAGTAG	TTGTCTTCAC	AAATGGTGAT	GCAATTAAAT	CAGTTAAGTT	2100
AGAAAAACA	GGTTCTCTTG	CAGCTAAAAC	AGCAGTTGCT	AAAGTAGAAT	TGTAATATAC	2160
TTGAGGTTGG	AAGCTGTATT	CCAACCTCTT	ATTTTGGGAG	AAAAGAATGA	AATTTTAAAC	2220
ACTCAATACT	CACAGTTGGA	TGGAGAAAGA	AGCAGAGGAA	AAATTCCAGA	TTTTGCTTGA	2280
AGATATTCTT	GAAAAGGACT	ATGATTTGAT	TTGTTTTCAA	GAAATCAATC	AGGAGATGAC	2340
CTCGTCAGAG	GTGGAGGTTA	ATGACCTTTA	TCAAGCTTTG	CCAGCAGCTG	AGCCTATTCA	2400
CCAAGACCAT	TATGTTAGAC	TCTTGGTTGA	AAAGTTGTCT	GAGCAAGGGA	AAAATTACTA	2460
CTGGACCTGG	GCCTATAACC	ATATCGGCTA	TAACCGCTAC	CACGAAGGTG	TGGCTATCTT	2520
GTCTAAAACA	CCTATTGAAG	CCAGAGAAAT	TTTGTTTCA	GATGTGGATG	ATCCAACAGA	2580
CTATCATACT	CGCCGTGTTG	CCCTAGCTGA	AACTGTAGTC	GATGGCAAGG	AGCTAGCAGT	2640
TGCCAGTGTT	CATCTCTCTT	GGTGGGATAA	AGGTTTCCAA	GAAGAATGGG	CACGATTTGA	2700
GGCTGTCTTG	AAAAAATTGA	ACAAGCCACT	TTTACTAGCT	GGAGATTTCA	ACAATCCGGC	2760
TGGACAGGAA	GGTTACCAAG	CTATTTTAGC	TAGTCCATTA	GGCTTACAAG	ACGCATTTGA	2820
AGTTGCTCAA	GAGAAAAGTG	GTAGCTATAC	TGTTCCGCCT	GAAATTGATG	GCTGGAAAGG	2880
GAACACTGAA	CCCCTTCGAA	TGATTATGT	CTTTACTACC	AAAGAGTTAG	CGGTGGAAAA	2940
TTTACATGTC	GTATTTGATG	GTAACAAGAG	TCCACAAGTG	AGTGATCACT	ATGGCTTGAA	3000
TGCTATATTA	AACTGGAAAT	AATAACTGAA	AAGAGGTTGG	AACTATAAAA	TTCCAGCCTT	3060
TTCTTACTAG	AGAAGCTACT	GGAAATAGCC	TAAATAAGTG	AGACTACTGT	AATGGAATAA	3120
AATATGGTAT	AATTGATAAG	GTAGATAGAA	TCGAGGATGT	TATGTCATTT	ACGAAATTC	3180
AATTTAAAAA	CTATATTAGA	GAAGCCTTGA	AGGAGTTAAA	ATTTACAAC	CCAACAGAGG	3240
TGCAAGACAA	GTTGATTCCCT	ATTGTTTTGG	CAGGTCGTGA	CCTAGTAGGA	GAATCAAAAA	3300
CAGGTTCAGG	TAAGACTCAT	ACTTTCTTGT	TACCGATTTT	CCAGCAATTA	GATGAAGCTA	3360
GCGATAGTGT	ACAAGCAGTG	ATTACTGCAC	CGAGTCGTGA	GTTGGCTACT	CAAATTTACC	3420
AAGTAGCGCG	TCAGATTTCA	GCTCACTCAG	ATGTCGAAGT	TCGTGTGGTT	AATTATGTGG	3480
GTGGTACGGA	TAAGGCTCGC	CAGATTGAGA	AATTGGCAAG	CAATCAGCCT	CATATTGTTA	3540
TTGGAACACC	AGGCCGTATC	TACGACTTGG	TTAAATCTGG	TGATTTAGCT	ATTCATAAAG	3600
CCAAGACATT	TGTTGTTGAT	GAAGCAGATA	TGACCTTGGA	TATGGGATTC	TTGGAAACTG	3660

1055

TTGATAAGAT	TGCTGGCAGT	CTTCCAAAAG	ACTTGCAATT	CATGGTCTTC	TCAGCGACTA	3720
TCCCACAAAA	ACTGCAACCA	TTCTTGAAAA	AATACTTATC	AAATCCTGTT	ATGGAGAAAA	3780
TTAAGACCAA	AACGGTTATT	TCTGACACCA	TTGATAATTG	GTTGATTTTCG	ACCAAGGGAC	3840
ATGATAAGAA	TGCTCAAATT	TACCAGTTGA	CTCAGTTGAT	GCAGCCGTAT	TTGGCAATGA	3900
TTTTTGTTAA	CACTAAAACG	CGTGCTGATG	AATTGCATTC	ATATCTGACT	GCTCAAGGCT	3960
TGAAGGTTGC	AAAAATCCAT	GGCGATATTG	CCCCTCGTGA	ACGCAAGCGA	ATCATGAATC	4020
AGGTGCAAAA	TCTGGATTTT	GAGTATATTG	TCGCAACAGA	TTTGGCAGCG	CGTGGGATTG	4080
ACATTGAAGG	TGTCAGCCAT	GTCATCAATG	ATGCCATTCC	GCAAGACTTA	TCTTTTTTTTG	4140
TTCATCGTGT	TGGTCGTACT	GGACGAAATG	GCCTACCAGG	TACAGCTATT	ACCCTTTATC	4200
AGCCAAGTGA	TGACTCGGAT	ATCCGTGAGT	TGGAGAAATT	GGGAATCAAG	TTTAGTCCTA	4260
AGATGGTCAA	AGACGGGGAA	TTTCAAGATA	CCTATGACCG	TGATCGTCGT	GCCAACCGTG	4320
AGAAAAAACA	AGATAAACTT	GATATCGAAA	TGATTGGTTT	GGTTAAAAAG	AAAAAGAAAA	4380
AAGTCAAACC	GGGTTATAAG	AAGAAAATTC	AATGGGCGGT	TGATGAAAAG	CGCCGTAAAA	4440
CCAAGCGTGC	TGAAAAATCGC	GCTCGCGGTC	GTGCAGAGCG	TAAAGCTAAA	CGCCAAACAT	4500
TTTAATAGAA	ATTGTTGGAG	TATTGAGCTC	CAACTTTTTT	ATTTATGAGA	ACGAACTATC	4560
TAAACCGAAA	CACTACATTA	AAGACTGCAA	ATTGCGATTA	AAAATGGTAT	AATGATAAAG	4620
TTATATAGTC	CCGATAAGAT	GGTAGGTATT	TATTACGAAG	AGTTTTCCCTA	TCAGTACTTT	4680
GTAACTCTAT	AACAATATTT	TTTAAGGGGG	GACATTTTTTA	TGTCAGAGCG	TAAATTATTC	4740
ACGTCTGAAT	CTGTATCTGA	GGGGCATCCG	GATAAGATTG	CAGACCAAAT	TTCAGATGCG	4800
ATTTTGGATG	CTATTTTAGC	AAAGGATCCA	GAGGCGCACG	TTGCTGCTGA	AACAGCTGTA	4860
TATACTGGTT	CTGTCCACGT	TTTTGGTGAA	ATTTCTACAA	ATGCCTATGT	GGATATTAAC	4920
CGTGTGGTTC	GTGATACCAT	TGCAGAGATT	GGTTATACCA	ATACAGAATA	TGGATTTTCT	4980
GCTGAGACGG	TGGGAGTACA	CCCATCTTTG	GTGGAACAAT	CTCCTGACAT	CGCTCAAGGT	5040
GTTAACGAAG	CCTTGAGAGT	TCGTGGAAAT	GCTGATCAAG	ATCCACTGGA	CTTGATTGGA	5100
GCAGGTGACC	AAGGGCTCAT	GTTTGGAATT	GCAGTAGATG	AAACAGAAGA	GCTTATGCCA	5160
TTGCCAATTG	CACTCAGTCA	TAAATTGGTT	CGTCGTCTGG	CAGAACTTCG	TAAGTCTGGA	5220
GAAATTAGCT	ATCTCCGTCC	AGATGCAAAA	TCACAAGTTA	CAGTTGAGTA	CGATGAAAAT	5280
GACCGTCCGG	TACGTGTAGA	TACAGTCGTT	ATTTCTACTC	AGCATGATCC	AGAGGCCACT	5340
AATGAACAAA	TCCATCAAGA	TGTGATTGAC	AAGGTCATCA	AAGAAGTTAT	TCCATCTTCT	5400

1056

TATCTTGATG	ATAAGACAAA	ATTCTTTATC	AATCCGACAG	GTCGTTTTGT	AATCGGTGGT	5460
CCTCAAGGGG	ACTCAGGTTT	GACTGGTCGT	AAGATTATTG	TAGATACTTA	TGGTGGCTAC	5520
TCTCGTCATG	GTGGTGGTGC	CTTCTCTGGT	AAAGATGCGA	CTAAGGTGGA	TCGTTCAGCC	5580
TCTTATGCGG	CTCGCTATAT	TGCCAAGAAT	ATCGTTGCAG	CAGACCTTGC	TAAGAAGGCA	5640
GAAGTGCAGT	TGGCCTATGC	TATCGGTGTT	GCGCAACCTG	TTTCTGTTCG	TATCGATACT	5700
TTCCGTACAG	GAACAGTAGC	TGAAAGTCAA	CTTGAAAAAG	CGGCTCGTCA	AATCTTTGAC	5760
CTTCGCCCTG	CAGGGATTAT	CCAAATGCTG	GACCTCAAGC	GTCCAATTTA	CCGTCAAACA	5820
TCGGCTTACG	GTCACATGGG	ACGTACAGAT	ATTGATCTTC	CATGGGAACG	TTTGGATAAG	5880
GTAGATGCTT	TGAAAGAAGC	AGTAAAATAA	GATTTTAAGA	GGGGAACGTC	CTCTCTTTTT	5940
TATAGTTTTT	AACTATACTG	GGATACTGTT	CTGAAAATCC	ATTTTGCGAA	AGTAGAGATT	6000
TACATGTATA	GTAGATTGAA	ACTAGAATAG	TACACCTCAA	CTTCTAAAAC	ATTGTTAGCA	6060
ATCAATTTGA	CTGTCCTGAT	CGATTTCTCC	TGTTCTTGTT	TCATTTTACT	ATATTTCTTT	6120
AAAAATGATA	AAGGTTAAGA	TTTCTCCTCG	TAATAGATAA	TCTTGGGGAT	ATTTCAATCC	6180
AAAGTTTTAT	TCGTTATCAC	TTGACTATTG	CAAGGTTTTC	TAGAGCAACA	GAGTCATGGA	6240
ATGGACTCAT	GGTTGAGATT	TCTCCTTGTT	GCTTGGACTT	CATTCAAAAG	TCTGTTACCC	6300
AAGCCTTGTT	CAAACCTTCTA	ATACACTAGC	TGTTTCCATA	GCATGACTTC	TGTACTAGAC	6360
TTTCTTTTCC	GAATAAATAG	ATAGAACCAC	AGAATCTAGT	AAACCTAGAA	TTAAAATTAT	6420
GGTATAATAT	TAGCAATAAA	AGAAATCTGG	AGGATTAGAA	TCATGGTATC	AACGAAAACA	6480
CAAATTGCTG	GTTTTGAGTT	TGACAATTGC	TTGATGAATG	CAGCAGGTGT	GGCTTGATG	6540
ACGATAGAGG	AGTTAGAAGA	GGTCAAAAAC	TCAGCGGCAG	GAACCTTTGT	TACTAAGACA	6600
GCGACCTTGG	ACTTCCGTCA	GGGGAATCCT	GAGCCACGCT	ACCAAGATGT	TCCACTTGGT	6660
TCCATCAACT	CTATGGGCTT	GCCAAATAAT	GGCTTAGACT	ATTATTTGGA	TTATCTTTTA	6720
GATTTGCAGG	AAAAAGAGTC	GAACCGAACT	TTCTTCTTAT	CTCTGGTCGG	CATGTCTCCA	6780
GAGGAAACCC	ATACTATTTT	GAAAAAAGTC	CAAGAGAGTG	ATTTTCGTGG	TCTGACTGAG	6840
CTAAATCTTT	CCTGTCCAAA	TGTTCCAGGT	AAACCTCAGA	TTGCCTATGA	TTTTGAGACA	6900
ACAGACCGGA	TTTTGGCAGA	AGTGTTTGCT	TACTTCACCA	AACCTCTTGG	AATTAAATTG	6960
CCACCTTATT	TTGATATTGT	TCACTTTGAC	CAAGCGGCAG	CTATTTTCAA	CAAATATCCG	7020
CTCAAGTTTG	TCAACTGCGT	TAACTCTATC	GGAAACGGCC	TCTATATAGA	AGACGAATCT	7080
GTCGTTATTC	GGCCTAAGAA	TGGTTTTGGT	GGAATTGGTG	GAGAATACAT	CAAACCGACT	7140
GCTTTAGCCA	ATGTTACGCG	CTTTTATCAA	CGTTTAAATC	CTCAAATCCA	AATTATCGGA	7200

1057

ACAGGTGGCG TTCTGACTGG TCGAGATGCC TTTGAACACA TCCTCTGTGG AGCAAGTATG 7260
 GTGCAGGTGG GAACGACCCT TCACAAAGAA GGCGTCAGTG CTTTGTGACCG CATTACCAAT 7320
 GAACTGAAAG CAATCATGGT GGAAAAAGGC TACGAGAGCT TAGAAGATTT CCGTGGGAAA 7380
 TTGCGCTATA TTGACTAAAT TAAATCGAAA AATCTGAAGA AAGGAGAGAC GATGCTAGCC 7440
 ATTGAAGAAA GTCAGAAGTT GACTTTATCA AATTTACCGA GCCTGAGCCT ATTTACAGGG 7500
 ACAGATCAGG GTCAGTTTGA AGTGATGAAG AGTCAAATGT TGAAACAGAT TGGGTATGAT 7560
 TCTGCTGACC TCAACTTTGC CTACTTTGAT ATGAAAGAAG TAGTTTACAA GGATGTGGAA 7620
 CTGGAGTTGG TCAGCCTTCC TTTCTTTGCG GATGAGAAAA TCGTGATATT AGATTATTTT 7680
 ATGGATATCA CGACTGCTAA GAAACGCTTT TTGACAGATG ATGAGCTTAA GTCATTTGAG 7740
 GAATACCTTG ACAATCCTTC TCCAACAACC AAGTTGATAA TCTTTGCAGA AGGAAAGCTG 7800
 GATAGCAAAA GACGGTTAGT CAAATTACTT AAGCGTGATG CCAAGGCCTT CGATGCAGTA 7860
 GAAGTAAAAG AACAAGAATT GCGCCAGTAC TTCCAAAAGT GGAGTCAGAA ACAAGGTCTG 7920
 CAGTTTACCA ATCATTCTTT TGAAAATCTC CTCATCAAGT CGGGGTTTCA ATTTAGCGAA 7980
 ATCCAGAAAA ATCTTCTCTT TTTACAGTCC TATAAGGCGA ATTCTGTTAT TGAGGAAGAG 8040
 GATATTGTTA ACGCAATTCC CAAGACTTGC AGGACAATAT TTTTGATTTA ACTCAGTTTA 8100
 TTCTGACTAA AAAGATGGAT CAGGCGCGCG ATTTGGTGAG AGACTTGACC TTGCAAGGGG 8160
 AAGATGAAAT CAAACTGATT GCAGTCATGC TGGGACAATT TCGGACTTTT ACTCAGGTGA 8220
 AGATTTTGGC GGAGTCTGGC CAAACAGAAT CGCAGATTGC AAGTAGTTTA GGTAGTTATC 8280
 TGGGACGTAA CCCAAATCCT TATCAAATCA AGTTTGCATT AAGAGATTCG AGAGGACTTT 8340
 CTTTGAGCTT TTTGAAGCAA GCTATTTCCCT ATTTGATTGA GACAGACTAT CAGATTAAGA 8400
 CAGGTCTTTA TGAAAAAGGT TTCCTTTTGT AAAAGGCACT CTTACAGATT GCTAGTCAGG 8460
 TCAATTGACA TTTGTTGAAA CTACTAACCC GCGG 8494

(2) INFORMATION FOR SEQ ID NO: 164:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9707 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

CCGGTCAGTT CGTTCAGTAC AAGGAATCAT AATGAACGAT CAATCAGAAA AAAAGACTAG 60

1058						
AAAGAAGACT	GTATGGATAA	TCGACCAATT	GGTTTTTTTGG	ATTCGGGTGT	CGGGGGCTTG	120
ACCGTTGTGC	GCGAGCTCAT	GCGCCAGCTT	CCCCATGAAG	AAATCGTCTA	TATTGGAGAT	180
TCGGCGCGGG	CGCCCTATGG	CCCCCGTCCT	GCTGAGCAAA	TTCGTGAATA	TACTTGGCAG	240
CTGGTCAACT	TTCTCTTGAC	CAAGGATGTC	AAAATGATTG	TCATTGCTTG	TAACACTGCG	300
ACTGCGGTTCG	TCTGGGAAGA	AATCAAGGCT	CAACTAGATA	TTCCTGTCTT	GGGTGTAATT	360
TTGCCAGGAG	CTTCGGCAGC	CATCAAGTCC	AGTCAAGGTG	GGAAAATCGG	AGTGATTGGA	420
ACGCCCATGA	CGGTACAATC	AGACATATAC	CGTCAGAAAA	TCCATGATCT	GGATCCCGAC	480
TTACAGGTGG	AGAGCTTGGC	CTGTCCCAAG	TTTGCTCCCT	TGGTTGAGTC	AGGTGCCCTG	540
TCAACCAGTG	TTACCAAGAA	GGTGGTCTAT	GAAACCCTGC	GTCCCTTGGT	TGGAAAGGTG	600
GATAGCCTGA	TTTTGGGCTG	TACTCATTAT	CCACTCCTTC	GCCCTATTAT	CCAAAATGTG	660
ATGGGGCCAA	AGGTTTCAGCT	CATCGATAGT	GGGGCAGAGT	GCGTACGGGA	TATCTCAGTC	720
TTACTCAATT	ATTTTGAAAT	CAATCGTGGT	CGCGATGCTG	GACCACTCCA	TCACCGTTTT	780
TACACAACAG	CCAGTAGCCA	AAGTTTTGCA	CAAATTGGTG	AAGAATGGCT	GGAAAAAGAG	840
ATTCATGTGG	AGCATGTAGA	ATTATGACAA	ATAAAATTTA	TGAATATAAG	GATGACCAGG	900
ACTGGTATGT	TGGGTCTTAT	AGTATTTTTG	GTGGCGTTAA	CAGTTTGAGC	GACTATAAGA	960
CAGATTTTCC	TCTGTTTGAA	TTCTCCAAAA	TATTTGGAGA	TGAAGAGTAT	GGTTTCCCGC	1020
TTTCAGTTAC	TGTTTTACGC	TATGGTTCTA	TCTACCGTTT	GTTCTCCTTT	GTGGTAGACA	1080
TGCTTAATCA	AGAAATGGGA	CGAAACTTGG	AAGTTATTCA	ACGTCATGGG	GCCCTGCTCT	1140
TGGTTGAAAA	TGGGCAACTC	TTGTATGTAG	AATTGCCTAA	AGAAGGGGTC	AATGTTTCATG	1200
ATTTCTTTGA	GACAAGCAAG	GTCAGAGAAA	CCTTGTTGAT	TGCGACTCGT	AACGAAGGTA	1260
AAACCAAGGA	ATTCCGAGCT	ATCTTTGATA	AGTTAGGCTA	CGATGTGGAA	AATCTTAATG	1320
ACTACCCTGA	CCTGCCTGAA	GTAGCAGAAA	CAGGTATGAC	CTTTGAAGAA	AATGCCCCGC	1380
TTAAGGCAGA	AACCATTTCT	CAATTAACGG	GCAAGATGGT	TTTGGCAGAT	GATTCTGGTC	1440
TCAAAGTCGA	TGTCCTTGGT	GGCTTACCAG	GCGTCTGGTC	AGCTCGTTTC	GCAGGTGTGG	1500
GAGCAACTGA	CCGTGAAAAT	AATGCCAAAC	TCTTGACGCA	ATTGGCCATG	GTCTTTGAAC	1560
TCAAGGACCG	CTCGGCTCAG	TTCCACACAA	CCCTAGTCGT	AGCCAGCCCA	AATAAGGAAA	1620
GTTTAGTTGT	TGAAGCAGAC	TGGTCAGGTT	ATATTAACTT	TGAACCTAAG	GGTGAAAATG	1680
GCTTTGGCTA	TGATCCCCCTC	TTCCTTGTAG	GAGAAACAGG	TGAGTCATCA	GCTGAATTAA	1740
CCCTGGAAGA	AAAAAATAGT	CAATCTCACC	GTGCCTTAGC	CGTTAAGAAA	CTTTTGGAGG	1800
TATTTCCATC	ATGGCAAAGC	AAACCATCAT	TGTAATGAGC	GATTCCCATG	GCGATAGCTT	1860

1059

GATTGTGGAA	GAAGTCCGTG	ATCGCTATGT	GGGCAAAGTC	GATGCTGTTT	TTCATAACGG	1920
CGATTCTGAA	CTACGTCCGG	ATTCTCCACT	TTGGGAGGGC	ATCCGCGTTG	TTAAAGGGAA	1980
CATGGACTTC	TACGCCGGCT	ACCCAGAACG	TCTGGTGA CT	GAGCTTGGTT	CGACCAAGAT	2040
TATCCAAACT	CATGGTCACT	TGTTTGACAT	CAATTTCAAC	TTTCAAAAGT	TGGACTACTG	2100
GGCTCAGGAG	GAAGAGGCCG	CTATCTGCCT	CTATGGTCAC	TTGCATGTGC	CAAGTGCTTG	2160
GTTGGAAGGC	AAGATCCTCT	TTCTAAATCC	AGGTTCTATC	AGTCAACCAC	GAGGTACCAT	2220
CAGAGAATGT	CTCTATGCTC	GTGTGGAGAT	TGATGATAGT	TACTTCAAAG	TGGACTTTTT	2280
GACACGAGAT	CACGAGGTGT	ATCCAGGTTT	GTCCAAGGAG	TTTAGCCGAT	GATTGCCAAG	2340
GAGTTTGAGA	CTTTCTTGTT	GGGGCAGGAG	GAAACTTTTT	TGACCCCTGC	TAAAAATCTA	2400
GCTGTGTTGA	TTGATACCCA	CAATGCGGAT	CATGCGACCC	TCTTGCTCAG	TCAGATGACC	2460
TATACCCGTG	TTCCCGTTGT	GACAGATGAA	AAACAGTTTG	TTGGGACGAT	TGGACTCAGA	2520
GATATTATGG	CTTATCAGAT	GGAGCATGAC	TTGAGCCAAG	AAATCATGGC	GGATACGGAT	2580
ATCGTTCATA	TGACAAAAAC	GGACGTAGCG	GTTGTTTCGC	CTGATTTTAC	CATTACGGAG	2640
GTCTTGCACA	AGCTAGTAGA	TGAGTCCTTC	TTACCGGTTG	TGGATGCAGA	GGGTATTTTC	2700
CAAGGGATTA	TTACGCGCAA	GTCCATCCTC	AAGGCCGTTA	ATGCCCTCTT	GCATGACTTT	2760
AGTAAGGAAT	ATGAGATTCG	ATGCCAATGA	GAGACAGGAT	TTCAGCCTTT	TTAGAGGAAA	2820
AGCAGGGCTT	GTCTGTCAAT	TCCAAGCAGT	CCTATAAGTA	TGATTTGGAG	CAATTTT TAG	2880
ACATGGTAGG	TGAGCGGATT	TCTGAGACCA	GTCTCAAGAT	TTACCAAGCC	CAGCTAGCCA	2940
ATCTAAAAAT	CAGCGCCCAG	AAGCGAAAGA	TTTCGGCCTG	TAACCAATTT	CTATACTTTC	3000
TCTATCAAAA	AGGAGAGGTG	GACAGCTTTT	ACCGCTTGGA	ATTAGCCAAA	CAAGCTGAAA	3060
AGAAGACGGA	AAAGCCAGAG	ATTCTATACC	TAGACTCTTT	TTGGCAGGAA	AGCGACCATC	3120
CAGAGGGCCG	CTTGCTAGCG	CTCTTAATCC	TAGAAATGGG	GCTCTTGCCC	AGTGAGATTT	3180
TAGCCATCAA	GGTTGCGGAC	ATCAATCTGG	ATTTTCAGGT	GTTGCGAATC	AGCAAGGCTT	3240
CCCAACAGAG	GATTGTCACC	ATTCCCACGG	CCTTGCTTTC	AGAATTGGAA	CCCTTGATGG	3300
GGCAGACCTA	TCTTTT TGAA	AGAGGAGAGA	AACCCTATTC	TCGTCAGTGG	GCCTTTCGTC	3360
AGTTAGAATC	TTTTGTCAAG	GAGAAAGGTT	TTCCATCCTT	ATCAGCTCAA	GTCTTACGTG	3420
AACAGTTTAT	TCTAAGACAA	ATAGAAAACA	AGGTCGATTT	GTACGAAATT	GCAAAAAAAT	3480
TAGGATTAAA	AACAGTCCTG	ACCTTAGAAA	AATATAGATA	ATGGATATTA	AATTAAAAGA	3540
TTTTGAAGGA	CCCCTGGACT	TGCTCTTGCA	TCTGGTTTCT	AAGTACCAGA	TGGATATCTA	3600

1060

CGATGTGCCC	ATTACGGAAG	TCATCGAACA	GTATCTAGCC	TATGTCTCAA	CCCTGCAGGC	3660
CATGCGTCTG	GAAGTGACGG	GTGAGTACAT	GGTCATGGCT	AGTCAGCTCA	TGCTGATTAA	3720
GAGTCGTAAA	CTCCTTCCGA	AGGTAGCAGA	AGTGACAGAC	TTGGGGGATG	ACCTGGAGCA	3780
GGACCTCCTC	TCTCAAATCG	AAGAATATCG	CAAGTTCAAG	CTCTTGGGTG	AGCACTTGGA	3840
AGCCAAGCAC	CAAGAACGGG	CCCAGTATTA	TTCCAAAGCG	CCGACAGAGT	TGATTTACGA	3900
AGATGCGGAG	CTTGTGCATG	ACAAGACGAC	CATTGACCTC	TTTTTGTACTT	TTTCAAATAT	3960
CCTAGCCAAG	AAAAAAGAGG	AGTTTGCACA	AAATCACACG	ACGATCTTGC	GGGATGAGTA	4020
TAAGATTGAG	GACATGATGA	TTATCGTGAA	AGAGTCCTTG	ATTGGACGAG	ATCAATTGCG	4080
CTTGCAGGAT	TTGTTCAAGG	AAGCCCAGAA	TGTCCAAGAG	GTCATCACCC	TCTTTTGGC	4140
AACCCTAGAG	TTAATCAAAA	CCCAGGAGTT	GATCCTCGTG	CAAGAGGAGA	GTTTTGGAGA	4200
TATCTATCTC	ATGGAAAAGA	AGGAAGAAAG	TCAAGTGCCT	CAAAGCTAGA	CTTGATAGAG	4260
AGGAAAGATG	AGTACTTTAG	CAAAAATAGA	AGCGCTCTTG	TTTGTAGCGG	GTGAAGATGG	4320
GATTCGGGTC	CGCCAGTTAG	CTGAACTCCT	CTCTCTGCCA	CCGACAGGCA	TCCAGCAAAG	4380
TTTAGGAAAA	TTAGCCCAGA	AGTATGAAAA	GGACCCAGAT	TCCAGTTTGG	CTTTGATTGA	4440
GACAAGTGGT	GCTTATAGAT	TGGTGACCAA	GCCTCAATTT	GCAGAGATTT	TGAAGGAATA	4500
CTCTAAGGCG	CCTATCAACC	AGAGCTTGTC	TCGGGCTGCC	CTTGAGACCT	TGTCCATTAT	4560
TGCCTACAAA	CAGCCGATTA	CGCGGATAGA	AATTGATGCC	ATCCGTGGAG	TTAACTCGAG	4620
TGGAGCCTTG	GCAAAGTTGC	AGGCTTTTGA	CCTGATAAAG	GAAGACGGGA	AAAAGGAAGT	4680
ATTGGGGCGC	CCCAACCTCT	ATGTGACTAC	GGATTATTTT	CTAGATTACA	TGGGGATAAA	4740
CCATTTAGAA	GAATTACCAG	TGATTGATGA	GCTTGAGATT	CAAGCCCAAG	AAAGCCAATT	4800
ATTTGGTGAA	AGGATAGAAG	AAGATGAGAA	TCAATAAGTA	TATTGCCCAC	GCAGGTGTGG	4860
CCAGTAGGAG	AAAAGCAGAA	GAGCTGATTA	AGCAAGGCTT	GGTGACGGTT	AACGGCCAAG	4920
TGGTGCGTGA	ACTAGCAACC	ACTATCAAGT	CAGGCGACAA	GGTCGAAGTT	GAAGGTCAAC	4980
CTATCTACAA	CGAAGAAAAG	GTCTACTATC	TGCTTAACAA	ACCACGCGGT	GTGATTTCCA	5040
GTGTGACAGA	TGATAAGGGT	CGCAAGACGG	TTGTGACCTT	CTTGCCCAAT	GTCAAAGAGC	5100
GTATTTACCC	TGTGGGTCGT	TTGGACTGGG	ATACATCAGG	TGTCTTGATT	TTGACCAATG	5160
ATGGGGACTT	TACAGACGAG	ATGATTCACC	CTCGTAATGA	GATTGACAAG	GTTTATGTCTG	5220
CGCGTGTTAA	AGGTGTGGCC	AATAAGGACA	ATCTCCGCCC	CTTGACCCGT	GGTCTTGAGA	5280
TTGATGGTAA	GAAAACCAAG	CCAGCTGTTT	ATGAAATTCT	CAAAGTGGAC	CCAGTCAAAA	5340
ATCGCTCTGT	GGTGCAGTTG	ACCATCCATG	AAGGGCGTAA	CCATCAGGTT	AAAAAGATGT	5400

1061

TTGAAGCTGT	TGGTCTCCAA	GTAGATAAGT	TGTCTCGGAC	TCGTTTCGGA	CACCTAGACT	5460
TGACAGGACT	CCGTCCAGGA	GAATCCCGTC	GTCTTAATAA	AAAAGAAATC	AGCCAACACTAC	5520
ACACCATGGC	TGTAACATAAG	AAATAATGAA	ACGAATTTTA	ATAGCGCCTG	TGCGCTTTTA	5580
CCAACGTTTT	ATCTCACCAG	TCTTTCACC	CTCTTGTCGC	TTTGAGCTGA	CTTGTTCCAA	5640
CTACATGATT	CAGGCTATTG	AAAAACATGG	GTTTAAGGGG	GTATTGATGG	GCTTGGCTCG	5700
GATTTTACGT	TGTCATCCCT	GGTCGAAAAC	AGGTAAGGAC	CCCGTTCCAG	ACCGCTTTTC	5760
CCTTAAACGA	AATCAAGAAG	GGGAATGAGG	TGGGGTAAAT	AGATTTCAAA	ATGATAAAAA	5820
CGCATCCTAT	CAGGTTTGAG	TGAACTTGAT	AGGATGCGTT	TTAGAATGTC	AAAATTTTAT	5880
ACTCTTCGAA	AATCTCTTCA	AACCGCGTCA	GCTTTCATCT	GCAACCTCAA	AACAGTGTTT	5940
TGAGCAACCT	GCGGCTAGTT	TCCTAGTTTG	CTCTTTGATT	TTCATTGAGT	ATTAAATTGA	6000
GTTTGAAGTG	GCTTATTTCA	AAGCTTTTTG	TATGTCTTCA	ATCATGAGTT	TTGTTGATTC	6060
AAGTCCGCCT	CCGCTTAGAT	ACCAGAGGTC	TGGTGTTAGT	TGGATAATCT	TACCATTTTT	6120
AGCAGCAGGT	GTTTCAGCGA	TAAGGGCATT	TTCTAGGACA	CCGTCGTTGC	TAGAGTTGTC	6180
CCCACCGATG	GCAAGGGTAC	GGTTGATGAC	AAAGAGGATG	TCAGGGTTGA	TTTCTTTGAC	6240
ACTTTCAAAG	CTGACTTCTT	GTCCGTGGCG	TGAGTCTTCA	AATTTTGTAT	CAGTTGGTTT	6300
GAATTTCAAG	GTTTGGTACA	AGAAAGAGAA	ACGAGATTTG	GCACCAAAGG	CTGCCATTTT	6360
TCCTTCATTA	AGGAGGATCG	CAAGGGCTTT	TTTGTCTAGAG	CTTTCATTTT	TAGTAGCGAC	6420
TTCTTGATG	CTCTTGCTTA	GCTTGGTCAA	TTCTTCCTTG	GCTTTCCTGTG	TACCAGTTTC	6480
GCCGAAGGCA	CTTGCTAAGG	ATTTCGATATT	AGCCTTGCTA	GAAGTCCAGT	AGTCGTCCTT	6540
GCTTGCTTGG	AAGAGAACGG	TTGGGGCGAT	TTCTTTGAAT	TTGTCTACGA	ATTTTTGTGT	6600
ACGTGGCGAA	GCGATAATCA	AATCAGGCTC	AAGGGCGGCG	ATAGCTTCTA	AATCAGGTTC	6660
TTTCATAGAA	CCAACATTTT	TGACAGTTCC	CACTAGGTCT	TTTAGATAAG	TCGGAACAGT	6720
TTTTGTAGGC	ATTCCGACGA	TATTTTTTTC	AAATCCTAAA	GCGCGAATAG	TATCCGCAGC	6780
GCCGAGGTCA	AAGGTCACAA	TCTTTTCAGG	AACTTTGGA	AGTTTGACCT	CGTCCAGTGA	6840
ACTTTTAATG	GTTACCTCTG	TTGGAGCAGA	GCTACTGGTC	TCTGTCTGAC	TAGTGCTTGA	6900
GTTTGTACTA	CATGCACCAA	GTAGGAGCAA	GAAGCTGGCC	ACTAGGGCAG	TGAAATAAAG	6960
TTTAAGGGAT	GTTTTTCATA	TTTCTCCTTT	TTAAAATGTG	ATAACGATTT	AGGGAGTCTC	7020
TTAATCTTAT	TGACTAAGAG	ACTGAAGGTT	CTCTAACTTG	AGCTTTTATG	TTACTAGCTA	7080
TAGATACAGA	TCTTTTGTG	ATTGATATCA	GCTAGCGTGA	TGGGAATCTC	ATAAAGTTGA	7140

1062

CTGAGCAGGT	CAGCCTGCAT	GATTTGATCG	GTTCTTCCCT	TGCTAAAGAC	CTGGCCGTCC	7200
TTGAAGGCGA	CAATTTTCATC	TGCATACTGA	CTGGCCATGT	TGATATCGTG	GAGGACGATG	7260
ATAATGGTCT	TGCCGAGTTC	CTCCACCAGT	CGTCGAAGAA	TCTGCATCAT	GCTGACGCTT	7320
TGCTTGATAT	CGAGATTGTT	GAGTGGTTCG	TCCAGCAAGA	TAAAGTCCGT	ATCCTGGGCC	7380
AGTACCATAG	CGATAAAGAC	GCGCTGGAGT	TGCCCCCTG	ACAGGCTATT	GATGTAGCGG	7440
TCTTTTAAAGT	TGGTCAGTTC	TAAATAGTTC	AGAGTTTCTC	GGATTTTTTC	CCAGTCTTCT	7500
GATCTAAGTC	GACCTCGGCT	GTAGGGAAAA	CGTCCAAAAC	TGACCAGTTC	TTCAACAGTC	7560
AATTTGGCTT	GGTAATTGAT	TTTCTGTTTT	AGGATGGTTA	GTTCTTGGGC	CAGTTCTTGC	7620
GAATTCACG	TCTCGATTTC	ACGTCCTTTG	ATACTGAGAA	CTCCCTGATC	TTTCTTGGTT	7680
AGCCTGCTCA	TGATGGAGAG	GAGAGTCGAT	TTTCCAGCAC	CATTTGGACC	AATAAAGGCT	7740
GTCAGTTTTT	GAGGACTGAC	TTCAAGCGAA	ATGCCTTGCA	AAATATCCTG	TTTTTGAATG	7800
GATTTGTCAA	TGTTTTCCAG	TTTCACTGAC	GAGACCTCCT	ATATAGTAAG	ATAAAGAATA	7860
AGAAGCCACC	CACACTCTCA	ATGATCATAC	TGATACGAAT	TTCCAGTGCA	AAGACTCGTT	7920
CAATCAAGGC	TTGCCCCAAG	GTTAAGCTAA	TAAATCCAAC	CAGAATGGCC	ACTATAAAGA	7980
GTAACCTGTG	CTGATAGTCT	TTGACAATCA	GGTAGGTGAG	GTTGGCCAGT	ATAAAGCCGA	8040
AGAAGGCCAT	AGGTCCTACC	AAGGCAGTGG	CCGTTGAGGT	CAAAAGCACG	ATTCCCCAGA	8100
GGAGCTCTTT	CTGTTCTTTT	TCAACATCGA	GTCCCAATAT	CTGAGCCGTT	TCTCTTTGCA	8160
GGTGCAAGAC	ATCTAGAACG	ACTGCTTTTC	GAAAGAAAAA	GATTGTCAAA	GCGAGGATGA	8220
TCAGAGAACC	GATGGCTAGG	ATGGAAGTGT	TGAGATGTTG	AAAGGAGGCA	AAAAGACTAT	8280
TTTGCAGTTT	ATCGTATTCG	TTTGGATCCA	TTAGGACTTG	AAGGAAGGTG	CTGATATTTT	8340
GAAAGAGACT	TCTGAGCGCT	AGACAGATCA	GCAGGACGAA	GACCAGGTCT	TGCTTCATCA	8400
GTGTCTTCAA	GTAACCTTGT	AAGGCGAGAA	AGAAGAGGGA	CTGGACAAGA	AGTAAGACTA	8460
GGAATTCTAA	GATAGGGGAT	TTGCCAAGTT	GAAGAACTT	GCTTTCAAAA	ACCAGTAGTA	8520
GGGTTTGTAG	TAGGACGTAG	AAGGATTCAA	TTCCCAAAAT	ACTAGGCGTC	AGGAAGCGAT	8580
TTTCCGTCAG	GGTTTGAAAA	CTAATGGTCG	AAATCCCAGT	CGCGATGGCT	ACCAAGAGAT	8640
AAACGATGAT	CTTTTGGGAA	CGCAACTTCC	AAGCAAAGGC	TGACAAGTGA	GTGATGGGCC	8700
AAAAGTAGAG	AAGACAAGCT	CCGATGGCAA	GAATAATGAG	AATCCAGAAG	AGCTTGGTAT	8760
GTTTGCTTTT	AGTCTGCATC	TTTTCGTCCC	CCTCTCCAGA	GAAGTAGGAT	AAAGACGAGA	8820
CTACCGATGA	TTCCTAGCAA	GAGACTGACA	GACAACTCAT	AGGGCCTAAT	CAGAACTCGG	8880
GATAGGATAT	CGCAAGCCAG	AACTAGATTG	GCACCAACCA	GTGCGACCAT	GAGTTTGGTT	8940

1063

TGACTTAGAT TATCTCCATA GCGCTTGCGA ACAAGATTGG GAACGATAAC TCCGAGAAAT	9000
GGTAGGCCAC CCACGGTAAT CATGGTGACG CTTGTCGTTA GCGCCACCAG AAAGAGGGCC	9060
AGTTTTTCAA GTAGGGAGTA GGAAATCCCC AACTCTCGC TGGTTTCTTT CCCTAGATTC	9120
ATGATGGTGA AGGTTTGGA TAATTTCCAA ACGGTTATCA GGATGATGAG GCCTAAGAAG	9180
AGCCACTCAT ACTGATGGGT CTGAATCATG GAGAAGGAGC CCTGGGTCCA GGCAGTCATA	9240
CTCTGAACCA GATTGAAACG ATAGGCGATA ACTTCTGTGA CTGAGCCGAT AATCCCGCTA	9300
TAGATGATCC CAATCAGAGG CAACATCCAC CTTTCCTTTA CAGTAAAAAT GGTCATAAAG	9360
GCTAGGAAGA AGAGGGTGAA TACGATGGAT GAAACAAAAG CGAAGAGCAT CTTGTGGGTC	9420
AGACTAGCCG ATGGAAAGAC AAAAAGGCTC AGCACCATTC CCAGTTTGGC GGCTTCAGTC	9480
GTTCCAACCTG TACTCGGTGC AGCAAACCTGA TTTTGGGTAA TAGTCTGCAT GAGAAGGCCT	9540
GCCATACTCA TACTAGAGGC AGTCAGGAGA ATACTGATAG TTCTTGGGAG ACGGGACTCT	9600
TGAAAGAGGA GCCAGGTCTG CTGGTCGAAA TCAAATAGCT TTCCCATGA AAAATCACTG	9660
GTCCCAATGC TAATAGAGAG AAAGACTAGG AGTAGAAGTA AGCCAGG	9707

(2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5910 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

CCGCAATTAT GCTTGAAAAG GAGTATACTT ATAAGTAACG CAAACGTTTG CGTCTGAAAA	60
ATACGCAACG TTCCATTATT TTAACACACG AGGTGCTATT ATGAAAAAAC GTCAAAGTGG	120
TGTGTTGATG CACATCTCTT CTCTTCCAGG AGCTTACGGA ATCGGATCAT TTGGTCAAAG	180
TGCTTACGAC TTCGTTGATT TCTTGGTCCG TACAAAACAA CGTTACTGGC AAATCCTTCC	240
ATTAGGAGCA ACTAGTTACG GGGATTCTCC TTACCAATCT TTCTCAGCCT TCGCAGGAAA	300
CACTCATTTT ATCGATTTAG ATATCTTGGT GGAGCAAGGT TTGTTGGAAG CAAGTGACCT	360
TGAAGGAGTT GACTTTGGTA GCGATGCGTC TGAAGTTGAC TATGCTAAAA TCTACTATGC	420
ACGTCGTCCT CTTTGTAGAAA AAGCGGTGAA ACGTTTCTTT GAAGTCGGAG ATGTTAAAGA	480
TTTGTAGAAA TTTGCTCAAG ACAACCAATC ATGGCTTGAG CTCTTTGCTG AGTATATGGC	540
TATCAAAGAG TATTTTGACA ATCTTGCTTG GACTGAATGG CCAGATGCAG ATGCTCGTGC	600

1064

TCGTAAAGCT	TCAGCACTTG	AAAGCTATCG	TGAGCAATTG	GCAGACAAGT	TGGTTTACCA	660
CCGTGTGACT	CAATACTTCT	TCTTCCAACA	ATGGTTGAAA	TTGAAAGCTT	ACGCTAACGA	720
CAACCACATC	GAAATCGTTG	GGGACATGCC	AATCTACGTA	GCGGAAGATT	CAAGTGATAT	780
GTGGGCAAAT	CCACATCTCT	TCAAAACAGA	TGTCAATGGT	AAGGCTACTT	GTATCGCAGG	840
ATGCCCCACCA	GATGAGTTTT	CTGTAACTGG	TCAGCTTTGG	GGTAATCCAA	TCTATGACTG	900
GGAAGCAATG	GACAAAGACG	GCTACAAATG	GTGGATTGAA	CGCTTGCGTG	AAAGCTTCAA	960
AATCTACGAT	ATCGTTCGTA	TCGACCACTT	CCGTGGCTTC	GAATCTTACT	GGGAAATCCC	1020
TGCTGGTTCC	GATACAGCAG	CACCTGGTGA	GTGGGTGAAA	GGTCCAGGTT	ACAAGCTTTT	1080
TGCAGCCGTT	AAGGAAGAAC	TTGGTGAGCT	AAACATCATC	GCAGAAGACC	TTGGCTTCAT	1140
GACAGATGAA	GTGATCGAAT	TGCGTGAACG	TACTGGCTTC	CCAGGAATGA	AGATTCTTCA	1200
ATTTGCCTTC	AACCCAGAAG	ACGAAAGCAT	TGATAGCCCA	CACTTGGCAC	CTGCTAACTC	1260
AGTTATGTAC	ACAGGAACAC	ACGATAACAA	TACGGTTCCT	GGTTGGTACC	GTAATGAGAT	1320
TGATGATGCG	ACTCGTGAGT	ACATGGCTCG	TTACACGAAC	CGTAAAGAAT	ACGAAACAGT	1380
GGTACACGCT	ATGCTTCGTA	CAGTATTTTC	ATCAGTTAGC	TTTATGGCAA	TTGCAACTAT	1440
GCAAGATTTA	CTAGAATTGG	ATGAGGCAGC	TCGTATGAAC	TTCCCATCTA	CCCTTGGTGG	1500
AAACTGGTCT	TGGCGTATGA	CTGAAGATCA	ATTGACACCA	GCTGTGAGG	AAGGTTTGCT	1560
TGACTTGACA	ACAATTTATC	GCCGAATTAA	TGAAAATTTG	GTAGATTTAA	AGAAATAAGA	1620
CAATAATCAG	GAGACAACCTA	AACATGTTAT	CACTACAAGA	ATTTGTACAA	AATCGTTACA	1680
ATAAAACCAT	TGCAGAATGT	AGCAATGAAG	AGCTTTACCT	TGCTCTTCTT	AACTACAGCA	1740
AGCTTGCAAG	CAGCCAAAAA	CCAGTCAACA	CTGGTAAGAA	AAAAGTTTAC	TACATCTCAG	1800
CTGAGTTCCT	GATTGGTAAA	CTCTTGTCAA	ACAACTTGAT	TAACCTTGGT	CTTTACGACG	1860
ATGTTAAAAA	AGAACTTGCA	GCTGCAGGTA	AAGACTTGAT	CGAAGTTGAA	GAAGTTGAAT	1920
TGGAACCATC	TCTTGGTAAT	GGTGGTTTGG	GACGTTTGGC	TGCCTGCTTT	ATCGACTCAA	1980
TTGCTACTCT	TGGTTTGAAT	GGTGACGGTG	TTGGTCTTAA	CTACCACTTT	GGTCTTTTCC	2040
AACAAGTTCT	TAAAAACAAC	CAACAAGAAA	CAATTCCAAA	TGCATGGTTG	ACAGAGCAAA	2100
ACTGGTTGGT	TCGCTCAAGC	CGTAGCTACC	AAGTACCATT	TGCAGACTTT	ACTTTGACAT	2160
CAACTCTTTA	CGATATTGAT	GTTACTGGTT	ATGAAACAGC	GAATAAAAAC	CGCTTGCGTT	2220
TGTTTGACTT	GGATTCAGTT	GATTCTTCTA	TTATTAAAGA	TGGTATCAAC	TTTGACAAGA	2280
CAGATATCGC	TCGCAACTTA	ACTCTCTTCC	TTTACCCAGA	TGATAGTGAC	CGTCAAGGTG	2340
AATTGCTCCG	TATCTTCCAA	CAATACTTCA	TGGTTTCAAA	CGGTGCGCAA	TTGATCATCG	2400

1065

ACGAAGCAAT	CGAAAAAGGA	AGCAACTTGC	ATGACCTTGC	TGACTACGCA	GTTGTCCAAA	2460
TCAACGATAC	TCACCCATCA	ATGGTGATTC	CTGAATTGAT	TCGTCTTTTG	ACTGCACGTG	2520
GTATCGATCT	TGACGAAGCA	ATCTCAATTG	TTCGTAGCAT	GACTGCCTAC	ACTAACCACA	2580
CAATCCTTGC	TGAAGCGCTT	GAAAAATGGC	CTCTTGAATT	CTTGCAAGAA	GTGGTTCCTC	2640
ACTTGGTACC	AATCATCGAA	GAATTGGACC	GTCGTGTGAA	GGCAGAGTAC	AAAGATCCAG	2700
CTGTTCAAAT	CATCGATGAG	AGCGGACGTG	TTCACATGGC	TCACATGGAT	ATCCACTACG	2760
GATACAGTGT	TAACGGGGTT	GCAGCACTCC	ATACTGAAAT	CTTGAAAAAT	TCTGAGTTGA	2820
AAGCCTTCTA	CGACCTTTAC	CCAGAAAAGT	TCAACAACAA	AACAAACGGT	ATCACTTTCC	2880
GTCGTTGGCT	TATGCATGCT	AACCCAAGAT	TGTCTCACTA	CTTGGATGAG	ATTCTTGGAG	2940
ATGGTTGGCA	CCATGAAGCA	GATGAGCTTG	AAAAACTTTT	GTCTTATGAA	GACAAAGCAG	3000
TTGTCAAAGA	AAAATTGGAA	AGCATCAAGG	CTCACAACAA	ACGTAAATTG	GCTCGTCACT	3060
TGAAAGAACA	CCAAGGTGTG	GAAATCAATC	CAAATTCTAT	CTTTGATATC	CAAATCAAAC	3120
GTCTTCACGA	GTACAAACGC	CAACAAATGA	ACGCTTTGTA	CGTGATCCAC	AAATACCTTG	3180
ACATCAAAGC	TGGTAACATC	CCTGCTCGTC	CAATCACAAT	CTTCTTTGGT	GGTAAAGCAG	3240
CTCCAGCCTA	CACAATCGCT	CAAGACATTA	TCCATTTAAT	CCTTTGCATG	TCAGAAGTTA	3300
TTGCTAACGA	TCCAGCAGTA	GCTCCACACT	TGCAAGTAGT	TATGGTTGAA	AACTACAACG	3360
TTACTGCAGC	AAGTTTCCTT	ATCCCAGCAT	GTGATATCTC	AGAACAAATC	TCACTTGCTT	3420
CTAAAGAAGC	TTCAGGTACT	GGTAACATGA	AATTCATGTT	GAACGGAGCT	TTGACACTTG	3480
GTACTATGGA	CGGTGCTAAC	GTGGAAATCG	CTGAGTTGGT	TGGAGAAGAA	AACATCTACA	3540
TCTTCGGTGA	AGATTCAAGAA	ACTGTTATCG	ACCTTTACGC	AAAAGCAGCT	TACAAATCAA	3600
GCGAATTCTA	CGCTCGTGAA	GCTATCAAAC	CATTGGTTGA	CTTCATCGTT	AGTGATGCAG	3660
TTCTTGCAGC	TGGAAACAAA	GAGCGCTTGG	AACGTTTTTA	CAATGAATTG	ATCAACAAAG	3720
ACTGGTTCAT	GACTCTTCTT	GATTTGGAAG	ACTACATCAA	AGTCAAAGAG	CAAATGCTTG	3780
CTGACTACGA	AGACCGTGAC	GCATGGTTGG	ATAAAGTCAT	CGTTAACATT	TCTAAAGCAG	3840
GATTCTTCTC	ATCTGACCGT	ACAATCGCTC	AGTATAACGA	AGACATCTGG	CACTTGAACT	3900
AATACTCTTC	GAAAATCTCT	TCAAACCACG	TCAGCTTTAT	CTGCAACCTC	AAAGCAGTGC	3960
TTTGAGCAAC	TGCGGCTAGC	TTCCTAGTTT	GCTCTTTGAT	TTTCATTGAG	TATAAGATAC	4020
AAATTTATAC	TAATACATTT	TGTAAAAAAG	CGAGTTTCGA	TTGAAATTCG	CTTTTTTAAT	4080
GATGTAGATT	TGGGTCAATC	TTGTCTAAAA	ATAGGGAAAT	CCTAGATACA	GTGAAGGCTT	4140

1066

TAAATGCTGG	TTTTTACTGT	CCTCAGCCTT	ATATTTTTTTC	GTAGTTGGTT	ACCTCATATC	4200
TATTATATTC	GCTTACATAA	AGTATTATAA	TATAATTGTA	GGAAAGAAGG	TGTTTTTATG	4260
ATATACACAC	TTAAATTGGT	GTTGTTTATT	ACCTTTCTTG	TAATAAGCTT	GTTACCTGAT	4320
AAGATTTTTG	GAAAAAATAA	AAAAATTGG	AAAATAGTTT	TTGCAATATT	GACGGCAGTG	4380
GCAGCATTGT	CATTTATGTA	CTAAGTTATT	TTAAGAATGT	AGGGAAATAA	ACCCTACATT	4440
CTTTTTAGTT	TTTTCTGTTT	TCTAAATTCT	ATTTATCCAA	GCGATTCAAC	ATTTCTTGCT	4500
TCTTCGCTTC	AAGTTCTGCA	CGCTTTTCTT	CGATTTCTGC	ATGTTTTTTC	TCGAGTTCAG	4560
AACAACTTGC	ACCATTGCTA	AATTCTTTTC	GCCATCAGGA	GATAGGGTGA	GTCGACATGT	4620
CTATTACTCA	CCCAAAGCAG	TCCTACAAAG	CAGGAATTTT	CTGTTACTTT	TTTGGAATA	4680
GTAACGTTTA	TACAGCTTTG	ACACTTCGTA	TCAAAGCGCC	AAACACACTC	CGAGGGGTTT	4740
ACAGAAAGCA	GAAAAGGAAT	GATCTGGTAT	AAGATCATTC	CTTTTCyCTC	TTTTTCTTTA	4800
AGTAATTATA	TACAATGTAC	GACGAAGTCG	TCATTGCAAT	GCTGATCCAC	CACCTAAAGG	4860
GAACTTTAAA	CAACATTGAT	AAGATAAAGA	ATATAAACAA	CGAAAATACG	TTATACCCAA	4920
TTAATTTTAT	TGTATATCTC	ATGATTAAAA	GTAAATCCTT	CCGTTGTTAG	GAATGGCATC	4980
ATTTTTATCC	CATAATTGTG	CTAAATAAGT	CCCCGGTGAT	AATAAATTCA	TAGCGAATTC	5040
TAAAGCAACA	TCATTTACAA	ACCAACTACC	TAGATATCTA	GAAATTGCTG	AACGAATAGC	5100
ACTTTTTGCT	GCATGTTTTT	CTTTTACTTT	AATTAGATTT	GCAAGGCCTG	CAGTAGTTCC	5160
TCCTAATGCT	AAAGCTATTG	CAGTATCTAA	TAGAGCACCC	ATTTGATTAA	CTGTAATACC	5220
TTGCCAAACT	GCTCTAAATG	GAGAGTATGT	AGGTGGGATT	GTATAATCGC	CTTGTAATTG	5280
TCGGTTAATT	ACTTCTTTGA	TCCATTGTTG	TGAGACGTCT	GGATGAAAAG	ATTGGATTTC	5340
GTTTGCAAGT	GTATTGATTT	GTTCTTCTGT	TAGAGAAAGT	ACAGGTTGAA	GTTCCATATT	5400
TGTTTCAATT	TGTGATACTT	GTTCAGAAGC	GTATACAGCT	GAAACACTTG	GAATCGCTGA	5460
TACAATTAAC	ACAATTGACG	TCAAAAAAAC	CGAAATAAAT	TTCATTAATT	TGTTTCATGAG	5520
CTTTTCTCCT	TTTTATTTGC	ATCTGCTTAC	ATTTTATCAT	ATACTGTTAT	TATAGTCAAA	5580
AAAATATGCT	ATTATGTTAA	AAAAATATTT	TTCAAAATAT	AAATGGACGG	ATTTATTTTG	5640
GATTTTATTT	GTTATTTTGA	CCTGCCTCTA	TATTGGTAAC	CATGATTTGT	TTACTCTCAA	5700
TCATCAAGAA	TTCTCTTTTC	GTGGTAGCGT	TTGGGGTCTG	GTACTGGCCT	TATATCACTT	5760
ACTATTCATT	GATAAGTTTG	TTATATCGAA	TCGAAAATAA	AGATTAGAGC	TATGCTTGAC	5820
TGTGTACTTT	TAGGATTTAT	TTTGGAGGAA	GATTTTGTCT	CTATTATTTA	TTATTTTAAA	5880
TTTATTTATT	TTGTATAAGA	TCTATTCTTT				5910

1067

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

GGCATAGCGA CTCATTTTTT CAACTGTCCA GGCTGGATAC CAGACTAATT TAACCTCAGT	60
ATCCGTTACT TCTGGAACCT CTATCATAGC ATCATAAATC TGGTCTGTCA AAAGGTCTGC	120
TAAGGGACAA CCCATAGTTG TCAAAGTCAT GTCAATCTCT GTTTGCCCTG TGTCACCGTC	180
AAAACGAATC TCATAGATCA AACCAAGATT GACAATATCG ATTCCCAACT CAGGGTCGAT	240
GACTTCTTCC AAGGCTGTTA AAATCCGTGT TTTGATGTTT TCAATTTGCT CTTCTGTATA	300
AGCCATATTT TCCTCACTCT TAGTCTTCAA TAAAATCACG AAGCGGTTTG CTACGACTTG	360
GTTGGCGTAG TTTTCTCAA GCCTTTGCTT CAATCTGACG GATACGCTCA CGAGTTACGT	420
TAAAGACTTT CCCCACATCT TCAAGTGTGC GCATTTTTTCC ATCATCTAGT CCAAACGTA	480
GACGCAGAAC ATTTTCTTCA CGGTCTGTAA GAGTATCTAA GATTTTCATCC AATTGCTCAC	540
GCAAGACGAT ACGAGTCGTA TAATCCACTG GATTTTCAAT CACTTCATCT TCGATAAAGT	600
CTCCAAGGTG GCTATCGTCC TCTTCACCGA TAGGAGTTTC AAGAGATACT GGTTCCTGGG	660
CAATCTTCAA GATTTTCACGA ACCTTATCAG GTGTCATATC CATTCGTTCA GCAATCTGTT	720
CTGGTGTCGG ATCTTGCCCC AATCTTGAA GGAGATTCCG CTGTTACGA ACCAATTTAT	780
TGATAGTTTC AACCATGTGA ACTGGGATAC GGATGGTACG AGCTTGGTCC GCAATAGCAC	840
GAGTGATAGC CTGACGAATC CACCAAGTTG CATAAGTTGA AAAGTTGAAC CCTTTAGAAT	900
AGTCAAACCT GTCAACCGCC TTCATCAAGC CCATATTTCC TTCTTGAATC AAGTCAAGGA	960
ACTGCATACC ACGACCGACA TAGCGTTTGG CAATGGAAAC AACCAAACGA AGATTGGCTT	1020
CCGCAAGACG TTGTTTGGCT TCGATATCAC CAGCTTCAAC AGCCAGTGCC AACTCTTTCT	1080
CCTCTTCATT GGTCAAGAGA GGAACGACCC CTATTTCTTT CAAGTACATA CGGACAGGGT	1140
CATTGACCTT AGCAGAAGTT GACCCAATCA AGTCCTCATC GCTGAGTTCT GGTCTTCTT	1200
CATTGCTGAG AACACGCGCA CTTGGATTTC CTTGTTATC TGTGATAGAA ATGCCTGCAT	1260
CCTGAATCCG TTGCAAGAGA TCTTCAATCC CATCAGCGTC CAAGGTAAAA GGAATAACCA	1320
GACTTGCATT GATTTTCATCA TCTGTTGCTG TCCCTTTTTG CTTATGATTA CGGATAAATT	1380

1068

CTGCTACCTG	TACGTCAAAT	GTTGTTACTT	CTTTTTGTTT	TGTTGCCATT	ATTACTCCAT	1440
TCTTCTCTTT	TGGGAAATTA	AACGTTCCAA	TTCTTCTAGG	GCTGTATCTG	TATCTCCTAC	1500
ATGGCTAGCT	TCCTGCACCT	TCTTTTTGAT	TCTCATATTG	TCCTGATTCA	AGAGAGCCTT	1560
GTTTCGAGTC	ATCTCTACTT	CACTAAGTTC	CTGCGGCGAT	ATCTCAGCAG	GCAAATCCTG	1620
AGCTAAAACT	TGGTACCAAG	CTCTTTCAAC	TTCTCTGTC	TGCTCTGCTA	AACTTCTGG	1680
AGGAAGATTT	CCATACTGGC	CAAGCAAGTC	ATATAAGACC	TGAAATTCAG	GTGTAGCAAA	1740
TGCAAAGTCT	TCTCGCAAAC	GGTAATCGTT	CAAAACAAGA	GGGGATTCCA	TCATCCGATA	1800
GAGTAGATGG	GCTTCTGCCC	TCATAATAGC	CGATAACTGC	TTGGTGACAG	GCATGGTGAT	1860
TGGCGTCGGT	CTGGAAATTC	CTTCCATGCG	ATTCTGCCTT	TGCACCTGAC	GACTCTCATT	1920
AACAATCTGC	TCAATCTGGG	TATAATCAAA	GGACGCCAGA	CTGTCAGCTA	AAATATGAAT	1980
ATAGCTGTTT	TGAGCAGCGA	TGGACTTTTC	TTGAACAATC	AAGGGAGCTA	TTTTTTCAAG	2040
AAACTCAATC	TGAGCCTGCA	GATTTTCACT	GTTTTTCAGG	TTGTACTGAT	GAATGTAGAA	2100
CTCAATCGGA	CTAATACGAG	TTTTCGTTAA	TAGATAGGCC	AAGTCTTCTG	GACCATTTTT	2160
TTGTAGATAC	TCATCAGGAT	CCAAGTTATC	AGGCATGCTG	ACGATTTGCA	CAGGCATATC	2220
ACCAATTTCA	TCCAATGCTT	TCAATGTCGC	GGCTTGCCCA	GCCTTATCTC	CATCGTAAAC	2280
AAGAACCAAT	TTCTTGGTTA	ACCTTTTCAG	ATGCTCAACA	TGCTCTCGAC	TCAAGGCTGT	2340
TCCCATCGAC	GCCACAGCAT	TTTCGATTCC	AGCCCGATAG	GCTGCAATAA	CATCCATGAA	2400
TCCTTCCATC	AGGTAAATCT	CACTAGCTTT	TCCAGAAGAT	CTTTTTGCCC	TATCCATATG	2460
ATATAATTCG	TAACTTTTGT	TAAAAATTGC	AGTCGATCGG	CTGTTTTTAT	ACTTAGAAGT	2520
TTGTGAATCC	GTTTTTTGCC	AGATACGACC	TGAGAAGGCA	ATGACCTTTC	CTTGGTCATT	2580
TGTCAGGGGA	AACATAATGC	GATTGTGAAA	GGTGTCTACA	AATTGATTGG	CATCCGAGAG	2640
ATAAACAGG	CCTGAATCCA	GTAAATCCTC	TTCACGATAC	TGATCAGACA	AACGTTGATA	2700
GAGATAGTTT	CGTTCTGGAG	GTGCTAAACC	AATCCAAAAA	TGTTTAAGCA	CTTCATCTGT	2760
CAACCCCCGC	TGATAAAGGT	AATTTCTGGC	CTCTTCGCCC	ATAGTCGTTG	TCATGAGAAT	2820
AGCATGGTAA	AATTTGGCTG	CATCTTCGTG	CATATCATAA	AGAGCTTGGT	GAGGTGAGGC	2880
TGACTTCTGC	TCACTATAAA	GCGGTTTTTC	AACCTCAATT	CCAACACGCT	GACCTAAGAT	2940
TTGGACTGCT	TCTATAAAGG	GAACCCCTTG	GTACTCCTCG	ATGAACTTAA	AGACATCACC	3000
TGAGCGACCA	CAACCGAAAC	AGTGATAAAA	CTGCTTGTC	TCTACAACAT	TGAAAGATGG	3060
TGTTTTTTCA	CCATGAAAAG	GACAGAGCCC	TAGATAGTTC	CGTCCTGCCT	TTTGTAAGA	3120
AATCACATCT	CCTATGACTT	CCACAATGTT	GGCATTGTTT	TTGATTTCTT	CAATGACTTG	3180

1069

TTTGTCAACC	ATACACAATA	CCTCCATGTT	ATCATAGTTT	ACTTTATATA	GTATACTTTA	3240
TTTCAGAAAA	AAAGTAAACC	ATTTCACTCA	TTTTCCCTAC	TTTATTCAAA	GAGTTGATAA	3300
TAATCAGAGA	TTTTCATTTT	TGCTTTTTCT	TCTTGGTTTA	AATCTTGGAT	AATTCGTCCT	3360
TCTTTCATGA	CAATCAAGCG	ATTGCCGTAT	TTGAGAGCAT	CTTCCATATG	ATGAGTAATC	3420
ATAAGGGCTG	TTAGCTGATC	TTTCTTAACA	AATTCATCTG	TCAATTCCAT	CAAAGCAACA	3480
CTAGTCTTTG	GATCCAGGGC	AGCAGTATGC	TCATCTAACA	GGAGTAATTC	AGGTCGCTTC	3540
AAGGTTGCCA	TCAAGAGACT	CAAAGCCTGT	CTTTGTCCAC	CTGATAAGAA	CTCAATCGGT	3600
GTATTCAAGT	GTTTCTCAAG	ACCATTTCCCT	ACTTTTTTCAA	TGGTTGCCTG	AAATTCATCC	3660
TTATAGCTAG	TCAAGCGTCG	TGGTAACAAT	CCACGCTTTT	CACCACGAAA	CTTGGCGATT	3720
AAAAGATTTT	CAGCGACCGT	CATACGGGGA	GCTGTCCCCA	TCTTTGGATC	TTGGAAGACA	3780
CGAGACAGGT	ACTTGGCACG	CTTCTCGGGT	GAAAACCTTAG	TGAGATCTTC	ACCTAAAATA	3840
CGGATAGTTC	CACTAGTTAG	TGATAAGGTC	CCTGCTATAG	TGTTAAAGAG	AGTTGATTTT	3900
CCAGCACCAT	TTCCGCCCAA	AATCGTGATA	AAGTCCCGTT	CAAAAATTTT	TAAGGAAACA	3960
TCATTTAAAA	TAATCTTTTC	TTCATCAAAG	CCATTTTAA	CGATTTTGGT	TGCATTTTTT	4020
AATTCTACAA	TTGCTGTCAT	TTGCTTAACT	TGGCTCCTTT	CAAGATTGTT	TGCTTAAATG	4080
TTGGAATCAT	GAGGCAGACT	GCTAAAATCA	AGGCACGTGA	TAAACGAAGG	TAACCTGTAT	4140
TAAAGCCAAG	TGCGATAACT	GCCCACACTA	AAAATTGATA	AGCGATAGAA	CCTACAACGA	4200
TAGTAACCAA	ACGCTCTGCC	AAGCTCAAAC	TCTTGAAAAT	AACTTCTCCA	ATAATCAAAC	4260
TTGCAAGCCC	CACAACGATA	ACCCCGATCC	CTCGAGACAC	ATCGGCATAA	CCTTCTTGCT	4320
GAGCAATGAG	GGCACCTGCA	AGGGCAATCA	CACCATTTGA	TAAGACCAAG	CCCATGAGCT	4380
CCATGCGTCC	AGTATGAATC	CCGAACTTC	TAGCCATATC	AGGATTATCC	CCTGTAGCAA	4440
TATAGGCTTG	TCCGAGTTTA	GTGTCCAAGA	AAAAGAGCAT	GAGAGCAATA	ACAATACTCA	4500
CAAAGATGAG	ACCTGTCAAG	AGTTGATTCA	AATCCGAATC	AAAAGGCAAA	ACATCCTGAA	4560
TTTGCTTGGT	TCCAAGCAGG	CCTAAATTCT	CACGTCCCAT	AATCAAGAGC	ATGATTGAGT	4620
GACAAGAAGT	CATCACCAAA	ATCCCTGAGA	GCAAGGTTGG	GATCTTCCCT	TTTGTATAAA	4680
GAAGGCCTGC	TGCCATTCCA	GCCAAACAAC	CTGCTCCTAC	AGCAACAAGT	GTCGCTAAAA	4740
ATGGGTTCAC	GCCTTTGGTT	ATCAAAGTGA	CAGCAACAGC	TCCCCCAAGA	GGGAAGGAAC	4800
CTTCTGTCGT	CATATCTGGA	AAGTTTAAAA	TCCTAAATGT	CATAAAGATT	CCCAGACCTA	4860
GAATAGCCCA	GACAAATCCT	TGAGAAATAA	TGGAAACAAT	CATATTTTAT	TTAATCCTTT	4920

1070

CTATATTCAT CTTTTTAAAA AATGGGAAGA GTCTCCTCCT CCCTACCTTA TTTATTCGAT	4980
GACTTGTCCT GCTTCTTTGA GAACAGACTC AGGAATAGTA ATACCTAGTT CTTGTGCTAT	5040
TTTTTTTATTG ATGACTGACT TACCAGTTGA AAAGACATTG ACTGGGGTAT CGGCTGGTTT	5100
TGCACCTTTC AAGACTTGCA CAATCATTTT ACCTGTTGCC ACACCAAGGT CATGTTGGTC	5160
AATTACAAC TATGCCAAAC CACCTACTTC TACCATAGCT GTCGCACTGG GATAAATTGG	5220
TTTCTTAGAA CTTTGATTGC TAGAGACAAC CGTTGGAAAT CCTGATGCAA TGGTGTTATC	5280
AATTGGAACC CAAATAGCAT CTACCTTGCT AGTCATAACA GTGACAGTTG AGGCAATTTC	5340
ATTTGTTGAA GGAAGTCAA ATGTTTCCAC TGTCAGACCT GCCTTTTCAG CATAAGCCTT	5400
AAATTC	5406

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CAGCTTGCTC TTAATTATTAT AGCAGATGTT ATAGCTGGAA TTATCTTGTA TTTCGTCTGC	60
AAATGGCTAG ATGGTAAGAA GTAGACCGAA TGAAGTGCCT ATAAACACCC GTTAAATCGC	120
TAAGATACGT CAAAAAAGCC CTTAACTATG GCACTAGTTA GGGGCTTTGG TGTTCCTAATG	180
AACCTTATAC ACTAACTACA TTCTAGCATA TAAGCCAGCA TATTTCAAGA GTTTTATTTA	240
TTGTTTAAAG TTCTGAAAGG TCTATAATGA AGTTAGCCAT CTAGTATCAA AAAACCGACT	300
AGCTCTTATG AACTAGTCGA TTTCTCATCA ATGCGCCAAC ATTTCTTGGG CGATTTCTTG	360
GCCAGATAGG TTATCTGGGT AGTAGGTTGG CCAGTTGTCC ATTTCTTCAA AGAGGGCTTC	420
TTGGCTTGTC CCTCCAAAGA AGATATGGAA ATGTTCTGCC TTAAGTGGGG CAACATTGTG	480
GTCACATAAC TGAACATACT TGAATTGTCC AGCGTCAGCA TCTGTGGCTT CAAAGAGGAA	540
ACGCACGCCA CGATTGCCTT TCTTGTAAGT CAAAATTTTC TTACCGACAT ACTTGTAAGT	600
GTATTTCTTG CTTTGTCCAC CTTGAACAAA TTCCATAGTA TTATCAGTAA TGTTAATCTT	660
AGTCACATCT GTATGATAGC CTTTTGTATA GTAAGCCTTG TACTCAGCCT GGGTCATCTT	720
ACCAGTCAAC TTAGCCTTGT AGTCAAAGAC TTGGTCAAAC GTGCCGTCTT CAAGGAAAGG	780
ATAAACTGAT TGCCAGTTAC CTGCATAGTC ACTCAAGGTG CGGTCCTTGA CAGCTGCATC	840
CTCGAAGTAA CCATTTTGGA CTGTCTTGGT ATCCTCTGCC TTTTCAGGTT CAATTGCTGG	900

1071

GCCTTCTTGG	TCTGTTGTTT	GTTTCAAAGC	CTTGAGGTTT	TTCTCCATCA	CGGAAATGTA	960
GTTTTCTCCA	GCCTTGGTGT	CCTCTTCTGT	CAGACTTTCT	AAAGGATTGA	GGACATCAGT	1020
TTTGACACCT	GCTTCTTTTG	AAAGTGTGTT	AGCAAGGGCT	TGTGAGGCAT	TTCTTCAAAA	1080
TAGATATAGG	CGATTTTATT	TTTCTTGACA	TACTCTGTCA	ATTCTGCCAA	GCGAGCAGCT	1140
GATGGCTCTG	CATCTGGAGA	AAGTCCTGAG	ATTGCGACTT	GTTTGAGTCC	ATAGTCCAAG	1200
GCAAGATAGT	TAAAGGCTGC	GTGTTGAGTC	ACAAAGCTCT	TTTGTTTTGC	TTGAGACAAA	1260
CCTTCTGCGT	AAGCCTTATC	CAAGGCTTGC	AATTTTTCGA	TATAGGCAGC	TGCATTCTTC	1320
TCAAAGGTCT	CTTTTTTATC	AGGATAATCT	GCTGACAAGC	TGTCGCGGAT	GTGCTCTACT	1380
AGTTTAATGG	CACGAACCTG	TGATAACCAA	ACATGGGGGT	CAAACCTCATG	GTGATGACCT	1440
TCTTCTCCAT	GGTCATGGTC	TCCCTCTTCT	TCCTCGCCAC	CTGGCAAGAG	CAACATATCG	1500
CCTGTCGCCT	TGATGGTTTT	CACTTTTTTC	TTATCCAAGG	TATCTAGCAA	TTTAGGTACC	1560
CATGTTTCCA	TGTTTTTCATT	TTCATAAACG	AAGGTATCTG	CATCTTGGAT	TTTGGCAACT	1620
GCCTTGGCAG	ATGGTTCGTA	TTCATGAGGT	TCTGTCCCAG	CACCGATTAG	GAGTTCCTACA	1680
TTAGCCGTAT	CTCCTGCGAC	TTGCTTGGTA	AATTCATAGA	CAGGGTAAAA	GGTTGTCACG	1740
ATATTGAGTT	TACCATCTGC	CTGTTTTTGA	TTGGAACAAG	CCACTAAAAA	CAAGGCACAT	1800
AGACTGGCTA	GTAATAAGCT	AATTTTTTTC	ACGTTCGTCT	CCTATTTGAT	AAAACGTCTT	1860
ACTAAACTGA	TTAGTATAAA	GACAGTTACA	AAAATAATGG	TAATACTTGC	ACTTGCAGGT	1920
GTTTCTGCAT	AGTAGGAAAT	GTAAAGTCCT	GCTACCATTC	CCAAAAAGCC	AATCGCACTG	1980
GCAAGCAGCA	TAACCGATTT	AAAGTTTTTC	CCCAGACGCA	GGGCAATACT	AGCTGGCAAG	2040
ACCATAATGG	TCGATACCAG	AAGAGCTCCT	GCTGCAGGAA	TCATAAGGGC	AATAGCCACC	2100
CCTGTCACCA	TGTTAAAAAG	AATGGACATG	GTACGAACTG	GCAAGCCATC	CACAAAGGCC	2160
GTATCTTCGT	CAAAAGTTAA	GATATACATA	GGACGAAGAA	AGAGAAAGGT	CAAAATCAAA	2220
ACAACCGCCG	CAATGACAAA	GAGGGAAATG	ACCTGTTCTT	CACTGATAGT	CACGATCGAA	2280
CCAAAGAGAT	ATTGGTCCAA	ACTCATTGAA	CTCGAGCTTT	TACCCTTGCT	CATGACAATC	2340
AGAGAAACAG	CCAGACCTGT	TGACATGAGG	ATAGCTGTCC	CGATTTCCAT	AAAGCTCTTG	2400
TAAACCGTAC	GGAGATACTC	CAGAAAGACC	GCCGCAATCA	AGACAATGGC	AATAGTAGAA	2460
ACAGTTGGAG	AAATCCCCAA	AACCAGACCA	AAGGCTACAC	CTGAAAGTGA	GACGTGGCTA	2520
AGGGTATCAC	TCATCAAACCT	CTGACGACGC	AAGATGAGGA	AGGTTCCCAA	TACCGGTGAG	2580
AAAAGACTCA	TAGCAATAAC	CGCCAAAAAG	GCGCGTTGTA	TAAAGTCGTA	AGATAATAAA	2640

1072

CTAAGCATGG	CCCACCTCCT	GGCCATTCTC	ATGAACATTG	AAACAACGCC	ATGGCGAGTC	2700
TTGGTTACGG	ACTAGATGAA	TATTGCGATC	CGCATAATCC	TTAACTTCTT	CAGGGTCATG	2760
GGTAATCATC	AAAACAGCCT	TGCCATGATG	ATGGGCGCTG	TGGTGCATGA	GTTCGTAAAA	2820
TTCATTTTTA	CTTCCTGCAT	CCATCCCCGT	TGTCGGCTCG	TCTAGGATAA	ACACATCAGG	2880
GTCAGAAGCA	AACATACGCG	CAATTACCGC	TCGCTGCTTT	TGTCCCCCAG	ATAGAGACCC	2940
CAAGCGTTTG	TCTCGATGTT	CCCACATGCC	AACTGAGTCC	AGACTAGCCT	TGATATGCTC	3000
CTCATCATGA	GCATTCAAAC	GACGGAACCA	GCCTTTTCTC	GGATAGCGAC	CCGACTTGAC	3060
AAATTCATAG	ACCGTACTTG	GAAAACCAGC	ATTAAAACTG	GCAATTTGTT	GAGGAAGATA	3120
GGCTATTCTC	AATTTCTTAC	CTTGCGTATT	TGTCTTTGAA	ATAGCCACCT	TTCCAATGCG	3180
TGGTTGCAGA	ATTCCAAGAC	TAGCCTTGAT	GAGCGTCGTC	TTAGCCGCTC	CATTTTCCCC	3240
AGTCAAGGTA	ACAAATTCCC	CACTATCAAC	ACAATAATTG	ATATGTTCAA	GAACAGGCTC	3300
CTTATCATAA	TAGAAGGACA	AATCCTCTAC	CGTAATATAT	CTCATTATTT	GATTTCTCCT	3360
ACTAAAGCAG	TCAAAAACCG	CTGAATCACT	TTTTGTTCAT	TTGGAGTAAA	CTGAGTCGCC	3420
ACTTGTTTCAT	AGGTAAAAAG	TGTATGCTCA	TGGTGATGGT	GGTGCTCCTC	AGCGATTGGA	3480
CGAGCCAAGT	CAGTCAACTG	ATAAAAAATC	ACACGCGCAT	CTTTAGAATC	TTTAGATGTT	3540
TCCAACATCC	CTTCCTTGAC	CAAAGACTTA	ATGGCCTTGG	TAAGTCCCGC	CTGACTGACA	3600
TTGAGACGAC	GGGCCAATTC	TGAATTTGTT	AAAGATTCCCT	CTGACAAGAG	CATAAGGATA	3660
TGCTCCTGAG	TATTGGTCAG	GGCCACCTCG	CTAGTGCAAT	GACCTATTAG	GATTTTCATGC	3720
TGATTTTCCG	CCTGCAAAAT	CACCTCATTC	AAAAAAGCAT	TGATATCCTT	TGCTAGCTGT	3780
CTCATATCTG	ACTCCTTTCC	TTTTAGACTT	CTCTTTTTTA	AGAGAAAAAT	ACTATTCTTT	3840
GACATTTTGT	TTACCAGTTA	ATTATATCAC	AAGCAAAAAA	AGAGTCAAGA	AAAAACGTGA	3900
AAACTAGTTT	CATTCTTGAA	CTCTTCTATA	TTATATTATC	TATTGAAATT	CTTTGACATC	3960
TCCATCATAA	GTCGCCCAAT	CTTTGCTGAA	AAAGCGCTCA	TTCAGATGGT	AAGTCGGAGC	4020
TGGTGTGGGA	TTGGATAGGA	AAGGATCAAC	TGCCTTGTC	AAAGCCAACC	AACCCAACCA	4080
ACCAAGGTGA	ATGGTGTCTT	TCATAAAGAA	AGGCTCCCCG	CCGTCCTTAG	AAAAATCTGC	4140
TATATTGGTA	AAACCTTGAC	TTTCTAACTG	GTAGCGAATC	TTCTGCACCG	TTTGTTGGTA	4200
CATATCCTCT	CGTAGACCAG	CATAGTTCAT	CCATTTTTTA	TTAACAGGTG	GAATGATAAA	4260
AATCGGGTTT	ACCTTAGATT	TAGAAAACCTG	TGTTAAAACC	AACTGCAAGT	CATTATACTC	4320
TGGCGACTTG	AGATAGGTAA	AGCTTTTCTG	AGAATCCTTT	AATTTCTTCA	AATCCTTCTT	4380
GATCTGCTCA	TTATAGAAAT	AATTTTCCAT	TCCCATCTCA	TTATTGGAAG	TATTTTTTTC	4440

1073

AGCATCTGCT	TTGACAACAT	CTTCTATTGC	CTGATAAGAA	AACTGGTCTG	GCAAGATTTT	4500
TAAATACTTA	GCTACATGCT	TATCGTAGTT	AACATAGCCT	CTAACCGAAA	ACTGACCAAA	4560
AAAGGAAGCT	TGGCGTTCAT	TAAAACGAGC	CAATAATTCA	ATCATTTTCAT	TGTCTGCTGT	4620
CGACAATTCT	TCTTTACTTG	CCAACCTCTG	AACCAGGTCC	TTCATAGCTA	CGTTTGGGAA	4680
CTGTTGCAGT	AAGCGAGTCG	CTGCATATTG	ACTAGCCTGA	TCCCCAGATT	GATGTTTCAG	4740
AAAAC TAGTC	AACTGGTCTC	CATTAAAATA	CTGCTGGAAG	GCTGCTGGAT	CATAGCCATT	4800
TTTACTGAAC	CACTGAGGTG	AGATAACATA	CACAACTTGT	TTATTCTCCA	GCTGTGGTAA	4860
CATCTGTTGC	ATTCCAAAAT	ATTGGTTAAG	CGATGCAGCT	CCCCCCTGTC	CTAAAAGATA	4920
AGGACGGTAG	GAACGATTGT	ATTTCTCAGC	TAATACCGCA	GGATGAGCAC	CGTCAAAACG	4980
AAGCCATTCA	CTAGAGCCAA	AGAAGGGAAC	AAAACGCACA	TTTGGATCAG	ATAGTGCTCT	5040
GACTTTTTGA	CTTCGCTCCT	TAAAAC TATC	GATAGTAGTA	GCCACTGCTG	AACGCTTTTC	5100
AGCTCCTAGA	TTATGATGCA	TCTCAGTAGG	ATAAAAGAAA	ATGAGCAGAA	AAACCAACAA	5160
ACCAGCGATC	AAGACCGGTC	CGAAGATCAT	CCATAAGCGT	TTAAGCATTT	TGTAGCTCCA	5220
CAATACCAGC	TATGATTTTA	TTAGCTGTAT	TCCAGTCGTC	ACGACCAAAC	TCTGTTACAG	5280
GGACACGAAT	GTCAAAACGG	TTCTCAATCT	CCACAATCAA	CTCAACCGTT	CCCATACTAT	5340
CCAAGACACC	TGCATCAAAA	AGATCTTCAT	CCATCATGTC	AGAAACATCT	TCCATAAACA	5400
ACTCATCAAT	AATTTCAATA	ACTTCTGATT	TGATATCCAT	ATTTTATTTT	CTTTTATTTT	5460
TTAAACCATA	GATTATTCAA	GAATCCAGAA	AAGATTAAGA	ATGACAACAT	GACAACATGG	5520
AAAGTGACAA	CCATGCCAAG	CAACTGAATC	CAGCGATTCT	CAGGTAGGGC	AGCCTTCCCT	5580
GCTTTTTTCC	GTTCCCTTATT	GAGCGTTTTT	TTCTTGCGAA	CCCAGGCATC	ATTGATGACC	5640
AAGCCTAGTC	CATGAAAGAG	TCCATAGGCG	ATATAGTACC	AGGTCACACC	ATGCCAAAAT	5700
CCCATAATCA	GCATATTTAC	AATGTAGGCC	ATGCTTGAGG	TTACATTACG	ATTTTTAAAG	5760
ACTTTCTTTC	TGGTTAACAC	CATCACCATT	CGCATAAAGA	CAAAGTCACG	GAACCAGAAG	5820
GACAGACTCA	TATGCCAGCG	ATTCCAAAAC	TCCTTTAAAT	CCCTTGATAA	AAAGGGCTTG	5880
TTAAAGTTGA	TAGGGCTACG	GATTCCCATC	AAGTTTGAGA	TGGCCAAAGC	AAACATAGAA	5940
TAACCTGCAA	AGTCAAAGAA	GAGTTCCAGA	CCAAAAGTAT	ACATAACTGC	CAAGGCATAG	6000
AGATTAAAGA	AGCCACCTGA	CTGCAAGGCT	AAATTCTTCA	GAGGAGGTAG	TAAGGTCTCT	6060
CCTAAAACAT	GAGCTAGGAT	AACTTATAC	AAAAAGCCCC	ACATGATATA	GCGGACAGAT	6120
TCATCCAGCA	TATCCATCAA	CTCATCTCGC	TCAGGAATAG	CCTGATAATT	TTCATTAAAT	6180

1074

CGCTTAAAGC	GATCGATTGG	ACCACTCGAG	AAAGTTGGCA	TGAAGAGAAG	GAAACGGAGG	6240
AATTCCCAGA	GGGTAAAATC	CTTAATCACT	CCATCTCTCA	GCTCGATGAC	AATTCCAACC	6300
GAACGAAAGG	TCAGGTAAGA	AATTCCCAAG	AACCCAAGCA	AAGACTGCGT	TCCATTGATA	6360
GCTGGTTGCA	CCTTGACAAA	GATAATCGGA	AGTAGGGACA	GAAAAC TAAC	TAAGTAGAAG	6420
ACCCACTTGC	CATCCTTGCT	TTTTTCGATA	TGCTTGTAGA	AAAGCAGGAG	CAATATTTCC	6480
CAGCAAAGGT	AAATACCCAA	GGCAGCTAGT	TGATTGGTCT	TTCCACCCAC	CAACATGGTG	6540
ACAATAAAGA	AGAGACTTAC	CAACACTTCA	TACCAGGCAA	AGCGTTTCTT	GAAAAAGAGA	6600
CCTATAAAGA	TGGGCAAGGT	TGCAGCAATC	ACATAAACAA	AATACTGAGG	ATTGCCATAT	6660
GGCTCTAAAT	GAGGAAGCTG	TTGAAAAAAC	TCCATCATCT	CTTATTCACC	TCGTTAATCA	6720
ATCCTTTGAT	GTCAATCTTT	CCATTTGGAG	TTAGTGGCAA	ACTGTCTCGG	TAAAGGAATT	6780
TAGATGGCAT	CATATAGGAC	ATCATGATGT	CTGTCAGGTC	TTCTTGATG	GCCTTGGTAA	6840
TATCGATATC	TCGCTCAAAC	TGCTCACGAA	CACCGTCTTT	TAAGATGACA	TAAGCCAATA	6900
GATTTTGTAC	CTTGTGGTCC	TTGTTATAGC	GCGGTACTGC	GACAGCAGAT	TCGATAAAGC	6960
GAGACTTGTT	GAGGTTTTGA	GAGACATCTT	CTAACTCAAT	GCGGTAACCG	TTAAACTTAA	7020
TCTGGAAGTC	CATGCGTCCG	CCGTAGAGAA	GCAAGCCCTC	ATCTGTCATG	GTTCCACAT	7080
CGCCTGTGTG	ATAGGCTGGC	AGATCTTCAA	ACTCAAAGAA	GGCTTCTGCT	GTTTTTTCAG	7140
GATTGTTTAT	ATAACCTTTT	GAAACAGCTG	GCCCAGAAAC	AATGATTTCT	CCCTGCTCAC	7200
CATTTGGCAG	TTTATTTCTT	TCCTCGTCAA	TGATAAAGGT	TGGAGAATCA	GCCTTGGTAT	7260
AGCCGATTGG	TAGGCGTTTG	AGAGTCGCTA	ACATCTCGTC	TGTCACGGCA	ACTGCTGACA	7320
GAGCTACTGT	CGCTTCTGTT	GGGCCGTAAG	CATTGATGAT	ACGGGCATTT	GGGAAACGCT	7380
CGCGCAGTTT	TTGAGCTGTT	TTGACCGTCA	ATTCTTCACC	ATCAAAGTAG	AAATGCGTGA	7440
TTCCAGGCAT	TTTCTCACTG	TTGAAGTATT	CAGACAACAT	GGCCATATCT	GCAAAGGATG	7500
GTGTTGATGT	CCAGATAGCG	ATTGGCAATG	AAAAGATAGC	CGCAAAGAGT	TGCTTAAACT	7560
CCTGAGTGAT	GACTGAAGGA	AGAGTGAAAA	GCGTACCACC	AAGTGCCAAG	GTCGGTGCCC	7620
AATACATGAC	AGACAAGTCA	AAAGAATAAG	GTGGCTGTGC	CAGCATTTGC	GGACGACTCG	7680
GTGTCGCAAA	TTCCTTATCC	GTAATCATCC	AGTTTGTAAG	GCTGAGGAGA	TTATCATGTG	7740
AAATCTGCAC	TCCCTTAGGC	TTACCAGTCG	TACCAGAAGT	AAAGATAATG	TAGTAATTAT	7800
CATCTCCCTT	GACTGGATGC	GTGATTTTAT	AGTTATTCCC	TTGGGCAAAG	GCTTCTTGAA	7860
CCTGAGCTAG	ATTTATCATT	GGTGTAGAAA	CCTGCTCCAA	GGGAAAGGCT	GAAATGGCAA	7920
TAATCAAGCT	TGGCTCTGCT	ACTTCTAAAA	TAGCTGAAAC	TCGCTCCAAG	GCCGAATGGC	7980

1075

TATCAATTGG	AATGTAGGCA	TGACCTGACT	TAGTCAGCGC	TACAAAGGTT	GCCAACATTT	8040
CATATTCTTG	GCCACCAAAA	ACAACCACAG	GAGACTTCTC	AGGCAAGCCT	AGTTGGTCAA	8100
TGACTGCAGC	CAAACATATCC	GAATCAGCCT	TTAAATCGCC	ATAAGTGTGT	TCCTGCCCCA	8160
AAACATTATA	GACAGGATAG	CTAGGCTGTG	TCTGAGCAAA	ATGCTCAATG	GTTTCAATCA	8220
TATCTGCTAT	TGGTTTATTT	GACACAATAG	GGATTCTCCT	TCAAGTTAAA	ATTCATTATA	8280
GATAAAGCTT	CCTTGACCCT	GACCAAGATA	GCTAAAGAAG	TAAAGCAGCC	CTAGAAAGAT	8340
AAGAAAATAC	AAGGCTGTCC	GACCAAGAAA	GAGGTACAAT	TCTTTTCTCT	GTTTCATCAA	8400
GAAAAACCAT	TCATTTCTGT	AATTTTTCGC	TAAAATAAGA	GTGATTCTTA	CTAGCTTATT	8460
TTTCTACCAT	TGTACCACTT	TATATAGTAT	CTTTTCAATT	GTTTACCGTA	TGTTTCCAAT	8520
AGATTTTCAGC	TTATTTTAAG	GATTATACAG	TTTTTCTATG	TATATTTTCA	AATAGAGTGA	8580
TCCTGCTTCA	AAACTCCATT	TCAGGAGACA	ATGAAGTAAA	TCTTCCCATA	ATAAAACACA	8640
CAATATCAAG	TTTTTTCAAC	ACCTGATACT	ATGCGCTTTT	CTGATTTTTA	AAGACTTTTT	8700
AACCACTCTC	TCATTTAAAA	TAATCTCGTC	TGATATAAAT	TAAAATAGCT	TCTATCATCA	8760
GACAAATGGC	TGATAGCCAA	AAACTGATGC	TAATACCAA	ACTCTCAGTA	ATATAGCTCA	8820
TTAGCAAAAC	AAATACTGAA	AATGCTAATG	TAGAAATCAC	TTCAAGAACG	GAATAGACAT	8880
TAATAAATG	ATTTTCCTCT	ACTGTTTCCT	GAAGAAATAC	ACTTTCAGGA	ACTTCTTTTA	8940
GTTGCGATAA	CATACCAACT	AAAGCTGAAA	ATAATAAAAA	CATCTGTGCG	TTTGGAAAAT	9000
ATAGAATAGT	CAGTGTCACT	ATTTCCATAG	CTACAAGAGG	AAAAAGAATA	CTTTCCCCCC	9060
AAATCATTC	TACCTCTCTC	AACTAGATGT	AACTTACAAA	ACCCCTGACC	TCATGAGCCA	9120
CTTCTTCCT	CCTCATGAGG	TCAGTTTTAC	TTTCTGCTGT	TCCAGTATCG	TTTTTCCTCG	9180
CTAGATTTCC	TCAAAAGGGC	AGACTCCTCC	CTTGGTGCGT	CACACGATTT	TTTCATCTCG	9240
ACTGTTCTTT	AATGCATCAT	TAACGACGCT	TTTCTTCTAG	GTGGTTCATA	AGGAACAGGA	9300
AGATTCAGGT	TGACTTTTCT	AATCCTAGAA	TAAAGTGCTG	AAAACAATTC	GGAATAGGCA	9360
TAGAGACTAG	ACAATTTGAG	GAGCTGCTTG	CGTCCTGTTC	GAACACATTT	TCCCACCACG	9420
TGAAGAAAAA	GATGGCGGAA	GCGTTTGATT	GTTAAAGTTT	GGAAGTCACC	TCCAGCTAGA	9480
TGTTTGAGAA	AAAGATAGAG	ATTGTAGGCG	ATACAGCTCA	TCATCATACG	AACTTCGTTT	9540
TTGATTAAGG	TTGAACTATC	CGTTTTATCG	CCAAAAATC	CCTCCTTCAT	CTCCTTGATG	9600
AAATTCTCGG	CTTGACCACG	TCCACGATAA	AGCTGAAACT	GGTCTTGGcT	gTTCCACTCG	9660
TCATATTTGT	AACGAGAGAA	ATAACATCGT	AGAACAAGTA	TCCTTCTTTT	C	9711

1076

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3025 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

CCCCTTTGTC AAAACTGTAA AATTAACGAC TCAACAATTC ATCTTTACAC CAATCTCAAT	60
GGAAAACAAA AACAAATTGA CCTCTGTCAA AACTGCTATA AGATTATCAA AACAGATCCT	120
AACAATAGCC TCTTCAAAGG TATGACGGAT CTGAACAATC GTGACTTCGA TCCCTTTGGT	180
GATTTCTTCA ATGATCTAAA CAATTTTCTAGA CCTTCTAGCA ATACTCCTCC TATTCCCCCA	240
ACCCAATCAG GTGGAGGTTA CGGTGGAAAC GCGGTTATG GTTCCCAAAA TCGTGGATCT	300
GCTCAAACCTC CGCCACCTAG CCAAGAAAAA GGCCTGCTGG AAGAATTTGG TATTAATGTA	360
ACTGAAATTG CCCGTCGTGG AGACATTGAC CCCGTTATTG GCGCGACGA TGAGATTATC	420
CGTGTCATCG AGATTCTCAA TCGTAGAACC AAGAATAATC CTGTCCTTAT CCGTGAACCT	480
GGTGTCGGAA AAACGGCCGT TGTCGAAGGT CTAGCTCAGA AAATTGTCGA TGGCGATGTG	540
CCACATAAAC TCCAAGGTAA ACAAGTCATC CGTCTGGATG TGGTTAGCTT AGTTCAAGGA	600
ACGGGGATTC GAGGACAATT TGAAGAACGC ATGCAAAAAC TCATGGAAGA AATTCGCAAA	660
CGTGAAGACA TCATCCTCTT TATCGATGAA ATCCATGAAA TTGTTGGTGC TGGTTCTGCG	720
AGTGATGGTA ATATGGACGC AGGAAATATC CTCAAGCCAG CCCTTGCTCG TGGAGAACTG	780
CAACTAGTCG GTGCTACTAC CCTCAATGAA TACCGTATCA TTGAAAAGGA TGCTGCCCTC	840
GAGCGTCGTA TGCAGCCTGT TAAAGTCGAT GAACCAACGG TGGACGAAAC AATCACTATT	900
CTCAAAGGGA TTCAAAAGAA ATACGAAGAT TACCACCACG TTCAATATAC AGATGCTGCG	960
ATTGAAGCAG CTGCAACTCT TTCCAATCGC TACATCCAAG ATCGCTTCTT GCCTGACAAG	1020
GCCATTGACC TCCTAGATGA AGCTGGTTCT AAGATGAACT TGACCTTGAA TTTTGTGGAT	1080
CCTAAAGTAA TTGATCAGCG CTTGATTGAG GCTGAAAATC TCAAGTCTCA AGCTACACGA	1140
GAAGAAGATT TTGAGAAGGC GGCCTACTTC CGCGACCAGA TTGCCAAGTA TAAGGAAATG	1200
CAAAAGAAAA AGATCACAGA CCAGGATACT CCTAGCATCA GCGAGAAAAC TATTGAGCAC	1260
ATTATCGAGC AGAAAACCAA TATCCCTGTT GGTGATTTGA AAGAGAAAGA ACAATCTCAA	1320
CTCATCCATC TAGCCGAAGA TCTCAAGTCT CATGTTATTG GTCAAGATGA TGCAGTCGAT	1380
AAGATTGCCA AGGCTATTCT CCGTAATCGT GTCGGACTTG GTACCCCTAA CCGCCCAATC	1440

1077

GGAAGCTTCC	TCTTCGTTGG	GCCAACCTGGT	GTCCGGTAAGA	CAGAACTTTC	CAAACAACCTG	1500
GCTATCGAAC	TTTTTGGTTC	TGCTGATAGT	ATGATTCGCT	TTGATATGAG	TGAATACATG	1560
GAAAAACATA	GTGTGGCTAA	GTTGGTCGGC	GCTCCTCCAG	GTTATGTTGG	CTATGATGAG	1620
GCTGGTCAAT	TAACTGAAAA	AGTTCGCCAC	AATCCATATT	CTCTCATCCT	TCTCGATGAA	1680
GTGGAAAAAG	CTCAGCCAGA	TGTTATGCAC	ATGTTTCTTC	AAGTCTTGGA	CGATGGTCGT	1740
TTGACAGACG	GGCAAGGACG	CACCGTTAGC	TTCAAGGATG	CCATCATTAT	CATGACCTCA	1800
AATGCAGGTA	CAGGAAAGAC	CGAAGCTAGC	GTTGGATTTC	GTGCTGCTAG	AGAAGGACGT	1860
ACCAATTCTG	TCCTCGGTGA	ACTCGGTAAC	TTCTTTAGCC	CAGAGTTTAT	GAACCGTTTT	1920
GATGGCATT	TCGAATTTAA	GGCTCTCAGC	AAGGATAACC	TCCTTCAGAT	TGTCGAGCTC	1980
ATGCTAGCAG	ATGTTAACAA	GCGCCTCTCT	AGCAACAACA	TTCGTTTGGA	TGTAACCTGAT	2040
AAGGTCAAGG	AAAAGTTGGT	TGACCTAGGT	TATGATCCAA	AAATGGGAGC	ACGCCCACTT	2100
CGTCGGACTA	TTCAAGACTA	TATTGAGGAC	ACAATCACTG	ACTACTACCT	TGAAAATCCA	2160
AGCGAAAAAG	ATCTCAAAGC	AGTTATGACT	AGCAAGGGAA	ACATTCAGAT	TAAATCTGCC	2220
AAAAAAGCTG	AAGTTAAAAG	TTCTGAAAAA	GAAAAATAAA	TCCTATAAAA	AAGGAGTAGA	2280
AAATGAAATT	TTTCTGCTTC	TTTTTTTACT	AAAATAACTG	TAATTTCTTG	ACAGCTTGCC	2340
CTTTGTCCAT	TATGATATAT	AGTAGACTGA	ATCTGAAATA	GTACGAAACA	ATTGCTAAAA	2400
CATTTATAGA	AATTAATTTT	ACTTTCCCAA	TCGATTGTGT	CTCATCTTAT	TTCAATCTGC	2460
TATAGTCAAT	TGAAACAAGA	ACAAGACAAA	AGAGCCTCAT	AAAAGGTATT	GCAACTTGGT	2520
AATACCTTTT	TGAGGTGCTT	TTTGATATGA	GCCCATGTTT	TCTCAATAGG	ATTGTACTCA	2580
GGTGAGTAGG	GAGGAAGAGG	TAAAAGTTTA	TACCCAAACT	CTTCACACAA	GAGTTCTAAC	2640
TTACCCATTC	TATGGAATCT	TGCATTATCC	ATAATAATAA	CCGATGGTGT	GGTTAATGTT	2700
GGTAAGAGAA	ACTTCTGAAA	CCAAGCTTCA	AAAAAGTCGC	TCGTCATCGT	CTCTTCGTAA	2760
GTCATTGGAG	CGATTAACTC	ACCATTCAAT	TGTTAGACCT	GCAACCAAAG	AAATTCTCTG	2820
ATATCTTCTT	CCAGATACTT	TGCCTCTTCT	TAACTGACCT	TTTAATGAGC	GACCATATTC	2880
TCGATAAAAA	TAAGTATCGA	ATCCTGTTTC	GTCAATCTAA	ACAGGTGCTA	GGTGCTTTAA	2940
ACTATTAAAA	TTCTTAAGAA	ATAAGGCTAC	TTTTTCTGGG	TCTTGTTTAT	AGTAGGTGTA	3000
GTTCCTTTTT	TTTTCGAGTG	TAGCC				3025

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4104 base pairs

1078

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

TTTAAGGTTT TAAAAAAGT TTTCGAAAGG TTTCTTCTTT ATTTTTTAAG GGAGAGATAA	60
CGTTGATATC TAAATCGTGG TCAAAGCCGG CAATTTTTC TTTAGATGTG TATTGGTGAA	120
TATCATAATC TAAATCAGTT TTAGGACTGC TCTCCAAAAA TCCTGAGTCT GAGCCGTAGA	180
CGGAATCCAA ACAGAGGTAA ACTTGCCTGT ATCAATACTG TGTTCCTCCA TGAAGTAGAC	240
ACCAACGTAG ATGCCGATGT TTTTAGCACC CAGTGATGCT AGTTTGTCTC GAAAGTTTTC	300
GACACCTTCG TTCATATTAG ACATGGTTTT GTCTTCCACG TCAAGCCAAT AGTAACTAGG	360
GCTGTAAGGA GAGGCAGCAT TGTAAGAAAC TTCGGCAGCC TTTTCCATTT CTTGGACACT	420
TTTTCCAGCT ACATAAGCGT AGACAGCAAC TGGGACATTC CGCTTTTGAA GTTCAGTGAT	480
ATGACTCTTA TAGGCCTTGT CTATTCCATT GATAAATGAA GCATCATTTT CTTTTGTCGT	540
TTGAGCACCA CTGTGAACAC GAACAATAGC ACCTGAAATA TTTTGTGAGA GGGCATCGTA	600
GTTGATTTCC TCAGGACGCT GCCAGCCAGA GAGGTCAATA ATCGGTTTGT CTAAGTGTTT	660
CAAAGCCTGT GCTTCAATCT GTGCTATATT GGATTTTGTT TTAAACGATT GGCTGTCATT	720
AAGTGGCGGA TTGATGATTA AAATGAACAT CATAATCCCA AAAAACTAA ATAAAATAAG	780
TGGATGAATT TGTTTTCTCA TATCTTATAA TTCTACCTA AAAATCAAAA AAAATCAAAA	840
AAATGGGTTA AGGAAGAGAC TTTAGAGCAT TTTTTCATTC AAGAGTGGG AATGATTGTA	900
AATATGGTAT AATAAAAGGG AATTTCTACA GAAAAGAGAA GATTATGTCA AATTTTGCCA	960
TTATTTTAGC AGCGGGTAAA GGGACTCGCA TGAAATCTGA TTTGCCAAAA GTTTTGCACA	1020
AGGTTGCGGG TATTTCTATG TTGGAACATG TTTTCCGTAG TGTGGGAGCT ATCCAACCTG	1080
AAAAGACAGT AACAGTTGTA GGACACAAGG CAGAATTGGT TGAGGAGGTC TTGGCTGGAC	1140
AGACAGAATT TGTGACTCAA TCTGAACAGT TGGGAAGTGG TCATGCAGTT ATGATGACAG	1200
AGCCTATCTT AGAAGGTTTG TCAGGACACA CCTTGGTCAT TGCAGGAGAT ACTCCTTTAA	1260
TCCTGGTGA AAGCTTGAAA AACTTGATTG ATTTCCATAT CAATCATAAA AATGTGGCCA	1320
CTATCTTGAC TGCTGAAACG GATAATCCTT TTGGTTATGG ACGAATTGTT CGTAATGACA	1380
ATGCTGAGGT TCTTCGTATT GTTGAGCAGA AGGATGCTAC AGATTTTGAA AAGCAAATCA	1440
AGGAAATCAA CACTGGAACA TACGTCTTTG ACAACGAGCG TTTGTTTGAG GCTTTGAAAA	1500
ATATCAATAC CAATAACGCT CAAGGCGAAT ACTATATTAC AGACGTCATT GGTATTTTCC	1560

1079

GTGAACTGG	TGAAAAAGTT	GGCGCTTATA	CTTTGAAAGA	TTTTGATGAA	AGTCTTGGGG	1620
TAAATGACCG	TGTGGCGCTT	GCGACAGCTG	AGTCAGTTAT	GCGTCGTCGC	ATCAATCATA	1680
AACACATGGT	CAACGGTGTT	AGCTTTGTCA	ATCCAGAAGC	AACTTATATC	GATATTGATG	1740
TTGAGATTGC	TTCGGAAGTT	CAAATCGAAG	CCAATGTTAC	CTTGAAAGGG	CAAACGAAAA	1800
TTGGTGCTGA	GACTGTTTTG	ACAAACGGTA	CTTATGTAGT	GGACAGCACT	ATCGGAGCAG	1860
GAGCGGTCAT	TACCAATTCT	ATGATTGAGG	AAAGTAGTGT	TGCAGACGGT	GTGATAGTCG	1920
GTCCTTATGC	TCACATTCGT	CCAAATTCAA	GTCTGGGTGC	CCAAGTTCAT	ATTGGTAACT	1980
TTGTTGAGGT	GAAAGGATCT	TCAATCGGTG	AGAATACCAA	GGCTGGTCAT	TTGACTTATA	2040
TCGGAACTG	TGAAGTGGA	AGCAACGTTA	ATTTGCGTGC	TGGAAC TATT	ACAGTCAACT	2100
ATGACGGCAA	AAACAAATAC	AAGACAGTCA	TTGGAAACAA	TGTCTTTGTT	GGTTCAAATT	2160
CAACCATTAT	TGCACCAGTA	GAAC TTGGTG	ACAATTCCCT	CGTTGGTGCT	GGTTCAACTA	2220
TTACTAAAGA	CGTGCCAGCA	GATGCTATTG	CTATTGGTCG	CGGTCGTCAG	ATCAATAAAG	2280
ACGAATATGC	AACACGTCTT	CCTCATCATC	CTAAGAACCA	G TAGGAGCCT	ATCATGGAGT	2340
TTGAAGAAAA	AACGCTTAGC	CGAAAAGAAA	TCTATCAAGG	ACCAATATTT	AAACTGGTCC	2400
AAGATCAGGT	TGAATTACCA	GAAGGCAAGG	GAAC TGCCCA	ACGGGATTTG	ATTTTCCACA	2460
ATGGGGCTGT	CTGTGTTTTA	GCAGTAACGG	ATGAACAAAA	ACTTATCTTG	GTCAAGCAGT	2520
ACCGCAAAGC	TATCGAGGCT	GTCTCTTACG	AAATTCCAGC	CGGAAAATTG	GAAGTAGGAG	2580
AAAACACAGC	CCCTGTGGCA	GCTGCCCTTC	GTGAATTAGA	GGAAGAAACA	GCCTATACAG	2640
GGAAATTAGA	ACTCTTG TAC	GATTTTTTATT	CAGCTATTGG	CTTTTGTAAT	GAGAAGTTAA	2700
AACTATATTT	AGCAAGCGAT	TTGACAAAAG	TGGAAAATCC	GCGTCCGCAG	GATGAGGATG	2760
AAACCTTGGA	AGTCCTTGAA	GTGAGCTTAG	AAGAAGCGAA	AGAATTAATC	CAATCAGGTC	2820
ATATCTGTGA	TGCCAAGACA	ATTATGGCTG	TTCAGTATTG	GGAGTTGCAG	AAAAAATAGA	2880
GGAGGTCAGT	ATGGGTAAAT	CTTTATTAAC	GGATGAAATG	ATTGAAAGAG	CTAATAGAGG	2940
CGAAAAAATT	TCAGGTCCTC	CTTTGCTAGA	TGATAATGAG	GAACTAAGA	TTTTACCAAC	3000
CTCTTCTTCC	CGTTTTGGTT	ATGCCAATCC	TAAGGATCAT	GGTTTTAGCC	AGGAAACCTT	3060
GAAGATTCAG	GTCGAACCAT	CTATTCATAA	AAGCCGTCGT	ATTGAAAATA	CCAAGAGAAA	3120
TGTCTTCAAT	TCTAAGTTGA	ATAAAATCTT	ATTTGCGGTC	ATCTTTCTCT	TGATTTTGCT	3180
TGTTTTAGCA	ATGAACTTT	TGTAATAGAA	AAGGAATTGA	AATGAAAATA	GGAATTATTG	3240
CTGCTATGCC	AGAAGAACTG	GCTTATCTGG	TCCAGCATTT	AGATAATGCC	CAGGAGCAAG	3300

1080

TTGTTTTTGG GAATACCTAT CATAACAGGAA CCATTGCTTC TCATGAAGTC GTTCTTGTAG	3360
AAAGTGGAAT TGGTAAGGTC ATGTCTGCTA TGAGTGTGGC GATTTTGGCT GATCATTTCC	3420
AGGTGGATGC CCTTATTAAT ACGGGTTCAG CTGGGGCAGT AGCAGAAGGT ATCGCTGTTG	3480
GGGATGTCGT GATTGCTGAC AAATTAGCCT ATCATGACGT GGATGTCACA GCTTTTGGCT	3540
ATGCTTATGG ACAAATGGCG CAACAACCGC TTTATTTCTGA ATCAGACAAA ACCTTTGTTG	3600
CTCAAATCCA AAAGAGTTTA TCTCAATTGG ACCAAAACCTG GCATCTTGGT TTGATTGCTA	3660
CAGGAGATAG TTTTGTGCA GGAAATGACA AGATAGAAGC GATTAAGTCC CATTTCCCAG	3720
AAGTTTTAGC CGTGGAGATG GAGGGGGCAG CTATTGCTCA AGCAGCGCAT GCCCTCAATC	3780
TCCCAGTCTT AGTCATCCGA GCTATGAGTG ACAATGCCAA CCATGAAGCA AACATCTTTT	3840
TTGATGAGTT TATTATCGAA GCTGGACGTC GCTCTGCCCA AGTCTTGTTG ACCTTTTGA	3900
AGGCTTTAGA TTAAGCGGAA ATTTGACAGT TTTTCTAGCT TATGATAAGA TTTAAGTAAA	3960
GAAAAGCTAG AAAACGTTTC AGAGGATATT ATGAGTATTG AAATGACCGT CAGTGAGATT	4020
GCAGAGGTCT TAGGATTATC TCGCCAAGCA ATCAATAACC GTGTCAAAGA ATTACCAGAA	4080
GAAGACACAG ATAAAAATGA CAAG	4104

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

CACGGATAGG CTCGGCTTTC ATCAGTCCTC AGGCTGATTT ACTAATAGCA ACTTTCCTCG	60
ACAAAGTCCA CAGCGATACG TnTGGGTATC AATCCTACGC TTACGCTGAT ACCTTTGCTG	120
GCAGGATTGG CAACGATAGA GCTTGATTGG CTTGGAGTTA CTATTGGGCA AGGATGGTAC	180
AAACCGTAAT CCATCCACTG CTTTCAACAG TTCCTTAAAA TCCCGATCCT TGTGTTGATA	240
GCCTTTCCT TGAAAATAGA GGTGATAATG ACAGAGTTCA TGTCGGACAA TTTTCCTAAA	300
AACGTCCAAC CCCAGTTCCT GATAAACCTT GGGATTAAAA TCCAAATGCC CATCTTTGGG	360
GAAAAATCGC CCACCTGTCG AACGTAGACG CCTATTCCAC TGGACATGAT GGATAAAAGG	420
TCTGCCGAAG TCTTCTAGTG AAACCTGCTT GACGTAATCA GTCAGTTTCA TTTGGAGCTA	480
GGAGAGACAG ATTAACTTTT TCACGTTTCA TATCAATTTT CTTAACCCAA ACGCTCACCA	540
AATCTCCAAC TGCCACCACT TGAAGAGGTT GTTTGATAAA CTTGCGACTC ATATGGGAAA	600

1081

TATGGATGAG	ACCGTCCTCA	TGAATTCCGA	TATCAACAAA	AGCACCGAAA	TCAACAACGT	660
TACGCACCAC	TCCTTCTAGC	TTTTGTCCAA	CCACTAAGTC	CTTGATATCT	AGGACATCTT	720
GGCGAaCACA	GGTGCGTCAA	AGGAATCACG	GAAATCTCGA	CCTGGTTTGA	GAAGATCTGC	780
AATGATATCT	TTAAGAGTTT	CTGGACCAAG	GTCTAACTCT	TGCGCCATTT	CCTTGACTGA	840
AAGCGACTTG	AGTTTGCTTT	GGGCTTCTTC	GTTTAGGTCT	TTAATATCTA	AACGTTTGAA	900
GAGTTCCTTA	ACTGCAGTGT	AATCTCTCTG	GTGAACTCCT	GTATTATCAA	GGATATTGCT	960
ACTTTCAGGG	ATACGAAGGA	AACCAGCAGC	CTGCTCAAAG	GCCTTGGCTC	CCAGACGAGG	1020
AACTTTCCTTG	ATTTGGGCGC	GTGAAGTGAT	TTTTCCTTCT	TCCTCGCGGT	ATTTGACAAT	1080
ATTTTCAGAG	ATAGTTTTGT	TGAGTCCAGC	TACGTGTGAA	AGAAGAGCTG	GGCTAGCTGT	1140
ATTGACATTG	ACACCAACTT	GGTTAACCAC	TGTATCGACA	ACAAAGTCCA	GACTCTCAGA	1200
TAGTTTCTTC	TGACTGACAT	CGTGTTGGTA	TTGACCGACA	CCAATTGACT	TAGGATCGAT	1260
TTTGACCAAT	TCCGCAAGAG	GATCTTGCAA	ACGACGGGCG	ATAGAAATGG	CAGAGCGTTT	1320
TTCAACGGTC	AAGTCTGGAA	ACTCCTGACG	AGCAAGTTCG	CTGGCAGAAT	AGACAGAAGC	1380
ACCACTTTCA	TTAACGATAA	CATAGCTGAC	TTCAGGGAAA	TCTTTCAGAA	CTCCGCTAC	1440
AAAAGCTTCA	CTTTCACGAC	TGGCCGTTCC	ATTTCCAATG	GCAATAATCT	CTACACCGTA	1500
TTGACCAATT	AAATCTGCTA	AATCTTTCTT	GGCTTCTTCG	ATTTGACGAG	CTGATGCTGG	1560
TTTAACAGGA	TAAATAACCT	GAGTTGTCAG	CATTTTTCCT	GTTGCATCCA	CGACAGCTAG	1620
CTTGGCACCT	GTACGAAAGG	CTGGGTCAAA	TCCAAGAACC	ACGCGCCCTT	TCAGTGGAGC	1680
AACCAAGAGG	AGATTGCGCA	GATTGTCAGA	AAAAAGTTGG	ATAGCTCCTT	CTTCAGCTTT	1740
CTCAGTTAAT	TCTGTCCGAA	TACGACGCTC	GATAGCAGGC	AAGACCTTTT	TCTTAACGGA	1800
TTGCTGAACA	ACTTCATCAA	TATAAGCATT	TTTCACCTTG	AAACGAGTAG	CAAAGAAGGC	1860
AAGAATACGG	TCCGTCGCAT	GTTCAAAACC	GATCTTCAAG	ACACCAAGTT	TCTCCCCACG	1920
ATTGAGAGCC	AAGGTACGAT	AGCCTTGCAT	AGTTCCAACT	GTCTCTGAAA	AATCATAATA	1980
AATCTGAAAA	ACCTGCTTTT	CATCAAGACT	TTCATCCTTG	GCTTGAGAAG	TAAGTTTAGA	2040
GTGTCTCAGC	ACTTCCTGAT	AAGTCATAGA	ACGCAAGGTC	ACATCTTCCG	ATAAGGCTTC	2100
GACCAAAATA	TCAACTGCAC	CGGTCAAGGC	TTCCCTTGCCA	GTCGCAAATC	CTTCACAGAC	2160
GAACTTTTCA	GCTTCTTTCT	CTAAGTCAAC	TATATTCTGC	AAAATCAAGC	GAGCAAGAGG	2220
AAAGAGTCCA	GCTTCACGGG	CAATGGTTGC	CTTGGTACGA	CGCTTTTCCT	TATAAGGAAG	2280
ATAGAGTTCT	TCAACGTCTG	CTAATTTTTC	GGCAACTAAG	ATAGCTTCTT	CCAATTCCTT	2340

1082

GGTCAACTTA	CCTTGTTCTT	GAATCTTAGC	TAAGACAGCT	TCCTTACGGT	CATTGAGATT	2400
TGTCAGACTT	TTATCCAAAT	CAATAATAGC	CTTAATCGCC	ACCTCATCCA	GACTACCAGT	2460
CATGTCCTTG	CGATAACGCG	CGATAAAGGG	AATAGTCGCC	CCTTCAGCTG	TCAAACCTTAG	2520
AACGGTATCA	ATTTGCTTTA	ACGTCACTCC	CAAATCCTGA	GAGATTTTTT	CATATTTTTT	2580
ATCCATAAAT	CTATTATACC	ACAAGCTAAA	CGTTTCAAAT	TAACTCGTAG	AACATTTAAA	2640
AAATATGTAG	GAAATAGATT	TATATGCTAC	AGCGCAATAA	CTTGCACTTA	AAGAGCATTG	2700
CCACCTTTTT	TTAACCAAGC	CATGATATCA	AAAGTATTTA	ATGGATCAGA	CATAATAGCC	2760
AGTTCTGGAA	GATGTCCTG	ACCTGGAATA	ACACATTGAC	TTTTCAAATT	TTTATATGGA	2820
CGATTGACTA	AAATTAATTT	ATTAGAATAA	GGAAGATTAT	CCATCTTATT	TAAAATTTCT	2880
TCACTAGCTG	AATCTTTATT	ATCAAAATTA	AAATAAAGAT	TATTCCAATT	TATGCGTTTT	2940
TTTCTTTTTT	CCCCTTAGT	TCGTGCTTCT	TCAATACTAG	AATAATGTAG	AAAATGAATA	3000
TCTATATCTC	CTAAGTGCCC	CAAAGGATAA	ACTTCATGAG	TCCAGCTCGG	TGAAATAAGT	3060
TCCTCTTCGA	AAACAAGTTC	TTGTTCCATA	TAATAACGAA	AATGCTTTGT	AAGTTTATAA	3120
TAATCATCAG	GAAGAATAAA	TAAACCAACA	AAAGGTGTTT	TATATTGAAA	ACCAAGCTGT	3180
TTATAAATTA	ATCCTCCAAC	ACAATTATTA	CTTATAATCG	TAAAATCTAA	TCTATCAAGC	3240
TCAAGAAAAG	GGAAAATTCC	TTTCTCTGCA	GCTATTAACT	TATGATAAAC	AATATCAGAA	3300
TCTAAATATT	CACCGTCATT	TTTTAACCBA	GCACTAAAAT	TTGCCAATTC	TTGAATATAT	3360
TGTTTTTTCG	CTCTTTCTAT	ATCATAGTTT	TCTAAGACGG	CGCAATCTTT	GATTCTATTT	3420
TCATAATTTT	CTAATATGAT	TTTGTAGGAG	TCTTTTAGAG	GTTTAGCATC	TATAACAGGT	3480
TTATAGATAT	ATGTCGGGAA	ATTAATATAG	GTTGCAGTTT	TAGAGTGAAT	ATAAAGTCTC	3540
CAAATAAGGT	TGTTTATATC	AAATTGATTT	ATTTTTTCGT	AAAGCTTACT	ATTGAATAAT	3600
TTTCCAAATA	ATGAGCGATA	TTGTTTTCTA	ATTGATGAT	CTGTATCATC	CATCTTTTGT	3660
AAAACCTGAA	CATTCGTAA	ATTTTCTGTC	AACCAATTAT	CCCCCAGAAA	AGGATAAAAG	3720
TAAAATACTC	CATCAACCAA	ATCAGCAAAA	TGACCAAGAA	CAACATCAGA	ATCGGATAAT	3780
TTTATCGCAT	GATACATCTT	TTCAAATGTC	CAATCAAATA	ATGAATCATT	TGAAGATAGA	3840
AACGTAATAT	AATCTCCTGT	AATCATATCA	GACAACTCAG	CAAAAGAATT	CTCATCTATA	3900
ATCTTAATAT	TAAATGATAG	ATTCATCTGT	TGGCTAATGG	AAGCTATCTC	CTCTGTAGAT	3960
TGATTTACAA	TAATAACTTC	TATATCTTTT	AATGTTTGTC	TCTCCACTAT	TGACAAAGAC	4020
TCTAATAAAC	TATTTTTATC	TCCTTGATGT	AACAAAACAA	CACTAATTGA	GTAAGTCAGT	4080
TTGACTACCT	CCCATAATTT	TCTGATAATG	ATTTTCTTTT	TATTTAATTA	TAGCACAATT	4140

1083

ATGATATATA	TCAGGTAATA	TCAAGCTATA	TTATCTCTTA	GCTACTCAAT	TTGAAATTTT	4200
AACTTTTCCC	TTTTCCGCAA	AATAATAGTA	TAATAGAGGT	AGAATCTAGA	ATCGAGGTAC	4260
ACCTATGGCT	GTCAAATTTA	CAAAACGAGA	CGACTTGGAC	AAGATGTTTG	AAGAGTTTGC	4320
TAAACTCCCT	GATTTGAAAC	AAGTTACTTT	CCCTGATGAC	AAAGAGAAAA	AAGTCAAAGC	4380
AGAAAAGAAA	AACTAGATGA	CTGCTTTTCA	ACAACTCCCA	TCTAGTGTAC	TTCAAACCTGG	4440
AGCCATTTTT	CTCTCCATTA	TCATTGAAGC	CCTTCCCTTC	GTTCTGATAG	GAAGCATTGT	4500
CTCAGGGCTG	ATTGAAGTTT	ATATCACACC	TGACAAGGTT	TATCATTTTC	TCCCTCGAAA	4560
TCGTTGGGGG	AGAATCTTTT	TTGGGACCTT	TGTCGGTATA	CTTTTCCCTT	CTTGTGAATG	4620
TGGAATCGTC	CCCATCATCA	ATCGTTTTCT	GGAAAAAAG	GTTCCAAGTT	ACACGGCCGT	4680
TCCTTTTCTT	GTGACAGCAC	CTGTTATCAA	TCCCATTGTT	CTTTTTCGCA	CCTATTCTGC	4740
CTTTGGCAAC	TCCTTCCATG	TCGCCCTATT	ACGAGCTCTG	GGTTCCATTC	TTGTGGCTGT	4800
AATACTAGGA	ATTTTTCTAG	GATTTTTCTG	GCAAGAACCG	ATTCAGAAAG	AAAATCGTCT	4860
GGCTTGTCAT	GAGCATGATT	TTTCTTACTT	GAGTTCTGCA	AAAAAAGTTT	TTCAAGTCTT	4920
TGTGCAGGCC	ATTGATGAAT	TTTTTGATAC	GGGGCGTTAT	TTGGTATTTG	GCTGCCTCTT	4980
TGCTTCTATA	ATACAGGTCT	ACGTTCCGAC	TCGGATTCTG	ACCTCTATCA	GTGCGACCCC	5040
TCTTTTGGCC	ATCCTGCTCT	TGATGATTTT	AGCCTTTCTT	CTTTCGCTCT	GTAGTGAGGC	5100
GGATGCCTTT	ATAGGTGCTT	CTCTTCTCTC	GAGTTTCGGT	TTGGCACCAG	TTCTGGCCTT	5160
TCTCGTCATT	GGTCCAATGC	TGGATATCAA	AAATATTCTC	ATGATGAAAA	ATTACTTGAA	5220
AGCACGATTT	ATCAGTCACT	TCATAACAAT	TGTAACCTCT	GTCGTCTTAG	TCTATTCTCT	5280
CTTGATTGGA	GTTATCCTAT	GATTCGATTT	TTAGTTTTAG	CTGGCTATTT	TGAACTGACT	5340
ATTTACCTCC	ATCTGTCGGG	CAAATAAAC	CAGTACATCA	ACATGCACTA	TTCCTATCTG	5400
GCCTATATCT	CCATGGTGCT	TTCTTTTATC	TTGGCTATCG	TTCAATTGTA	TATCTGGATG	5460
AAGCAAGTCA	AAACCCACAG	TCATCTGAAC	AGCCGATTAG	CCAAGATAAC	GAGTATTTCT	5520
CTTCTGGCTA	TTCCACTTGT	CATCGGCTTA	ACTTTCCCAA	CTGTTAGCTT	GGATTCTCAG	5580
ACTGTTTCTG	CTAAAGGTTA	TCATTTCCCC	CTATCGGAAG	GAACGGATCT	AGCCATTGAG	5640
ACAAGCGAAG	GGACGACAAG	CCAATATTTG	AAACCAGATA	CCAGTTCTTA	TTTTTCAAAA	5700
TCAGCCTATG	AAAAGGAAAT	GCGAACGGCG	GCGGATAAAT	ACTTATCCCA	AGATAGTATT	5760
CAGATCACTA	ATGAAAATA	TATGGAAGTC	ATGGAGGCTA	TCTACGACTA	TCCAGATGAG	5820
TTTGAGGGCA	AGACAATCCA	GTTTACAGGC	TTTGTCTATA	ACGACCCAG	TCATGCCAAT	5880

1084

AGTCAATTTT	TGTTCCGATT	CGGCATTATC	CACTGTATCG	CAGATTCTGG	TGTCTATGGA	5940
TTGCTGACCA	AGGGCAATAC	CCGGCAGTAT	GAAAACAACA	CTTGGATAAC	AGCCAAAGGA	6000
AAACTGGTCA	ATCACTACCA	TAAAGAACTC	AAACAAAACC	TTCCAACCTT	GGAAATCGAC	6060
AGCTTTACCA	AAGTCGATAA	ACCAGAAAAT	CCCTATGTAT	ATAGAGCTTT	TTAAGAAAAT	6120
CAAGATAAAA	ACGAACAAGT	TCTCTTCTGA	ATAACAGAAA	AAGAGCCTGT	TCGTTTTTTG	6180
TTATATGAAA	ATTAGTGACT	TGTAGATTTT	CATCTTATAC	CATTCCCAGC	AATACAAGTA	6240
GCTCATAGAA	AATAAGCGAG	CCACTCATTC	ATTAGACTAG	CGATTTCTTT	AGGTGCTTGA	6300
GTATAAAGCT	CATGGCCAAA	GTTTTCTAAA	AAAATAGTAT	CAAATAGTC	TGGCAATTCT	6360
TTTAGGGCTT	CCTCTCTCCA	TGTAGCTTCA	TTAGGATAGC	GAGGACTAAT	AAACAAGGTA	6420
TCTCCCCTT	CTCTCTTAAA	AGCTTGTATT	TTTCTCCGTA	GcGGAGTATC	GCTTCTATAT	6480
TTTCATAATT	TATAGCCAAC	TCATATCTAT	TATACTCAAC	ATTCCAGTGA	TAAGACTGTC	6540
TTACAGCTTT	CTCCATATTT	TCTGACCAAT	GCTTTGCTTC	AGATTTTTCT	TTAGAAGTAA	6600
GAACATCTAA	GTCCGAAACA	ATTTGAGATT	TGATATAATT	TTTAGTTTCC	TCTAACTCTG	6660
TATCCAAAGG	TAAAATCTTA	TCTAAATCTA	GATAGCCACC	ATCCAAAAGA	ATCAGTTTCT	6720
TTACTTCTTC	AAATTCCGAT	GCGAAATAAC	GAGCTAAATC	TCCTCCAAGA	GAATGGCCTA	6780
TCAGACAGAT	AGATTCTTCC	TCTACAATTT	CATTTTTTAA	CCATGATTTT	AATTCTGTTT	6840
CATCTCGAAG	ATGCTTTTCA	TATGGATTTA	GAAAATAGAC	CTGCGAATCT	AGTTCTTGAA	6900
GAAAATCCTT	GCTATGATAG	GCATTGCTTC	CCAAACCGCC	AATAAAATAT	TTTTTCATTC	6960
TCTACTTAAT	ACTATGCTTA	TTCATCTTTT	GTTCAAAGAT	AGTTGTGATA	ATCTGACGCA	7020
ATTCTTCGCG	TTTTTTTTCT	GGAATCTCAC	CACTTGTTTG	AGCTACAGCG	TAGAGTTCAG	7080
GGTATTCAAT	TGAAATGCGT	TTAATCGTAC	GTGTTGTAGC	ATGTTTTCTG	ACAAAAACG	7140
GGATTGCTT	AATCAAGTCT	TGTGGGACTA	GCGCCAGAAT	CTTCTCAGTA	GTTTCTTTGT	7200
CACTAATATT	AGACATTGTA	AGCCTTTTCT	TAATCATTTT	CTGTTCTTTT	TCTGTAAAAT	7260
CTTTTAATTC	CATTCGATTA	GTCCTCCTAT	TTTCTCTAAG	TTAAATTATG	TACTAATACA	7320
GATGAAACTA	CAAAGAATAA	ACTTTAAGAA	ATCTTCTCAC	TGATAAGATT	TTAGCATTAG	7380
ACTTCCTGCG	AAACAAAATA	TGGTATAGTA	GTTCTATGAA	TTATGAAGCA	AGTAAACAAC	7440
TAAGTGATGC	ACGATTTAAA	CGTCTTGTTG	GTGTTGAGCG	CACGACTTTT	GAAGAGATAT	7500
TAGCTGTATT	AAAAACAGCT	TATCAACTTA	AACACGCAAA	AGGTGGACGA	AAACCTAAAT	7560
TAAGCCTAGA	AGACCTTCTT	ATGGCCACTC	TTCAATATGT	GCGAGAATAC	CGCACTTATG	7620
AAGAAATTGC	GGCTGATTTT	GGTATTCACG	AAAGCAACTT	AATCCGTCGG	AGCCAATGGG	7680

1085

TTTAAGTAAC TCTTGTTCAA AGTGGTGTGA CGATTTCAAG AACTCCTCTC AGTTCTGAGG	7740
ACACGGTAAT GATTGATAGC CATTCCCATC AATATCGTAT CTTTGGACAT AGCCAATAAA	7800
TGTTTCATTT TTGCGTGGTT TCTGGCTATT AACGATTGAA ATAACCCACC AACTTATCAA	7860
AAATAGAAAT AAAAATCCTA AGATTACTGT CATATCATAA CACTATTAAA GTTTAACCCA	7920
CTTATCATTA TCCATGATAA AAGGCTTAGC CAGTCCCTCG CCTGTATAAT CCGCATACTT	7980
GGTGCCCAA TACTTGTAGC AATCTTCCTT ACTAGCAAAT TTAATCGCTT GG TAGGGCTC	8040
TTCGAAAGTC AATTTCTCTA CAAATAAGAA ACCGTCATCA GCAGGTACTA AGACCCCAAC	8100
GTGGCCTACA AACAGATACT CGCCATCCAA ATTGTCGTGC AAGACTACAG ACAGCATTCG	8160
AGCTTTTTTCA TTGAATTGAA ATTGTGAGAA GAATGCTTCC ATCTTTTCAG CGTGAACCTT	8220
GACATCTGTA GTTGACTCAG TTGGA ACTCT CGAAAATAGA ATATCAA ACT CTTCTTATC	8280
TTGTGAATCA AAGACCTTTC CTTTATCAAT CGCATCATTA TCTAGGAAAA GCAACTGGTC	8340
ATTCTTTTCA AGCTTTGGAA TGGTGACTGA ATTTTTCAAA AGACAATAAC TATTGATACG	8400
GCAGTTGGTC CCAACAAAAT CGCCCTTCTT TTGATTCCAG AGATGACTGA TTTTCTCAAC	8460
ATCGTATTCG GTGTGAGTAA AGGAAGTGAA ATCTCCTGAT AAGCCAGTTG AGCCGACAAT	8520
GGTATTATAG TCATTAACGA GATTAAAAA TGCATCAACA CTATTTGGAT CCAAGTGAGC	8580
TGATAAGAGA GATTTGACCT CTTCTGTACT TACCTGGTTG TTTAGGTTGG TGTATGAAGC	8640
TTTCCATGGA ACTTTCGCTG AACTGCTTTG CCTTTGATTC GTCCCCTCAG AAGTAGCATG	8700
TTGTTGTTGA CAAGCAGCCA AGCCTAAAA CAAGGCTGAA CAGATTCCTA ATGTGGCTAA	8760
TTTTCTTGAT TTCTTCATTT CTTTCTCCTA AATGTCTTGG ATTAAAGTTT CTTTAACTAT	8820
TGCTTTACAG ATATTGATTA CTTTCTCATT TAATGTGTTC ATCGTCTTTC CTCCGG	8876

(2) INFORMATION FOR SEQ ID NO: 171:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14736 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

CGCAAAC TTT CGCGGTCGGA AGGTAGTTTT ATGACACGAT TTGAGATACG AGATGATTTT	60
TATCTCGATG GAAAATCATT TAAGATTTTA TCTGGTGCCA TTCATTATTT TAGGGTTCCT	120
CCAGAGGATT GGTATCATTC GCTCTATAAC TTGAAGGCTC TTGGTTTTAA TACGGTAGAG	180

1086

ACTTATGTTG	CTTGGAATTT	ACACGAGCCT	TGTGAAGGTG	AGTTTCATTT	TGAAGGTGAT	240
CTGGATTTAG	AGAAATTTCT	CCAAATAGCG	CAGGATTTGG	GTCTCTACGC	AATTGTGCGT	300
CCGTCTCCAT	TTATCTGTGC	GGAATGGGAA	TTCGGTGGCT	TACCAGCTTG	GCTCTTGACC	360
AAGAACATGC	GAATTCGCTC	ATCCGACCCA	GCATATATCG	AGGCAGTTGG	TCGCTACTAT	420
GATCAGTTAT	TGCCAAGACT	GGTGCCTCGT	TTGTTGGACA	ATGGTGGCAA	TATTCTCATG	480
ATGCAGGTTG	AAAATGAGTA	TGGTTCCTAC	GGAGAAGATA	AGGCTTACCT	GAGAGCGATT	540
CGACAGCTAA	TGGAAGAGTG	TGGCGTAACC	TGTCCCCTCT	TTACATCAGA	TGGTCCATGG	600
CGAGCTACTC	TGAAAGCTGG	AACCTTAATT	GAAGAGGACC	TCTTTGTAAC	AGGAAACTTT	660
GGTTCCTAAGG	CACCTTACAA	CTTTTCGCAG	ATGCAGGAAT	TCTTTGATGA	ACATGGTAAG	720
AAATGGCCAC	TCATGTGTAT	GGAGTTCCTG	GATGGTTGGT	TCAATCGCTG	GAAAGAACCG	780
ATTATCACAC	GGGATCCTAA	GGAATTGGCA	GATGCAGTTC	GAGAGGTTTT	GGAACAAGGC	840
TCTATCAATC	TTTACATGTT	CCACGGTGGT	ACAACTTTTG	GTTTCATGAA	TGGTTGCTCA	900
GCTCGAGGAA	CTTTGGACCT	GCCACAAGTT	ACGTCTTATG	ATTACGATGC	CCTTCTGGAT	960
GAAGAAGGAA	ATCCAACCTG	TAAATATCTT	GCAGTCAAGA	AGATGATGGC	AACACATTTT	1020
TCAGAGTATC	CGCAGTTGGA	ACCACTCTAC	AAAGAGAGTA	TGGAGTTGGA	TGCTATTCCA	1080
CTAGTTGAAA	AAGTTTCTTT	GTTTGAAACC	TTAGATAGCT	TGTCAAGTCC	TGTAGAAAGT	1140
CTCTATCCTC	AAAAGATGGA	GGAGCTGGGA	CAAAGTTATG	GCTACCTACT	TTATCGAACA	1200
GAAACAAACT	GGGATGCAGA	AGAAGAAAGA	CTTCGTATCA	TTGATGGTCG	AGATAGGGCC	1260
CAGCTGTATG	TCGATGGTCA	GTGGGTAAAA	ACTCAATATC	AGACAGAGAT	TGGGGAAGAT	1320
ATTTTTTATC	AAGGTAAAAA	GAAAGGGCTA	TCTAGGTTAG	ATATCTTGAT	AGAAAATATG	1380
GGGCGTGTCA	ACTATGGGCA	TAAGTTCTTA	GCGGATACGC	AACGTAAGGG	AATTCGGACA	1440
GGGGTCTGTA	AGGATCTGCA	TTTCTTACTA	AACTGGAAAC	ACTATCCACT	CCCCTAGAC	1500
AATCCTGAGA	AAATTGATTT	TTCAAAAAGGA	TGGACTCAAG	GACAACCAGC	CTTTTACGCT	1560
TATGACTTTA	CAGTCGAAGA	GCCAAAAGAT	ACTTACCTAG	ACTTGTCTGA	GTTTGGTAAG	1620
GGGGTTGCCT	TTGTCAATGG	GCAGAATCTA	GGACGTTTTT	GGAACGTTGG	CCCAACTCTC	1680
TCACTTTATA	TCCCTCATAG	CTATCTCAAG	GAAGGTGCCA	ACCGCATCAT	TATCTTTGAA	1740
ACAGAAGGTC	AATATAAAGA	AGAGATTCAT	TTAACTCGTA	AACCTACACT	AAAACATATA	1800
AAGGGGGAAA	ACTTATGACA	ATTGTAGGAT	GCCGTATTGA	TGGACGTTTG	ATCCACGGAC	1860
AAGTAGCCAA	TCTTTGGGCT	GGAAAATAA	ATGTTTCACG	CATTATGGTT	GTAGACGACG	1920
AAGTTGTCAA	CAACGATATT	GAAAAGAGTG	GTTTGAAACT	TGCGACACCA	CCAGGTGTGA	1980

1087

AATTGAGTAT	TTTGCCAGTT	GAGAAAGCTG	CAGCCAATAT	TCTTGGTGGC	AAATACGATA	2040
GCCAACGTCT	CTTTATCGTG	GCTCGTAAAC	CAGACCGCTT	CCTTGGTTTG	GTAGAAGCAG	2100
GTGTACCACT	TGAAACCCTT	AATGTTGGGA	ATATGTCTCA	AACACCAGAA	ACTCGTTCCTA	2160
TTACACGTTC	TATCAACGTA	GTAGACAAGG	ATGTGGAAGA	CTTCCACAAA	CTGGCAGAAA	2220
AAGGTGTTAA	ACTTACTGCT	CAGATGGTTC	CAAATGATCC	AATTTTCAGAC	TTTTTTGAGCT	2280
TATTAATAA	GGAAAAAAT	TTTTAGGAGG	TCATTGTTAT	GATACAATGG	TGGCAAATTT	2340
TACTTCTCAC	TTTGTACTCA	GCTTATCAAA	TCTGTGATGA	GTTGACGATC	GTTTCATCTG	2400
CAGGTTCCCC	TGTATTTGCT	GGTTTCATTA	CTGGTTTAAT	CATGGGAGAT	GTGACTACTG	2460
GTTTACTTAT	CGGTGGTAAC	TTGCAACTGT	TCGTTCTTGG	GGTTGGTACC	TTCCGGTGGTG	2520
CTTCTCGTAT	CGACGCAACT	TCTGGTGCGG	TTCTTGCGAC	ACCTTCTCTG	TTTCACAAGG	2580
AATTGATGCA	CCGCTTGCCA	TTACTACAAT	CGCTGTACCA	GTAGCAGCTC	TCTTGACTTA	2640
CTTCGACGTT	CTTGGTCGTA	TGACTACTAC	CTTCTTCGCT	CACCGTGTGG	ATGCTGCAAT	2700
CGAACGCTTT	GACTATAAAG	GTATTGAACG	CAACTACTTG	CTTGGTGCGA	TTCCGTGGGC	2760
TCTATCTCGT	GCCCTTCCAG	TCTTCTTTGC	CCTTGCTTTT	GGTGGTGCCCT	TTGTACAATC	2820
AGTAGTAGAC	TTCGTTGAAG	CCTACAAATG	GGTTGCAGAT	GGCTTGACAC	TTGCAGGACG	2880
TATGCTTCCA	GGTCTTGAT	TTGCAATCTT	GCTTCGTTAC	CTTCCAGTTA	AACGTAACCT	2940
TCACTACCTT	GCTATGGGAT	TTGGTTTGAC	AGCTATGTTG	ACTGTTCTTT	ACTCATATGT	3000
AACAGGTCTT	GGTGGCGCTG	TTGCTGGTAT	CGTAGGTACT	CTTCCTGCTG	AAGTTGCTGA	3060
AAAAATTGGT	TTCGTGAACA	ACTTCAAAGG	TTTGTCTATG	ATTGGTATTT	CTATCGTAGG	3120
TATTTTCCTT	GCAGTGCTTC	ACTTCAAAAA	TAGCCAAAAA	GTAGCTGTAG	CAGCACCTTC	3180
TACACCATCA	GAAAGTGGGG	AAATCGAAGA	TGACGAATTC	TAATTACAAA	CTTACAAAAG	3240
AAGATTTTAA	TCAAATCAAC	AAACGTAGCT	TGTTTACTTT	CCAATTAGGT	TGGAACCTACG	3300
AACGTATGCA	AGCTTCTGGT	TACCTTTACA	TGATCTTGCC	TCAGTTGCGT	AAAATGTATG	3360
GTGATGGAAC	TCCTGAATTG	AAAGAAATGA	TGAAAGTTCA	TACTCAATTC	TTCAATACTT	3420
CACCATTCTT	CCATACCATT	ATCGCTGGTT	TTGACCTTGC	CATGGAAGAA	AAAGATGGTG	3480
TAGGTTCAAA	AGACGCCGTT	AACGGTATCA	AGACAGGTTT	GATGGGACCA	TTGCTCCTC	3540
TTGGGGATAC	AATCTTTGGT	TCACTTGATC	CTGCTATCAT	GGGGTCAGTC	GCAGCAACTA	3600
TGGCTATCGC	TGGCCAACCT	TGGGGGATCT	TCCTTTGGAT	TGCAGTTGCA	GTAGCGTATG	3660
ACATCTTCCG	TTGGAAACAG	TTGGAATTTG	CTTACAAAGA	AGGGGTAAAC	CTTATCAACA	3720

1088

ACATGCAAAG	TACCTTGACA	GCTTTGATTG	ACGCTGCATC	TGTACTTGGT	GTCTTCATGA	3780
TGGGTGCTCT	TGTAGCAACA	GTGATTAAC	TTGAAATTT	TTACAAGTTG	CCAATCGGTG	3840
AAAAGATGAT	TGATTTCCAA	GACATCTTGA	ACCAAATCTT	CCCACGTTTG	CTTCCAGCAA	3900
TCTTTACTGC	CTTTATCTTC	TGGTTGCTTG	GTAAGAAAGG	TATGAACTCT	ACTAAAGCTA	3960
TCGGTATTAT	TATCGTACTT	GCTTTGGCTC	TTTCTGCCCT	TGGTCACTTT	GCACTTGGAA	4020
TGTAATTCCT	TATGACTAAA	TCATTAATTT	TGGTGAGCCA	TGGTCGCTTC	TGTGAGGAGC	4080
TTAGAGGTAG	CACAGAAATG	ATTATGGGCC	CACAAGACAA	CATTTACACA	GTAGCTCTTC	4140
TTCCAGAAGA	TGGCCCAGAA	GAATTTACTG	CTAAATTTGA	AGCTGTTATT	GAAGGATTGG	4200
ATGATTTCCCT	AGTCTTTGCG	GATCTTCTCG	GTGGGACACC	TTGTAATGTG	GTGAGTCGCT	4260
TGATCATGGA	AGGTCGTGAT	ATTGACCTTT	ACGCAGGGAT	GAATCTTCCA	ATGGTGATTG	4320
AATTTATCAA	TGCGAGCCTT	ACAGGCGCAG	ATGCGGACTA	CAAGAGCCGT	GCTGCAGAAA	4380
GCATTGTGAA	AGTTAATGAC	CTGTTAGCGG	GCTTCGATGA	TGACGAAGAT	GAATAATACT	4440
CTTCGAAAAT	CTCTTCAAAC	TACGTCAACG	TCGCCTTGCC	GTAGGTATAT	GTTACTGACT	4500
TCGTCAGTCT	TATCCGGCAA	CCTCAAAACG	GTGTTTTGAG	CTGACTTCGT	CAGTCTTATC	4560
CGGCAACCTC	AAAGCAGTGC	TTTGAGCAGC	CTGCGGCTAG	TTTCCTACAG	ATTTTAGTTG	4620
GAACTCGATT	CAATTCATGT	GACAACGTGA	AAATCGTTAG	AGCATTTTAT	ATAGAATATA	4680
CATGGGAATG	TAGCTTACTC	CCATTCCCAT	ATTTAATAGA	AAAAGAGGAA	CTCAATGCTA	4740
CATTATACAA	AAGAAGACTT	GCTCGAATTG	GGTGCAGAAA	TCACTACGCG	TGAAATCTAC	4800
CAACAGCCTG	ATGTATGGAG	AGAAGCTTTT	GAATTTTATC	AAGCAAAACG	TGAAGAAATT	4860
GCAGCCTTCC	TACAAGAAAT	CGCTGATAAA	CATGACTATA	TTAAGGTTAT	CTTGACAGGT	4920
GCTGGGACTT	CTGCTTATGT	GGGAGATACC	TTGCTACCTT	ATTTTAAGGA	AGTCTATGAC	4980
GAACGCAAAT	GGAATTTCAA	TGCTATTGCG	ACAACAGATA	TCGTTGCCAA	TCCAGCAACC	5040
TATTTGAAAA	AAGATGTGGC	AACTGTCCTT	GTGTCTTTTG	CTCGTAGTGG	GAATTCGCCT	5100
GAAAGTTTGG	CGACTGTTGA	TTTGGCCAAA	TCCTTGGTGG	ATGAGCTTTA	TCAAGTGACG	5160
ATTACTTGTG	CAGCAGATGG	TAAATTGGCT	CTTCAAGCTC	ACGGTGATGA	TCGTAATCTC	5220
TTGCTCTTGC	AACCAGCTGT	CTCTAATGAT	GCTGGATTTG	CCATGACTTC	TAGCTTTACG	5280
TCTATGATGT	TGACAACTCT	CTTGGTCTTT	GATCCTACAG	AATTTGCTGT	TAAGTCTGAA	5340
CGTTTTGAAG	TTGTATCTAG	TCTTGCCCGT	AAAGTTTTAG	ACAAGGCAGA	AGATGTCAAA	5400
GAGCTCGTTG	ATTTAGACTT	TAACCGTGTC	ATCTATCTAG	GCGCTGGTCC	TTTCTTTGGA	5460
CTTGCTCATG	AAGCTCAGCT	CAAGATTTTG	GAATTAAC	CTGGTCAAGT	TGCGACCATG	5520

1089

TATGAAAGCC	CAGTTGGCTT	CCGTCACGGT	CCAAAATCTC	TTATCAACGA	CAATACAGTT	5580
GTTTTGGTCT	TTGGTACAAC	GACAGACTAC	ACTCGTAAGT	ACGACTTGGA	CTTGGTTCGT	5640
GAAGTTGCTG	GTGACCAGAT	TGCTCGTCGT	GTTGTGCTTT	TGAGTGATCA	AGCTTTTGGT	5700
CTTGAAAATG	TCAAAGAAGT	GGCCCTTGGT	TGTGGCGGTG	TCTTGAATGA	TATTTACCGT	5760
GTCTTCCCTT	ACATCGTTTA	TGCCCAACTC	TTTGCTTTAT	TGACTTCACT	CAAGGTAGAA	5820
AATAAACCAG	ATACACCGTC	TCCTACAGGT	ACAGTAAACC	GTGTAGTACA	AGGTGTCATA	5880
ATTCACGAAT	ATCAAAAGTA	AGACAGTGTT	TATGAATTCT	TGACAAGAGG	ATTTGTAAAT	5940
TATCAGATAA	ACCATAGATT	GTCAGTACGC	TTTCTATGGT	TTGTTTGCTT	GAGAGAAATA	6000
GTAAAAGGAG	AACAGAATGA	AAGCATACAC	AGAGCGTGTA	TTTGGAAATG	TTGAGGGTGA	6060
GGATGTCTTG	GCCTATCGAT	TTGAGACAGA	CGGTGGCTAC	CAACTTGAGG	TTATGACTTA	6120
TGGTGCGACT	ATCTTGCGCT	ATGTCGCACC	TGACAAGGCT	GGAAATTTTG	CCAATGTTAT	6180
CTTGGGATTT	GATGACTTTG	ATAGTTATGT	AGGCAATAGT	CCCAAGCATG	GAGCAAGTGT	6240
AGGTCCTGTA	GCGGGTCGTA	TTGCAGGTGC	GACCTTTGAG	CTCAATGGTA	AGACCTATGA	6300
CCTTGAGGTT	AATAATGCTA	GCAACTGTAA	TCACAGTGGT	TCAACTGGTT	GGGATTCCAG	6360
CTTGTTTGAA	GTTGAAGAAG	TAAGCGATCA	TGGCTTGACT	CTCTACACAG	AGCGTACAGA	6420
TGGGACAGGA	GGGTTCCCTG	GAAATCTCAA	GATTTGGATC	AGTTATCACT	TGGAAGAAAC	6480
TGGTGCCTAT	GAAATCAGCT	ACAAGGTAAC	GACCGATCAG	GATACGCTGG	TCAATCCAAC	6540
CAACCACAGC	TATTTCAACT	TGTCTGGTGA	TTTCACGCAG	ACGATTGACC	GTCATGTCTT	6600
CCAACTAAAC	ACAGAGGGCA	TTTACTCAAT	CGCTCCTGAC	GGTGTTCCTG	CCAAAACCTCC	6660
AGAAGCCAAC	CGTGATGTGG	TCAAACACGT	CTACAATGGT	ACCTTGTTGA	AGGATATCTT	6720
TGCAGAAGAA	GATGAGCAAA	TCCAGCTGGC	ATCAGGTTTG	GATCATCCAT	TTGCCCTTCC	6780
TGCAGGCCAT	GACAATGCTG	GATTCCTTTA	TGACCAAAT	TCAGGTCGCT	TCCTGCTTTT	6840
CAAGACAGAA	GCTCCTTGCT	TTGTGGTCTA	CACAGCAAAC	TTTGTGGATG	AAAGTGTCAT	6900
CATAGGAGGT	CAGCCAATGC	TACAGCACAA	TGGGATTGCT	CTTGAAGCGC	AAGCTTTACC	6960
AGATGCCATT	CACAGTGACC	TTAAAGGCCA	AGTCATTCTT	AAAGCTGGTC	AAACCTTCAC	7020
CAGTAAGACA	CGTTATGAAC	TTGTTGTGAA	GTAAAAGAGT	CATTGCGCCT	ACTTTTGGGA	7080
GCTAGGAATA	GGTACGCAGA	GACAAATAGT	AGGAAAATAT	GATATAACTA	AGCGTTGAAA	7140
GCTATCTGTT	AATATAATAT	TCAAAC TACA	ATAAGGAGTA	AGAAAGAAAC	GAAGAAAATT	7200
GTATTTGCTA	GTGCCTTGGC	TTTGACCTTG	GCTGGAGCAG	TTT TGACAAA	TGATGTTTTT	7260

1090

GCGAACGACA	GACTTGTGGC	AACACAAACT	ACTGATGGTA	AAAATGAAAA	TGTATTGACC	7320
TCAGAGGTGC	TAAAACCTTC	TAGTGGCAAT	GTTTTGGTTG	GAATCAAAGG	AGAATTTGTG	7380
GCTCCTCATC	AACAATCTAT	TTTGGATGCC	ATCAATGCTA	TCTGTAAAGA	AGCGGCTGAC	7440
GAAGGTTTGG	TAGATAAGTA	TGTCCCTATC	AAATGATCAA	CTGACCTAGA	AAAGGCAGCT	7500
TTTGCCAGAG	CTACAGAAGC	ATCTATAACC	ATGGATCATA	CCCGTCTTTC	TAGCAAAGAT	7560
CTTTGGAGTG	CCTTTCCAAC	TTCTAATAGT	ATAATGGGAG	AAAATTTGGC	ATGGAATCAT	7620
GACGGTTTTT	TAAAAGCTAT	TGAACAATGG	CGTGCTGAAA	AAGCAGATTA	TGTGGAGAAA	7680
AAAATAGTGG	TTCAGACAAC	GGGAAATCTG	GTCACATGA	GTCGCTAATT	AACCCTAAAT	7740
TTACACACAT	GGGGATGGCA	GCTTTTAAAA	ATCCTAACAA	TCAATACAAA	GCTATTACAA	7800
TTGCTCAAAC	TCTAGGTGAT	GATGCTTCTT	CAGAGGAATT	GGCTGGTAGA	TATGGTTCTG	7860
CTGTTCAAGT	TACAGAAGTG	ACTGCCTCAA	ACCTTTCAAC	AGTTAAAACT	AAAGCTACGG	7920
TTGTAGAAAA	ACCACTGAAA	GATTTTAGAG	CGTCTACGTC	TGATCAGTCT	GGTTGGGTGG	7980
AATCTAATGG	TAAATGGTAT	TTCTATGAGT	CTGGTGATGT	GAAGACAGGT	TGGGTGAAAA	8040
CAGATGGTAA	ATGGTACTAT	TTGAATGACT	TAGGTGTCAT	GCAGACTGGA	TTTGTA AAAAT	8100
TTTCTGGTAG	CTGGTATTAC	TTGAGCAATT	CAGGTGCTAT	GTTTACAGGC	TGGGGAACAG	8160
ATGGTAGCAG	ATGGTTCTAC	TTTGACGGCT	CAGGAGCTAT	GAAGACAGGC	TGGTACAAGG	8220
AAAATGGCAC	TTGGTATTAC	CTTGACGAAG	CAGGTATCAT	GAAGACAGGT	TGGTTTAAAG	8280
TCGGACCACA	CTGGTACTAT	GCCTACGGTT	CAGGAGCTTT	GGCTGTGAGC	ACAACAACAC	8340
CAGATGGTTA	CCGTGTAAAT	GGTAATGGTG	AATGGGTAAA	CTAGGCTCAG	GCCATAGGTA	8400
AAGCATTCAT	CTTACTTAGC	AAAAAGAATG	AACGATAAGA	AAGAGGTTGA	TGGCGAACAT	8460
TGGCCTCTTT	TGATTTATAA	AGATTGGATT	CTTGTCGCCT	CAATTTCAGA	CTTTTCTATT	8520
GTAAGCTAAT	ATTTTATAGC	CCATTAAAAG	CATAAGCGGT	AATCTAATTT	AAAAAATGCT	8580
GTAATTAGTC	TGAAGTCCAC	ACTTACTTGT	TGAGATGTTA	TCTCTGTTTT	TTATCGTTAT	8640
AATTTACTGT	ATTTTTTATA	GTATGCAGAA	TATTTTAAAG	TATATTTCAA	TAGAAATTTT	8700
TATCGATTTA	TTGTATAATG	ATAAGTAATT	GTTGAAAAGT	ACTCAGAAAA	TTCCATACTA	8760
TATTATTTTT	ATGTTTATAC	TTTTATGCTA	TAAAATATAG	ATTGATATAA	AGAATATAGA	8820
AAAAGCGAGG	TTAATATGAG	CCGAAAAAGC	ATTGGTGAGA	AACGCCATAG	TTTCTCGATG	8880
AGAAAGTTGT	CAGTGGGATT	GGTATCAGTT	ACTGTATCTA	GTTTCTTTTT	GATGAGTCAA	8940
GGGATTCAAT	CGGTATCGGC	CGATAATATG	GAAAGTCCAA	TTCATTATAA	GTATATGACC	9000
GAGGGTAAAT	TGACAGACGA	GGAAAAATCC	TTGCTGGTAG	AGGCCCTTCC	ACA ACTGGCT	9060

1091

GAAGAATCAG ATGATACTTA TTACTTGGTT TATAGATCTC AACAGTTTTT ACCGAATACA	9120
GGTTTTAACC CAACTGTTGG TACTTTCCTT TTTACTGCAG GATTGAGCTT GTTAGTTTTA	9180
TTGGTTTCTA AAAGGGAAAA TGGAAAGAAA CGACTTGTTT ATTTTCTGCT GTTGACTAGC	9240
ATGGGAGTTC AATTGTTGCC GGCCAGTGCT TTTGGGTTGA CCAGCCAGAT TTTATCTGCC	9300
TATAATAGTC AGCTTCTAT CGGAGTCGGG GAACATTTAC CAGAGCCTCT GAAAATCGAA	9360
GGTTATCAAT ATATTGGTTA TATCAAACT AAGAAACAGG ATAATACAGA GCTTCAAGG	9420
ACAGTTGATG GGAAATACTC TGCTCAAAGA GATAGTCAAC CAACTCTAC AAAAACATCA	9480
GATGTAGTTC ATTCAGCTGA TTTAGAATGG AACCAAGGAC AGGGGAAGGT TAGTTTACAA	9540
GGTGAAGCAT CAGGGGATGA TGGACTTTCA GAAAAATCTT CTATAGCAGC AGACAATCTA	9600
TCTTCTAATG ATTCATTCGC AAGTCAAGTT GAGCAGAATC CGGATCACAA AGGAGAATCT	9660
GTAGTTCGAC CAACAGTGCC AGAACAAGGA AATCCTGTGT CTGCTACAAC GGTGCAGAGT	9720
GCGGAAGAGG AAGTATTGGC GACGACAAAT GATCGACCAG AGTATAAACT TCCATTGGAA	9780
ACCAAAGGCA CGCAAGAACC CGGTCATGAG GGTGAAGCCG CAGTCCGTGA AGACTTACCA	9840
GTCTACACTA AGCCACTAGA AACCAAAGGT ACACAAGGAC CCGGACATGA AGGTGAAGCT	9900
GCAGTTCGCG AGGAAGAACC AGCTTACACA GAACCGTTAG CAACGAAAGG CACGCAAGAG	9960
CCAGGTCATG AGGGCAAAGC TACAGTCCGC GAAGAGACTC TAGAGTACAC GGAACCGGTA	10020
GCGACAAAAG GCACACAAGA ACCCGAACAT GAGGGCGAAG cGGCAGTAGA AGAAGAACTT	10080
CCGGCTTTAG AGGTCACTAC ACGAAATAGA ACGGAAATCC AGAATATTCC TTATACAACA	10140
GAAGAAATTC AGGATCCAAC ACTTCTGAAA AATCGTCGTA AGATTGAACG ACAAGGGCAA	10200
GCAGGGACAC GTACAATTCA ATATGAAGAC TACATCGTAA ATGGTAATGT CGTAGAACT	10260
AAAGAAGTGT CACGAACTGA AGTAGCTCCG GTCAACGAAG TCGTTAAAGT AGGAACACTT	10320
GTGAAAGTTA AACCTACAGT AGAAATTACA AACTTAACAA AAGTTGAGAA CAAAAATCT	10380
ATAACTGTAA GTTATAACTT AATAGACACT ACCTCAGCAT ATGTTTCTGC AAAAACGCAA	10440
GTTTTCCATG GAGACAAGCT AGTTAAAGAG GTGGATATAG AAAATCCTGC CAAAGAGCAA	10500
GTAATATCAG GTTTAGATTA CTACACACCG TATACAGTTA AAACACACCT AACTTATAAT	10560
TTGGGTGAAA ATAATGAGGA AAATACTGAA ACATCAACTC AAGATTTCCA ATTAGAGTAT	10620
AAGAAAATAG AGATTAAAGA TATTGATTCA GTAGAATTAT ACGGTAAAGA AAATGATCGT	10680
TATCGTAGAT ATTTAAGTCT AAGTGAAGCG CCGACTGATA CGGCTAAATA CTTTGTAATA	10740
GTGAAATCAG ATCGCTTCAA AGAAATGTAC CTACCTGTAA AATCTATTAC AGAAAATACG	10800

1092

GATGGAACGT	ATAAAGTGAC	GGTAGCCGTT	GATCAACTTG	TCGAAGAAGG	TACAGACGGT	10860
TACAAAGATG	ATTACACATT	TACTGTAGCT	AAATCTAAAG	CAGAGCAACC	AGGAGTTTAC	10920
ACATCCTTTA	AACAGCTGGT	AACAGCCATG	CAAAGCAATC	TGTCTGGTGT	CTATACATTG	10980
GCTTCAGATA	TGACCGCAGA	TGAGGTGAGC	TTAGGCGATA	AGCAGACAAG	TTATCTCACA	11040
GGTGCATTTA	CAGGGAGCTT	GATCGGTTCT	GATGGAACAA	AATCGTATGC	CATTTATGAT	11100
TTGAAGAAAC	CATTATTTGA	TACATTAAAT	GGTGCTACAG	TTAGAGATTT	GGATATTAAA	11160
ACTGTTTCTG	CTGATAGTAA	AGAAAATGTC	GCAGCGCTGG	CGAAGGCAGC	GAATAGCGCG	11220
AATATTAATA	ATGTTGCAGT	AGAAGGAAAA	ATCTCAGGTG	CGAAATCTGT	TGCGGGATTA	11280
GTAGCGAGCG	CAACAAATAC	AGTGATAGAA	AACAGCTCGT	TTACAGGGAA	ACTTATCGCA	11340
AATCACCAGG	ACAGTAATAA	AAATGATACT	GGAGGAATAG	TAGGTAATAT	AACAGGAAAT	11400
AGTTCGAGAG	TTAATAAAGT	TAGGGTAGAT	GCCTTAATCT	CTACTAATGC	ACGCAATAAT	11460
AACCAAACAG	CTGGAGGGAT	AGTAGGTAGA	TTAGAAAATG	GTGCATTGAT	ATCTAATTCTG	11520
GTTGCTACTG	GAGAAATACG	AAATGGTCAA	GGATATTCTA	GAGTCGGAGG	AATAGTAGGA	11580
TCTACGTGGC	AAAACGGTCG	AGTAAATAAT	GTTGTGAGTA	ACGTAGATGT	TGGAGATGGT	11640
TATGTTATCA	CCGGTGATCA	ATACGCAGCA	GCAGATGTGA	AAAATGCAAG	TACATCAGTT	11700
GATAATAGAA	AAGCAGACAG	ATTCGCTACA	AAATTATCAA	AAGACCAAAT	AGACGCGAAA	11760
GTTGCTGATT	ATGGAATCAC	AGTAACTCTT	GATGATACTG	GGCAAGATTT	AAAACGTAAT	11820
CTAAGAGAAG	TTGATTATAC	AAGACTAAAT	AAAGCAGAAG	CTGAAAGAAA	AGTAGCTTAT	11880
AGCAACATAG	AAAAACTGAT	GCCATTCTAC	AATAAAGACC	TAGTAGTTCA	CTATGGTAAC	11940
AAAGTAGCGA	CAACAGATAA	ACTTTACACT	ACAGAATTGT	TAGATGTTGT	GCCGATGAAA	12000
GATGATGAAG	TAGTAACGGA	TATTAATAAT	AAGAAAAATT	CAATAAATAA	AGTTATGTTA	12060
CATTTCAAAG	ATAATACAGT	AGAATACCTA	GATGTAACAT	TCAAAGAAAA	CTTCATAAAC	12120
AGTCAAGTAA	TCGAATACAA	TGTTACAGGA	AAAGAATATA	TATTCACACC	AGAAGCATTT	12180
GTTTCAGACT	ATACAGCGAT	AACGAATAAC	GTACTAAGCG	ACTTGCAAAA	TGTAACACTT	12240
AACTCAGAAG	CTACTAAAAA	AGTACTAGGA	GCAGCGAATG	ATGCAGCCTT	AGATAACCTA	12300
TACTTAGATA	GACAATTTGA	AGAAGTTAAA	GCTAATATAG	CAGAACACCT	AAGAAAAGTA	12360
TTAGCGATGG	ATAAATCAAT	CAATACTACA	GGAGACGGTG	TAGTTGAATA	CGTAAGTGAG	12420
AAAATCAAAA	ATAACAAAGA	AGCATTTATG	CTAGGTCTTA	CTTATATGAA	CCGTTGGTAC	12480
GATATTAATT	ATGGTAAAAT	GAATACAAAA	GATTTATCTA	CGTACAAGTT	TGACTTTAAC	12540
GGAAATAATG	AGACTTCAAC	GTTGGATACT	ATTGTCGCAT	TAGGAAATAG	TGGACTAGAT	12600

1093

AACCTGAGAG	CTTCAAATAC	TGTAGGTTTA	TATGCGAATA	AACTTGCATC	GGTAAAAGGA	12660
GAAGATTCAG	TCTTTGACTT	CGTAGAAGCG	TATAGAAAAC	TGTTCTTACC	AAACAAAACA	12720
AATAACGAGT	GGTTTAAAGA	AAATACAAAG	GCATATATAG	TCGAAATGAA	GTCTGATATT	12780
GCAGAAGTAC	GAGAAAAACA	AGAATCACCA	ACAGCCGATA	GAAAATATTC	ATTAGGAGTT	12840
TACGATAGAA	TATCAGCACC	AAGTTGGGGG	CATAAGAGTA	TGTTATTACC	ACTACTAACT	12900
TTACCTGAAG	AATCTGTGTA	TATTTTCATCG	AATATGTCTA	CACTTGCATT	CGGTTTCGTAT	12960
GAAAGATATC	GTGATAGTGT	GGATGGAGTT	ATTCTTTTCTAG	GAGATGCTTT	ACGAACTTAT	13020
GTAAGAAATA	GAGTTGATAT	AGCAGCGAAA	AGGCATAGAG	ACCATTATGA	TATTTGGTAC	13080
AATCTTCTTG	ACAGTGCTTC	AAAAGAAAAA	CTTTTCCGTT	CTGTGATAGT	TTATGATGGA	13140
TTCAATGTAA	AAGATGAGAC	AGGAAGAACT	TATTGGGCAA	GGTTAACGGA	TAAAAACATC	13200
GGCTCTATTA	AAGAATTCTT	CGGACCTGTT	GGGAAATGGT	ATGAGTATAA	TAGTAGTGCA	13260
GGAGCGTATG	CGyAtGGAAG	TTTAACGCAC	TTTGTGTTAG	ATAGATTATT	AGATGCTTAT	13320
GGAACGTCGG	TTTATACTCA	TGAAATGGTT	CATAATTCTG	ATTCTGCAAT	CTACTTTGAA	13380
GGAAATGGTA	GACGTGAAGG	ATTGGGAGCG	GAGTTATACG	CACTTGGTTT	ACTGCAATCT	13440
GTAGATAGTG	TAAATTCTCA	TATTTTAGCT	TTAAATACGT	TATATAAAGC	AGAAAAAGAT	13500
GATTTGAATA	GATTGCATAC	ATATAATCCG	GTGGAACGTT	TCGATTCGGA	TGAGGCGCTT	13560
CAAAGTTATA	TGCATGGATC	ATATGATGTA	ATGTATACAC	TTGATGCGAT	GGAAGCAAAA	13620
GCGATATTAG	CTCAAATAA	TGATGTTAAG	AAAAAATGGT	TTAGAAAAAT	AGAAAATTAT	13680
TACGTTCTTG	ATACTAGACA	TAATAAAGAT	ACACATGCAG	GAAATAAAGT	CCGTCCATTA	13740
ACAGATGAAG	AAGTAGCTAA	CTTAACATCG	TTAAACTCAT	TAATCGACAA	CGACATCATA	13800
AATAGACGTA	GCTATGATGA	TAGTAGAGAA	TATAAACGAA	ATGGCTACTA	TACTATAAGT	13860
ATGTTCTCTC	CTGTATACGC	AGCGCTAAGC	AATTCGAAAG	GTGCTCCTGG	AGATATTATG	13920
TTTAGAAAAA	TAGCTTATGA	ATTACTTGCG	GAAAAAGGTT	ATCACAAAGG	ATTCCTACCT	13980
TATGTTTCTA	ATCAGTACGG	AGCAGAAGCA	TTTGCCAGCG	GAAGCAAAAC	ATTCTCATCA	14040
TGGCATGGAA	GAGATGTTGC	TTTAGTGACA	GATGATTTAG	TATTTAAGAA	AGTATTCAAT	14100
GGTGAGTACT	CATCATGGGC	TGATTTCAAA	AAAGCAATGT	TTAAACAACG	TATAGATAAA	14160
CAAGATAATC	TGAAACCAAT	AACAATTCAA	TACGAATTAG	GTAATCCTAA	TAGTACAAAA	14220
GAAGTAACTA	TAACAACGGC	TGCACAAATG	CAACAATTAA	TTAATGAAGC	GGCTGCGAAA	14280
GATATTACTA	ATATAGATCG	TGCAACGAGT	CATACCCCAG	CAAGTTGGGT	GCATTTATTA	14340

1094

AAACAAAAA	TCTATAATGC	ATATCTTCGC	ACTACAGATG	ACTTTAGAAA	TTCTATATAT	14400
AAATAAGATT	GTAGAGTTTC	ATTGTTGAGT	AGTGTTTCTT	GTAAGGATGA	GGAGTCAGAT	14460
GACAAATCGA	CTCCTTTTTC	TTATGGATCG	ATGTAGAGAT	TTGATTGAAT	GCAGATTGCA	14520
GGAATCATCT	TCAACTCATC	AACGACCAAT	GGTGACAAGG	TGGATTTCAA	TCCCACAGAA	14580
AATGTTGATT	TGAGAAATAA	CTTTGCTAGT	CTAGTAAAAT	AAATACAAAA	CAATCCTAGA	14640
AGATTTTTTC	TGGGATTGTT	TTTTGCTGAG	TGGGATGCTT	CAAGTTGTCT	GGCTTGACTT	14700
TCTTGAGGGA	AGTTATATAA	TAGTTGTAAT	AATTAG			14736

(2) INFORMATION FOR SEQ ID NO: 172:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11770 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

ACAGGAAAGC	ACGATAGCAA	TCTCTTTGGA	AGATTTAAAA	AATATTCCTC	AAAGTTTCGC	60
TGTTGCTTAC	GGTGATACGA	AAGTATCTTC	GATTCTCTCT	GTCTTGCGTG	CTAATTTAGT	120
AAATCATTTG	ATTACAGACA	AAAATACAAT	TTTAAAAGTT	TTGGAAGAAG	ATGGGGATTT	180
GACTTTTAGA	GAGATTCTAG	GTGAGTGAAA	ATGATAGACT	GATTCAGTTT	ATCGTTTTTC	240
TTTTTAGTTG	ATTGCACATT	TGTGCTTATA	TAAACAAAAA	TAGTTTATCT	GTTGTTTTTG	300
GATTGACAAC	TTTATTATGT	AGTTGTATTC	TATAGTTACA	AAAGAAAATT	TTAAAATTTT	360
AAATGAAAAA	AGCTTTTTTAC	ATAGTGAAAT	GAGGAGGAAT	TTATGGAAAT	GATTGTTCCA	420
GATCAAATTA	TCATGGGTTT	AATTTTATAT	GCTGGTGATG	CGAAACAACA	TATTTATAAA	480
GCGTTAGATT	ACATAAAAAA	TGGTACATGT	GAACGGTGTG	AAGAAGAAAT	ACAGTTAGCT	540
GATGCAGCCT	TATTAGAAGC	TCATAATCTA	CAAACAAAAT	TTTTGGCACA	GGAAGCGTCT	600
GGTACAAAGA	CAGAAATTAC	AGCTCTCTTT	GTTCAATCAC	AAGATCATCT	CATGACCAGT	660
ATGACGGAGA	TTAATTTAAT	CAAAGAAATT	ATTAGTTTGA	GAAAAGAACT	TCATAAAAAA	720
TAATACTAGA	GTATTATCAT	TGTTATTAAC	ATAGAGGAGG	AAAACATAAT	GGTGAAGATT	780
GGTTTGTTTT	GTGCAGCAGG	TTTTTCTACT	GGTATGCTTG	TAAATAATAT	GAAAATTGCA	840
GCGCAATCTA	GTGGAGTTGA	GGCAGAAATA	GAGGCGTTTT	CTCAGTCTAA	ATTAGCGGAT	900
TATGCGCCAA	ATATAGATGT	TGCACTATTG	GGTCCACAAG	TTGCTTATAC	ATTAGATAAA	960
TCAAAAGAAA	TTTGTGATAA	GTGTGATGTT	CCGATAGCTG	TTATTCCGAT	GATGGACTAT	1020

1095

GGTATGTTAG	ATGGGAAAAA	AGTATTAGAT	TTGGCCCTAT	CTTTGATTAG	TGGGTAAGAA	1080
AAGGAGATTT	ATTATGTCAA	AGATGGATGT	TCAGAAAATC	ATTGCACCGA	TGATGAAGTT	1140
TGTGAATATG	CGTGGCATT	TAGCTCTAAA	AGATGGGATG	TTAGCAATTT	TGCCATTGAC	1200
AGTAGTTGGT	AGTTTGTTC	TGATTATGGG	ACAATTGCCG	TTCGAAGGAT	TAAATAAGAG	1260
CATTGCTAGT	GTTTTTGGAG	CTAATTGGAC	AGAGCCGTTT	ATGCAAGTAT	ATTCAGGAAC	1320
TTTTGCTATT	ATGGGTCTAA	TTTCTTGTTT	TTCAATTGCC	TATTCCTTATG	CTAAGAATAG	1380
CGGAGTAGAG	GCTTTACCAG	CTGGAGTTCT	ATCTGTATCT	GCATTCTTTA	TTTTGCTAAG	1440
ATCATCTTAT	ATCCCTAAAC	AAGGTGAGGC	GATTGGGGAC	GCTATTAGTA	AAGTTTGGTT	1500
TGGAGGCCAA	GGAATTATCG	GTGCTATCAT	TATAGGTTTG	GTAGTAGGAA	GTATTTATAC	1560
CTTCTTTATA	AAGAGAAAAA	TTGTTATTAA	GATGCCAGAA	CAAGTTCCAC	AAGCTATTGC	1620
CAAACAGTTT	GAAGCAATGA	TTCCAGCATT	TGTAATTTTC	TTATCTTCTA	TGATTGTATA	1680
TATTTTAGCG	AAGTCATTGA	CTAATGGCGG	AACATTCATA	GAAATGATTT	ATTCTGCTAT	1740
TCAAGTCCG	TTGCAAGGTT	TAAGTGGATC	TTTGTATGGT	GCTATTGGAA	TTGCATTCTT	1800
TATATCATTT	TTGTGGTGGT	TTGGTGTTC	TGGGCAATCG	GTAGTAAATG	GAGTAGTGAC	1860
AGCTCTGCTT	TTATCTAATC	TTGATGCTAA	TAAAGCTATG	TTAGCCTCTG	CTAATCTATC	1920
ATTAGAAAAT	GGTGACATA	TTGTTACTCA	ACAATTTTTA	GATTCATTTT	TAATTCTATC	1980
AGGTTTCAGG	ATTACGTTTG	GTCTTGTAAG	TGCCATGCTT	TTTGCAGCAA	AATCAAAACA	2040
ATACCAAGCC	TTAGGAAAAG	TTGCAGCTTT	TCCAGCAATA	TTTAACGTAA	ATGAGCCAGT	2100
TGTATTTGGA	TTTCCGATTG	TCATGAATCC	AGTTATGTTT	GTACCTTTCA	TTCTTGTTCC	2160
TGTACTTGCA	GCTGTGATAG	TATATGGAGC	TATTGCAACA	GGTTTCATGC	AGCCATTCTC	2220
AGGGGTAACA	TTGCCTTGGA	GTACACCAGC	TATTTTATCA	GGATTTTGGG	TGGGTGGATG	2280
GCAAGGAGTT	ATTACTCAGC	TGGTGATATT	AGCGATGTCT	ACATTGGTTT	ATTTTCCATT	2340
CTTTAAAGTA	CAGGATCGTT	TAGCTTACCA	AAATGAAATC	AAACAATCTT	AGAGGTATTT	2400
GTGTGTTACT	GTTAAACTCA	CACATTTGTG	CTAAAAATTA	GAGAGTTAAA	ATTTTCTAG	2460
TTAAAAGCTT	GAAAATTTCT	ATAAAAATCG	GTATTATATT	TTCGAAAGAA	ATAAAAATAT	2520
TTTCGAAAGA	AAGGTGCTTA	CGATGGTAAA	TACAGAAGTA	GCAAGAACAA	CAATCAAGAC	2580
AGAATATTTT	GGCAGCCTTA	CTGAAAGGAT	GAACAAATAT	CGAGAAGATG	TTTTAAATAA	2640
AAAACCTTAT	ATTGATGCTG	AGAGAGCAGT	TCTAGCAACA	CGCGCCTATG	AACGATACAA	2700
GGAACAACCT	AATGTCCTAA	AACGTGCATA	TATGCTGAAA	GAAATTTTGG	AAAATATGAC	2760

1096

TATCTATATT	GAAGAAGAAT	CTATGATTGC	GGGAAATCAA	GCTTCTTCCA	ATAAAGATGC	2820
TCCTATTTTT	CCGGAATATA	CGCTAGAATT	TGTTCTCAAT	GAGTTGGATC	TTTTTGAAAA	2880
GCGTGATGGA	GATGTTTTCT	ATATTACAGA	AGAAACAAAA	GAACAACCTA	GAAGTATTGC	2940
TCCGTTTTGG	GAAAATAATA	ATTTACGTGC	TAGAGCTGGT	GCCTTATTAC	CTGAAGAAGT	3000
GTCTGTTTAT	ATGGAAACAG	GATTCTTCGG	TATGGAAGGT	AAGATGAATT	CTGGAGATGC	3060
TCACCTAGCA	GTTAACTATC	AGAAACTTTT	GCAATTTGGT	TTAAGAGGTT	TTGAAGAGCG	3120
GGCTCGTAAA	GCAAAAGTAG	CTCTAGATTT	AACAGATCCA	GCAAGTATTG	ATAAATATCA	3180
TTTTTACGAC	TCTATATTTA	TCGTAATCGA	TGCTATTAAA	GTATATGCAA	AGCGCTTTGT	3240
TGCTCTTGCT	AAAAGTTTAG	CCGAAAATGC	AAATCCTAAA	CGTAAGAAAG	AATTACTTGA	3300
GATTGCAGAT	ATTTGCTCTA	GAGTCCCATA	TGAACCGGCA	ACTACTTTTG	CAGAAGCTAT	3360
TCAATCAGTT	TGGTTTATTC	AATGTATTTT	ACAAATTGAA	TCTAATGGCC	ACTCTCTTTC	3420
ATATGGCCGT	TTTGATCAAT	ATATGTATCC	ATATATGAAG	GCTGATTTAG	AAAGTGGTAA	3480
AGAAACAGAA	GATAGCATTG	TTGAACGTCT	GACAAATCTT	TGGATTAAGA	CAATTACAAT	3540
TAATAAGGTT	CGCAGTCAAT	CACATACATT	TTCTTCAGCA	GGAAGTCCTT	TATATCAAAA	3600
TGTTACAATT	GGTGGACAGA	CTCGAGATAA	GAAGGATGCT	GTTAACCCAT	TATCTTATTT	3660
GGTATTAAAA	TCAGTTGCAC	AAACCCATCT	ACCGCAACCT	AATCTAACTG	TACGTTACCA	3720
TGCAGGTTTA	GATGCTCGTT	TCATGAATGA	GTGTATTGAA	GTGATGAAAC	TTGGTTTTGG	3780
TATGCCTGCA	TTTAATAATG	ATGAGATTAT	TATTCCTTCT	TTTATTGCAA	AAGGAGTATT	3840
GGAAGATGAT	GCTTATGATT	ACAGTGCCAT	TGGATGTGTT	GAAACGGCAG	TTCCAGGGAA	3900
ATGGGGCTAT	CGTTGCACAG	GTATGAGTTA	TATGAACTTC	CCTAAGGTTT	TACTTATCAC	3960
GATGAATGAT	GGAATTGATC	CGGCTTCGGG	TAAACGGTTT	GCACCAAGCT	TTGGTCGTTT	4020
TAAGGATATG	AAGAACTTTT	CTGAATTAGA	AAATGCTTGG	GATAAAACAC	TAAGATATTT	4080
GACACGAATG	AGTGTTATTG	TTGAAAATTC	TATTGATTTA	TCATTGGAAC	GAGAAGTTCC	4140
TGATATTCTA	TGTTCAGCAT	TGACTGATGA	TTGTATTGGT	CGTGGAAAAC	ACCTTAAAGA	4200
AGGTGGAGCA	GTATATGATT	ATATATCAGG	ATTGCAAGTT	GGAATTGCAA	ATTTGTCGGA	4260
TTCATTAGCT	GCAATTAAAA	AATTGGTGTT	TGAGGAAGAA	CGTATAAGCC	CAAGTCAGCT	4320
TTGGCATGCA	CTGGAAACAG	ATTATGCCGG	AGAAGAAGGT	AAGGTCATTC	AAGAAATGTT	4380
GATTCATGAT	GCACCTAAGT	ATGGTAATGA	TGATGATTAT	GCTGACAAAT	TGGTTACTGC	4440
TGCTTATGAC	ATTTATGTTG	ATGAAATTGC	TAAATATCCT	AATACACGTT	ATGGAAGAGG	4500
GCCTATTGGA	GGAATTCGTT	ATTCAGGAAC	ATCTTCTATC	TCAGCCAACG	TAGGGCAGGG	4560

1097

ACGTGGAACA	TTAGCAACTC	CAGATGGACG	CAACGCGGGT	ACACCGTTAG	CAGAGGGTTG	4620
TTCACCATCA	CATAATATGG	ATCAACACGG	CCCTACATCT	GTTTTAAAAT	CTGTTTCAAA	4680
ATTACCAACA	GATGAAATCG	TAGGTGGGGT	TCTCTTAAAT	CAGAAAGTAA	ATCCTCAAAC	4740
GTTAGCCAAA	GAAGAAGATA	AATTAAAACT	AATTGCTTTG	TTACGAACAT	TCTTTAATCG	4800
TTTACATGGG	TACCATATTC	AATACAATGT	TGTTTCCAGA	GAGACGCTGA	TTGACGCTCA	4860
GAAACATCCT	GAAAAACACA	GAGACTTAAT	TGTTCTGTGT	GCAGGATACT	CTGCATTCTT	4920
CAATGTTCTT	TCTAAGGCAA	CCCAAGATGA	CATTATAGGA	CGTACTGAGC	ATACTTTGTA	4980
AAATAAAGAG	GTTCTTTTTA	TGGAATTTAT	GCTTGACACA	TTAAATTTAG	ATGAGATTAA	5040
AAAGTGGTCT	GAAATTTTGC	CGCTAGCTGG	GGTAACTTCA	AATCCCACTA	TTGCAAAAAG	5100
AGAGGGTTCT	ATTAATTTTT	TTGAACGAAT	CAAAGATGTA	AGAGAATTGA	TTGGCTCTAC	5160
ACCTCTATT	CATGTTTCAGG	TGATTTCTCA	AGATTTTGAA	GGCATCTTAA	AGGATGCTCA	5220
TAAAATTCGA	AGACAAGCAG	GAGATGATAT	ATTTATCAAA	GTACCTGTTA	CTCCAGCTGG	5280
ATTACGTGCA	ATAAAGGCGC	TAAAAAAGA	GGGCTACCAT	ATCACTGCAA	CAGCTATTTA	5340
TACAGTTATT	CAGGGATTAT	TAGCTATCGA	AGCAGGAGCG	GATTACCTAG	CTCCATATTA	5400
TAATAGAATG	GAAAATCTGA	ACATTGATTC	AAATCTGTGC	ATTCGTCAAT	TAGCTCTTGC	5460
TATTGATAGA	CAGAACTCTC	CTAGTAAGAT	TTTAGCTGCA	TCCTTTAAAA	ATGTAGCACA	5520
AGTAAATAAT	GCTTTAGCTG	CAGGTGCGCA	TGCTGTTACA	GCAGGAGCGG	ATGTTTTTGA	5580
ATCAGCTTTC	GCCATGCCAT	CTATCCAAAA	GGCGGTGAT	GATTTTTCTG	ACGATTGGTT	5640
TGTTATTCAA	AATAGTCGTT	CCATTTAGAT	AGAGAGGAAA	TACATATGAG	AATTTTTGCT	5700
AGTCCTTCTA	GATATATTCA	GGGGGAAAAT	GCCTTGTTTG	AAAATGCCAA	ATCAATTTTG	5760
GATTTGGGAA	ATTGCCCTAT	TCTATTATGC	GATCAGTTGG	TTTATGATAT	TGTTGGAAAA	5820
CGATTTGAAG	ATTACCTACA	TAGGTATGGT	TTCCATATTG	TTCTGGCGCT	ATTTAATGGT	5880
GAAGCTTCTG	ACAATGAAAT	CAATCGAGTT	GTTGCCTTGG	CTGAGAAAGA	AAATTGTGAT	5940
AGTATTATCG	GTCTTGGTGG	GGGAAAGACG	ATTGATAGCG	CAAAAGCTAT	TGCAGATTTG	6000
ATTGAAAAGC	CTGTTATTAT	TGCTCCAACA	ATTGCATCGA	CCGACGCACC	TGTATCTGCT	6060
TTATCTGTTA	TTTATACAGA	TGAAGGTGCA	TTTGATCATT	ATCTATTTTA	TTCTAAAAAT	6120
CCAGATTTAG	TTTTGGTTGA	TACAAAAGTT	ATTTCACAAAG	CCCCTAAGCG	TTTATTAGCG	6180
TCTGGTATTG	CAGATGGTTT	AGCAACTTGG	GTTGAGGCGC	GTGCGGTTAT	GCAGGCAAAT	6240
GGAAAACTA	TGTTGGGACA	ACAGCAAACA	TTGGCTGGAG	TTGCAATTGC	GAAGAAATGT	6300

1098

GAAGAAACGC	TGTTTGCAGA	TGGTTTACAG	GCTATGGCAG	CTTGTGAAGC	TAAAGTGGTG	6360
ACACCAGCAT	TAGAAAATAT	TGTTGAAGCT	AATACTTTAT	TGAGTGGTCT	AGGTTTTGAA	6420
AGTGGAGGAT	TAGCTGCGGC	GCATGCAATT	CATAATGGTT	TTACTGCATT	GACAGGTGAC	6480
ATTCATCATT	TAACACATGG	TGAAAAAGTA	GCTTATGGAA	CTTTAGTACA	ACTATTATTG	6540
GAAAATAGAC	CTAAAGAAGA	ACTTGATAAG	TATATTGAGT	TTTACAAAAA	AATTGGTATG	6600
CCAACAACCTC	TAAAAGAAAT	GCATTTGGAT	CAAGTTGGAT	ATGATGATTT	AATAAAAAGTT	6660
GGTAAACAAG	CAACTATGGA	GGGTGAGACA	ATTCATCAGA	TGCCGTTTAA	GATTTTCGCCT	6720
TCAGATGTTG	CTCAAGCTAT	TATCGCTGTA	GATGCCTATG	TAAATTCAAA	ATAAACAATA	6780
AGGACTACTG	TTTTCCAAAT	GGTAGTCTTT	TATTGATCCC	TGTATTGAAT	TCTATAGAAG	6840
ATTGAAATAG	GATGAGAACA	AATCGATTGG	GAAAGTAAAA	TTAATTTCTA	TAAATGTTTT	6900
AGCAATTGTT	TCGTACTATT	TCAGATTCAG	TCTACTATAT	GTTCTTCATA	AATCAAAAAG	6960
CGACATAGGT	TGTCGGCTAT	TTATTGTGAA	TACATTAATT	AGCATTCCAG	TTTTATCTTC	7020
GGTCTAAAAT	AAGTATTTTG	TGCTATACGA	GATAAGCTTC	TTGACTTACT	CCTTGATTTA	7080
CTGCATAACA	ATGGGATAAA	AAGTGGGAGA	TAGAGCAATT	CATAGTCATC	AAAATTAATG	7140
AGATACAGTA	TACAGTTTTT	CCTTTAAACA	CATTTCAAAT	TCCCTCAAAA	ATGGTATAAT	7200
AGTAACATCA	CAAATTTGGA	GAGAGACCAT	GAGTTTTTAC	AATCATAAAG	AAATTGAGCC	7260
TAAGTGGCAG	GGCTACTGGG	CAGAACATCA	TACATTTAAG	ACAGGAACAG	ATACATCAAA	7320
ACCTAAGTTT	TATGCGCTTG	ATATGTTCCC	TTATCCGTCT	GGAGCTGGTC	TGCACGTAGG	7380
ACACCCAGAA	GGTTATACTG	CAACCGATAT	CCTCAGTCGT	TACAAACGTG	CGCAAGGCTA	7440
CAATGTCCCT	CACCCAATGG	GTTGGGATGC	TTTTGGTTTG	CCTGCAGAGC	AATACGCTAT	7500
GGATACTGGT	AATGACCCAG	CAGAATTTAC	AGCGGAAAAC	ATTGCCAACT	TCAAACGTCA	7560
AATTAATGCG	CTTGGATTTT	CTTATGACTG	GGATCGTGAA	GTCAACACAA	CAGATCCAAA	7620
CTACTACAAG	TGGACTCAAT	GGATTTTCAC	CAAGCTTTAC	GAAAAAGGCT	TGGCCTATCA	7680
AGCTGAAGTG	CCAGTAAACT	GGGTTGAGGA	ATTGGGAACT	GCCATTGCCA	ATGAAGAAGT	7740
GCTTCCTGAC	GGAACCTCTG	AGCGTGGAGG	CTATCCAGTT	GTCCGCAAAC	CAATGCGCCA	7800
ATGGATGCTC	AAAATCACGG	CTTACGCAGA	GCGCTTGCTC	AATGACTTAG	ATGAACTAGA	7860
TTGGTCAGAG	TCTATCAAGG	ATATGCAACG	CAACTGGATT	GGTAAATCAA	CTGGTGCCAA	7920
TGTAACCTTC	AAAGTAAAAG	GAACAGACAA	GGAATTTACA	GTCTTTACTA	CTCGTCCGGA	7980
CACACTTTTC	GGTGCGACTT	TCACTGTCTT	GGCTCCTGAA	CATGAATTAG	TAGACGCTAT	8040
CACAAGTTCA	GAGCAAGCAG	AAGCTGTAGC	AGACTATAAA	CACCAAGCCA	GCCTTAAGTC	8100

1099

TGACTTGGCT	CGTACAGACC	TTGCTAAAGA	AAAAACAGGG	GTTTGGACTG	GTGCTTATGC	8160
CATCAACCCT	GTCAATGGTA	AGGAAATGCC	AATCTGGATT	GCAGACTATG	TCCTTGCTAG	8220
TTATGGAACA	GGTGCGGTTA	TGGCTGTGCC	TGCCCACGAC	CAACGTGACT	GGGAATTTGC	8280
CAAACAATTT	GACCTTCCAA	TCGTGGAAGT	ACTTGAAGGT	GGAAATGTCT	AAGAAGCTGC	8340
CTACACAGAG	GATGGCCTGC	ATGTCAATTC	AGACTTCCTA	GATGGATTGA	ACAAAGAAGA	8400
CGCTATTGCC	AAGATTGTGG	CTTGGTTGGA	AGAAAAAGGC	TGTGGTCAGG	AGAAGGTTAC	8460
CTACCGTCTC	CGCGACTGGC	TCTTTAGCCG	TCAACGTTAC	TGGGGTGAGC	CAATTCCAAT	8520
CATTCATTGG	GAAGATGGAA	CTTCAACAGC	TGTTCTTGAA	ACTGAATTGC	CGCTTGCTCT	8580
GCCTGTAACC	AAGGATATCC	GTCCTTCAGG	TACTGGTGAA	AGTCCACTAG	CTAACTTGAC	8640
AGATTGGCTT	GAAGTGAATC	GTGAAGATGG	TGTCAAAGGT	CGTCGTGAAA	CCAACACTAT	8700
GCCACAATGG	GCTGGTTCAA	GCTGGTACTA	CCTCCGCTAT	ATTGACCCGC	ACAATACTGA	8760
GAAATTGGCT	GATGAGGACC	TCCTCAAACA	ATGGTTGCCA	GTAGATATCT	ACGTGGGTGG	8820
TGCGGAACAT	GCTGTACTTC	ACTTGCTTTA	TGCTCGTTTC	TGGCATAAAT	TCCTCTATGA	8880
CCTCGGTGTT	GTTCCGACTA	AGGAACCATT	CCAAAACTC	TTAACCAAG	GGATGATTTT	8940
GGGAACAAGC	TACCGTGACC	ACCGTGGTGC	TCTTGTGGCA	ACCGACAAGG	TTGAAAAACG	9000
TGATGGTTCC	TTCTTCCATG	TAGAAACAGG	GGAAGAGTTG	GAGCAAGCGC	CAGCCAAGAT	9060
GTCTAAATCG	CTCAAGAACG	TTGTTAACCC	AGACGATGTG	GTGGAACAAT	ACGGTGCCGA	9120
TACCCTTCGT	GTTTATGAAA	TGTTTATGGG	ACCACTCGAT	GCTTCGATTG	CTTGGTCAGA	9180
AGAAGGTTTG	GAAGGAAGCC	GTAAGTTCCT	TGACCGAGTT	TACCGTTTGA	TTACAAGTAA	9240
AGAAATCCTT	GCGGAAAACA	ATGGTGCTCT	TGACAAGGTT	TACAACGAAA	CAGTCAAAGC	9300
TGTTACTGAG	CAAATTGAGT	CTCTCAAATT	CAACACAGCT	ATTGCCCAAC	TTATGGTCTT	9360
TGTCAATGCT	GCTAACAAGG	AAGATAAGCT	TTATGTTGAC	TATGCCAAAG	GCTTTATTCA	9420
ATTGATTGCA	CCATTTGCAC	CTCACTTGGC	AGAAGAAGTC	TGGCAAACAG	TCGCAGAAAC	9480
AGGTGAGTCA	ATCTCTTATG	TAGCTTGGCC	AACTTGGGAC	GAAAGCAAAT	TGGTTGAAGA	9540
TGAAATTGAA	ATTGTCGTCC	AAATCAAAGG	AAAAGTTCGT	GCCAAACTCA	TGGTTGCTAA	9600
AGATCTATCA	CGTGAAGAAT	TACAAGAAAT	CGCTTTAGCT	GATGAAAAAG	TCAAAGCAGA	9660
AATTGACGGT	AAGGAAATCG	TGAAAGTAAT	TGCGGTACCG	AATAAACTCG	TTAATATCGT	9720
CGTTAAATAA	CGAGTTTATT	AGCTCTATCT	GCCACCTTCA	ATAGTCCACT	GGACTATTGA	9780
AsCCAACATA	ATTAGTTAAC	ATTGTTGTGA	AATAAGATAG	GAGTCCTTCA	GAGTAGAATC	9840

1100
TGGAGGATTT TTTGAATCTT CTTATGAAAG TATGATATAC TATGGGCAAC TATAAAGTTT 9900
GAAAAGTGAA ATAAGGAGAA TAAGATGCCA GTAAATGAAT ATGGTCAAAT GATTGGGGAG 9960
TCAATGGAAG CTTATACTCC AGGTGAATTG CCTTCTTTTG ATTTCTTAGA AGGGCGTTAT 10020
GCTAGGATAG AGGCTCTTTC AGTGGAAGAG CATGCGGAGG ATTTATTAGC TGTTTATGGC 10080
CCTGATACGC CTCGGGAGAT GTGGACCTAC CTCTTTCAGG AGTCAGTAGC AGACATGGAG 10140
GAACTGGTCA GCCTTTTAAA TCAGATGTTG GCTCGTAAGG ACCGTTTTTA TTATGCAATC 10200
ATAGACAAGG CAACTGGTAA GGCTTTGGGA ACTTTTTCCC TCATGCGAAT TGATCAGAAT 10260
AACCGAGTAA TAGAAGTGGG AGCTGTCACT TTTTCTCCAG AGCTCAGGGG GACACGGATA 10320
GGAACAGAAG CCCAGTATCT CTTGGCTTGC TATGTCTTTG AGGAGCTTAA CTATCGTCGC 10380
TATGAGTGGA AATGCGATGC TCTTAACCTG CCATCCAGAC GAGCAGCGGA ACGTTTGGGA 10440
TTTATTTATG AAGGAACCTT CCGTCAGGCA GTGGTTTATA AGGGGCGTAC AAGAGATACG 10500
GATTGGTTGT CTATGATTGA TAAGGACTGG CCTCAAGTCA AAGCTCGATT GGAAATATGG 10560
TTGCGTCCTG AAAACTTTGA TAAAAATGGA CGACAGCACA AGAGCTTGAG AGAACTTTAA 10620
GAGGTGTTGA GATGATTACT ATTAAAAAGC AAGAAATTGT CAAGCTAGAG GATGTTTTGC 10680
ATCTCTATCA GGCTGTCGGT TGGACAACT ATACCCATCA AACAGAGATG CTGGAGCAGG 10740
CCTTATCTCA TTCATTAGTA ATTTATCTGG CACTTGATGG TGATGCTGTG GTGGGCTTGA 10800
TTCGTTTGGT TGGAGATGGT TTTTCATCAG TTTTGTACA GGATTTGATT GTTTTGCCTA 10860
GCTATCAGCG TCAAGGGATT GGTAGCTCCT TGATGAAAGA GGCTTTAGGA AATTTTAAAG 10920
AGGCCTATCA AGTCCAGCTG GCGACAGAAG AGACAGAAAA AAACGTGGGA TTTTATCGTT 10980
CTATGGGCTT TGAAATCTTA TCCACCTATG ACTGTACAGG AATGATTTGG ATAAACAGAG 11040
AAAAATAAAA AAACCTGTTT GTTCTTAAGC AAAGTTTAAG GATGGTCTAG TATCATATAG 11100
TCATTAAATA AAGACCTCCT AACTTTATTT AATAAAATCC TAAACTTTTT TCATCACAAT 11160
CTCCTAATGA AGCCACCCAA TCAGGTGGCT TTTTGTGCGT ACGACGGGCA TGTCTATAT 11220
CTGAGGTGTA AGTCCTCAGC CTGACTATCG TGAGGTAGCA GGGAGAGGAA GGGATAGCGA 11280
AATCGTGGCT CTACGAACAG GAACGTGATA GTAAGGCGTA TATAGCGGAT AAGGAGGCTT 11340
CAAACCTCTAA AGTCCAAAAA GGTAGTCGTA ACCTATATGT GTAAATCACG AGAGTAATTG 11400
AATTCGGACT AAGGTTTGTG TGAAAAAGAT AAATCTTCT AGAGTCTAAA GACTCTGCGT 11460
CAGATTCCT ATTTTCACTG TAACCTTTTA ACGTCCTCAT ATCTTGATA AACGAGGAAA 11520
GATGTACGAC TTATCCCGTG AGGTTTCATG AGCGCTGAAA GCGTAGTAAC AACGAATCAT 11580
GAGAAGTCAG CCGAGCCCAT AGTAGTGAGG AACTTCCGT AATGGAAGTG GAGCGAAGGG 11640

1101

GTGAATACTC AAACAGTCTG GGGAGAGACT GTTTGAGGTC TGTCGCTAGA AAGAGAAAAC	11700
GACAGATCGA AGTAATCCTA CTTCACTTGT GTCTGTAAAA TGAGTGGTCT GATAGAAGTG	11760
GACTTTGAGG	11770

(2) INFORMATION FOR SEQ ID NO: 173:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4185 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

CGCGAAACTA CTTTCTTAGT ATAACACTTT CAGAATCATT GTCAATAGAA ATGACTTGAT	60
TTTTTCAATT TTTTCAAGCT ATTTCCAAGG GTTGTAATAAT CGTCCCTGAT TCTGCAAGAT	120
AAGTAGTAAA CTAAGTACTA AAAACAAGGT TGCCAAGAGC AAGGTAATAT AGTCTCCTTT	180
TTTCAAGGCC TGATAACTAT ACCATGTGCG TTTTTTCTCT TTCCCAAAGC GGCGAACTCC	240
ATGGCAGTCG CAATGGTATC AATGCGTTCT AGCGAGCTAA AAATCAAGGG CGTAATAATG	300
AGCAGATTGC CTTTGATTCT TTGCATAAGA GAAGCTTTCT TGGATAATTC CATCCCACGC	360
GCCTCCTGAG ACATCTTGAT AGTAAAGAAT TCTTCCTGCA AATCTGGAAT ATAGCGCAAG	420
GTCAGGCTGA CAGAATAAGC AATCTTATAG GGCACACCAA TTTGATTAA ACTGGAAGCA	480
AACTGACTAG GATGGGTTGT CATCAAAAAG ATAATAGCCA GAGGAATGGT GCAAAGATAC	540
TTAATGGCCA AATTTAGCAG ATAAAAGAGC TCCTGGCTGG TTAGAGTGTA GACACCGATT	600
CCCTGCCAAA TCACACTTCT CTCTCCATAA AGTCCAACCC CATACTCGGG AGAAAAGAGA	660
TAGACCATCA AAACGTTTAA AACGGCAAAT ATCGTCGCAA AAACGGCTAC AAAGGAAACA	720
TCTTTAAAGC GAATTTCTGA TAAATAGAGG AGAAAGACTG AAAAGATGGC AATCAGCAAG	780
AGCATTCTGG TATCATAGCT AATCATGGCC GCCAATGATA CCAGAATGAA AAAGAGAAGT	840
TTCCCAGCTC CTGACAAGCG ATGAATCACA GTATCTCTAT GCTGGTAACC GATTAATTTA	900
GCTTGCATCC CTCTCTCCTT TCTTTGTAAA ATGCCGTTAA ATCCAGTGGA TCCACATCTA	960
GTTTCTTAGC CAAGTTAAAG ATGGAGGTTT CTTTGTAGATT GGCTTTTACT AACAGCTCAG	1020
GATCGCTCAA CAGACTGGCT GGAACAGTAT CGGCAATCAA TTCTCCATCC ACCATGACAA	1080
GGACCCGGTC TGAATAATCC AGCATCAATF GCATATCATG GGTAATCATG ACAATGGTAT	1140
GCCCTTTTGT ATGTAAGTCT TCGAGAAATT CCATAATCTC AGTATAGTTC TTCTGATCTT	1200

1102

GACCTGCAGT	CGGTTTCATCT	AGGAGAATAA	TTTCAGCTCC	TAAGACCAAA	ATTGAAGCAA	1260
TGGTGACACG	TTTTTCTGA	CCAAATGACA	GGGCAGAAAT	AGGCCAATTA	CGGAATTCAT	1320
AAAGTCCACA	GATTTTCAAG	GTTTCATATA	CTCTCGTTTC	AATTTCTTTC	TCATCCACAC	1380
CTCGCAAACG	GAGCCCTAGA	GCCACCTCAT	CAAAAATCAT	ATTGGTTGAA	ATCATTTGAT	1440
TAGGATTTTG	TAGCACATAT	CCTACTCGTT	CCGCCCCTC	TGCAACAGAA	TCGCCTTTTA	1500
TATCCTGTTT	TTCCCAAAGA	TAGCGTCCTT	CCGTCTGAAT	AAAGCTACTT	ATAGCCTTGG	1560
CTAGAGTTGA	TTCCCTGCT	CCATTTTTTC	CGACAATAGC	AATCTTTTCA	CCCTTTTTAA	1620
TATCTAAATG	TAGGGATTTT	AAAATCGGTC	TATCATCATA	AGAAAAAGAT	ACTTCCTCTA	1680
GTCTAAAGAG	TGACTGCAAT	GCTGGGGTTT	CTTTTGCCAG	TTCATTCTGC	AACTGAACCT	1740
GACCTTTTGA	GATAGACAAG	TTATCCAGAT	TCGCTAATTG	TTCTTCCTTG	ACTAAGTCCA	1800
CACCTAATTG	ACGGAGAGTC	GTTAGATAAA	GGGGTTCTCG	AATTCCATTT	TGAGTCAATA	1860
AATCAGTCGC	AAGCAACTGG	TCAGGGCTCC	CATTAAAAAG	GATACGACCA	TCGTTTATCA	1920
AGACAATCCG	ATCCACAGGG	CGATGCAGAA	CGTCCTCCAA	ACGGTGCTCG	ATAATAAGAG	1980
TCGTCTGCCC	CTCTTCCTTA	TGAATCTGGT	CAATCAATTC	GATAATATCC	TGACCTGACT	2040
TGGGATCTAG	ATTGGCGAGT	GGCTCATCAA	ACAAGAGAAT	CGGACTTTCA	TCAATCAAGA	2100
CACCAGCCAG	ACTGACTCGC	TGCTTTTGTC	CACCTGACAA	ATCCTGAGGA	CGCTGATCCA	2160
GTAAAGGAAG	AAGGTCCAGC	TTTTCAGCCC	ATTTATAAAC	ACGACCTTTC	ATCTCATCTA	2220
GGGCTGTCAC	ATCATTTTCC	AGAGCAAACG	CCAAATCTTC	TGCCACAGAC	AAGCCAATAA	2280
ACTGCCCATC	TGTATCCTGC	AAAACGTGTC	TAACCAGATG	AGACTTATCA	TAGATGCTCA	2340
TATCAAAGGC	TACTTGACCC	TTTATCAAAA	ATTCTCCATA	TGTCTGACCC	TTGTAAATAT	2400
TGGGAATAAT	CCCATTCAAA	CACTGACCCA	AGGTAGATTT	ACCTGACCCA	GATGGTCCAA	2460
CAATTAAGAC	TTTCTCTCCC	TTGTAAATGG	TCAAGTCTAT	CCCTTGCAAG	GTCGGTTCTT	2520
GTTGTGTTTC	ATACCGGAAA	GAGAAATCCT	TCCACTCAAT	TaTAGCTTCT	TTCATCTTAC	2580
TCTCTTCATT	CGCTTCTTAG	ACTTCTATTT	TATCATAAAT	CAAGCCCTTC	TTGCAGTCTC	2640
TCCTCTTAAA	ATCTTAGCGC	CAAAAAGATT	CCTATCCTAG	CTTACTTGCC	TAACATAATCT	2700
ATAAACATCG	AAAAAGACTA	GTTGCCCAGC	CTTCCCCATC	ATTTTATACT	CTTCGAAAAT	2760
CTCTTCAAAC	CACGTCAGcT	TCGCCTTGCC	GTAGGTATGG	TTACTGACTt	CGTCAGTTTC	2820
ATCTACAACC	TCAAAACCAT	GTTTTGAGCc	TGCTTCGTCA	GTTCTATCCA	CAATCTCAAA	2880
ACACTGTTTT	GAGCAACtGC	GGCTAGCTTC	CTAGTTTGCT	CTTTGATTTT	CATTGAGTAT	2940
TAGTCCTTTT	TCAAAC TTCC	TGCACGAGTT	TGGGTTCCTG	CATAGGCAAG	TAAGAGAAGA	3000

1103

G TTCCTGCAA TAGCTACAGA TACACCATTG GCAATTCCCC CAACAATCCC TTGTGCAAAT	3060
A CTTTTTCTG CCGCTTCTTG ATAAATCACA ACATCTCCAA GTGGTGCCAA GACACCCCAA	3120
A CAAGGGCAT TTGCAAGTAG TTGAATGAGA TTAAAAATAA GAATATCTTT CCAGTCAAAA	3180
A CACCATTGA TCACGCGAAC GTACTTTCTA AAAAGTCCCA CAACTAAACC AAAGAGTCCG	3240
C TAGCGATAA TCCAAGTCCA CCATAGACCA TAACCAACAA GAGAGTCCTT GATTGCATGA	3300
C CAATCAACC CGACAAGCAA ACCGATAATC GGTCCAAAAA TAATAGAAAG TAGCGCTTGT	3360
A CCGCATACT GAAGCTGGAT GCTTGATTTT GGAACAGGGG TTGGAATGTT GATCATCCCC	3420
A TGACGACAA AGAGGGCAGC GCCAATTCCG ACAGCAACAA CTTGTTTAAT TGTAAATTTG	3480
A TTTCCATAC TATTCTCCTA TTTTATCCTT CTATTTTCTT TATTTCAATG GTCCAAGATG	3540
A ACCGACACC TACATTATAG GCCTTGGCAA AGGAACCTTG GTTGATAGCC AAACCTAAAC	3600
G ATAGAGAGA GTTGATGTAA AGGATGGGTT GCCCAATTCT CACATCTGCA AATGATTTGC	3660
C ATAGACAAC CTGATTTTGA TAGACCAGCA TATCAGCATG ATAGATGGTC ACTTCAAAAC	3720
G ATCACCAAA TTCTGGTTCC AGCTTGTAAG ATTCTTCCCG TGTGATAGAG GTCCAAAGCG	3780
A ACCGAAACG CACATCCAGA ATATCAATGG CTCCCTTCAC CAGATGATCT TCTATGATGG	3840
T CGCTACGAC TGGAAGCTCT ACAATCTGTT CCACACTGAG CTCTGGCCCT ACTTCCTCAA	3900
A AGTAATGTG ACCACTGGCC AGTTTAGCAC CAGTATAGGC ATAGACATCA CGACCGTGGA	3960
A GGTATAAGA ATGCTCTGTG TTTTGACGCC TATTGGCCAC CTCAGAAATC TCACGAATGG	4020
C TACAATGCC AACGTGTTTC TTGATAAAGG AAAGCGTCCC ATTATCTGGC GTGACAATGT	4080
A TTGATTTTTT TGCAGTCTTG GCAACTACAC TCTTACGTTT CGAACCGACA CCTGGATCGA	4140
C AACCGATAC AAACGTCGTT CCCTCAGGCC AGTAATCCAC CGTCT	4185

(2) INFORMATION FOR SEQ ID NO: 174:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2069 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

TGATAGAGTT AAAGCCGCTG AGTCATTCAA TCCATCTCCA ACCATCAAAA TAGTGTGACC	60
TGCTTTCTGC AGTTTCTCTA CTAACCTAAA TTTCCCATCA GGTTTCAAGT CTGTATAGAC	120
CTGATCAAAG GGCAAATCTT TGAATAATTC CTCTGTCCTA ATCAAGGTGT CTCCTGTTGC	180

1104

CAGAATCAAT	TTTTyCCCCCT	GTGCCTTAAG	TTTATCCAAG	GCTGTTTTTG	CTTCTTTTCT	240
CAAAGGAGTA	TGAATGCAGA	ACATTCCAAT	CAATTCATTT	TGATAAGCCA	AGAATAAGAG	300
ATTGTAGTGA	CTCTTGTA	CTTCAATTAA	AGCATTTTGT	TCTGAACTGA	TATGAATCTG	360
CTCATCCTGC	ATCAAGACAT	AATTCCCAAT	AAGAACTGGT	TGGCCATCTA	TATGAGATTT	420
GATCCCCCTG	CTTGCGATAT	ATTGGAGTTT	CCCATGCATT	TCCTCATGTT	CAATTC CCTC	480
TATCTCAGCT	TGCTTGACGA	TGGCATTAGC	AATAGGATGA	TAAATGTGTT	CCTCAAGACA	540
GGCACTGATT	CTGAGAATAT	CTTCCTCACT	ATAGTCTCCA	AAAGGTAACA	CCTTTTCAAC	600
TATAGGATAA	CTAGTTGTGA	TTGTTCCGTG	CTTATCAAAC	AAGAAAGTAT	CAACTTCCAG	660
ATATTTCTCC	AGAACATCTC	CATCCTTAAT	CACCATTTCA	CGGTTCAACC	CTTCCTTGAT	720
AACTGTCAAA	TAAGCTACAG	GAGTAGAGAT	TTTCAAAGCG	CAGGAGAAAT	CGACCAATAG	780
GAAAGAAATA	GCCTTAGAAA	AAGAACCTGT	CAATAGGTAA	GTCAGCCCAG	CCCCCAAGAA	840
ATTATATTTG	ACGACTTTAT	CCGCCATCTT	GATGAAATAG	CGTTGTTTCG	TTTTCTTGTT	900
TTCTTCAGAT	TTCTTCATCA	ACTCAATCAG	CTGTAAAATA	CGGCTGTTCA	TCTGATTATC	960
TGTTACACGA	ATGCGTAACT	CTCCAGTTTC	TAATACTGTA	TTTGCACAAA	CCAAATCAGA	1020
CTCTCTTTTT	TCAACTGGAA	AACTCTCTCC	TGTCAAGGAA	CTTTCGTTGA	CCATACCTAA	1080
ACCTGAAACT	ACTTGTCAT	CAAACAGAAT	TTCATTTCCCT	TGAGATAAGA	TCAAGACATC	1140
TCCTATTTGA	ACATCGGAAC	TCTTGATACT	AACAACCGTA	TCGCCCTGTA	CTAGGAATAC	1200
ATCGCTCTCT	TTTGCAAGAA	GACTCTGTTC	TAAATCTGTT	GCAGTTTTTT	TCAAGGACCA	1260
CTGATCTAAA	TGATTCCCCA	AATCAAGCAT	AAACATGATA	TTGCTAGCTG	TCTTGATTG	1320
G TTCATAAAC	AAAGACAATA	AAATAGCCGA	ACAGTCCAAG	ACTTCCATCG	TTAGTyCCTT	1380
ACGCGCTAGT	GTTTGATAGG	CTTCTCTAAT	ATAACCCAAA	GCCTGATAAC	AAGTCCATAT	1440
ATAGCGAATA	GGATACGGCA	CAAACTACG	AAAAAGTACA	CGCTTAACCG	CTGCACCTGA	1500
AACAATAGAA	TAAGCACTCT	CTTCTCTACG	AATGGGAAGA	GTCATCAACT	CAGAACTTT	1560
CCCTTTATCA	ATTCTTTTTA	AAAAGGCTTC	TGCATTATCT	AATACAGAAA	AGCCTTCTTT	1620
TATGCGTAGA	GTAAAGTGCT	GTTGATCCAT	GTAAAACTGG	ATAGACTCAA	TCCCCTTTTC	1680
ATCTCTCGCC	AAGGAACGAA	GATAGTCTTG	AATATCCAAG	GTAAGTGAAA	AAGAAGATGA	1740
TAGTCGGATA	TGTTGGTATC	CTCTATGTAG	CACTTTAAAA	GACATATTAT	TCACCTATAA	1800
GGCTATCTAA	TTGCTCTTCT	TTTTTCTCTT	GCTCGTACAA	ATATTTGGCA	TCTTGCAAGA	1860
CATCGTCTCC	ATGTTGCTTC	ACAACAGAAA	CAGATGCATC	TAGCTCGTCT	TTCAACTTGT	1920
AAGCCTTAGC	CAAAGCTTTA	GAATAACCTT	TTTTAGCTTC	CTTACTTGCT	AAGATTTTCA	1980

1105

AACCAAGGGT ACCAAATGCG ACACCACCCA AAAATAATGA AGATTTTTTC GCAACTTTTG 2040
CAACGGTTAA TACTTCTTTT AACATAGGG 2069

(2) INFORMATION FOR SEQ ID NO: 175:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4597 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

AAATCTTGCG CAATAAAGCT CATCTCCATC TCCCGATTGA AACAGTCACT CCCC GGACTG 60
TTTCAACGTC CCAAGACATA ATCTTAGGCA GATTTCTAAA ATTACACTCA AAGTGGAAGT 120
CATTGAGCTT TCGAATGACA GTTGAAGTTG AAATGGCCAG CTGATGGGCA ATATCGGTCA 180
TAGAAATCTT TTCAATTAAC TTTTGCGCAA TCTTTTGGTT GATAATACGA GGAATTTGGT 240
GATTTTTCTT GACGATAGAA GTTTCAGCGA CCATCATTTT CAAGCAATGA TAGCACTTAA 300
AACGACGTTT TCTAAGGAGA ATTCTAGTAG GCATACCAGT CGTTTCAAGG TAAGGAATTT 360
TATAGGGTCT TTAATGTCTA GTAATTTTGT GATAAAATGT AATTGTTCCA TATGATTCTT 420
TCTAATGAGT TGTTTTGTCT CTTTTCATTA TAGATCTTAT GGGACTTTTT TTCTACCCAA 480
AATAGGCTCC ATAATATCCA TAGGGAATTT ACCCACTACA AATATTATAG AGCCCAAAGT 540
TTTAGGTCGC TTGATAATAT GCGTTTTTTG AATTTTATAG ACTGCTCGTT TAAACTCTAT 600
TTACTTCGTA CCTTCTGGAG CGAGACGGAA TATTAGTCAC ATACAAAATG AGTACTATTA 660
GGATTTTATT TTCATGTACA ATTTCAGCCA GTCTTGTTAT AATCAGCCTA TAGGAATCAA 720
GGAGGTGACT CTTATGGCTG TTTTTGTGTC TTTGGATGGA ATTGTGGTAG AAGTCCTTGA 780
TGTCTTTTCT TCTTTTAATG GGGATAGTGA GTTTTTCTTG TGTATAGCAT TTTGAATCTG 840
GAATAGGACG CCATGACTGC TAAAAGATTT CTATAAATTA ATTTGATTTT CCTAATCAAT 900
TTGTTTCATAT CTTATTTTCAT TCCACTATAA ACGTCTTAAA GACAAGAGTC AGTTTGTTAT 960
GGAACGCTCT CAGTTCGAGG AGATGTTCCA ACTTCAAAGT AGTCGCTTGA CGACGCAAGA 1020
AAAATTACAA TTGTTTACCT CTGTGTTTGC TGGCCGTTAT GATGTTTATG CTAAGAATTT 1080
TATCAATGAA CAAGGGAAAA TTCAGTATTT TCCTTCCTAT GATTATGGTT GGAAGCAGTT 1140
GCCACCTGAA AAACGGAGTT TCCAGACATT GACGAACTCC GTTTTGAAAT CTCATTTTCG 1200
TGGGGAGGCA GCTATCGGTA TCTTTCCTAT GCACTTAGAT GATAGCTGTT ATTTTTTGGT 1260

1106

ACTGGATTTG	GATGAAGGAG	ATTGGAAAGA	AGCTGGTTTA	ACCATTCGAA	GAATAGCCAG	1320
GGAACGCCAG	ATGGAAGCCC	ATTTAGAGAT	TTCTCGTTCG	GGTCACGGAC	TCCATATTTG	1380
GTTCTTCTTT	GAGGAAGCGA	TTCCGAGTCG	AGAGGCTCGC	TTGTTTGGA	AGAAACTGAT	1440
AGAACTGGCA	ATGCAGGAAA	GTATGCAACT	GTCCTTTGAT	TCTTTTGATC	GCATGTTTCC	1500
AAATCAGGAT	GTCCTTCCTA	AGGGGGGATT	TGGAAATTTG	ATTGCCTTGC	CTTTTCAAGG	1560
AGAAGCTTAC	CATCAAGGGC	GAACGGTCTT	TGTGGATGAA	CAGTTTCAGC	CTTATGAAGA	1620
CCAATGGAGG	TATCTACAAG	AAATTCAGAG	GATTTCAACT	GCTAAAGTGG	CACTGTTAAT	1680
CCAAGAGGAG	TTAGGCAAGC	AAGAATTGGA	TAAGGAGTTG	AAGGTCGTTT	TATCCAATAT	1740
GATCCAACCT	GAAAAATCGT	CTGTGACATC	CAAGGCACTT	TTTTCTTGAA	AAATATGGCT	1800
TCCTTTTCTA	ATCCCGAATT	TTATAGTAGA	TTGAAACTAG	AATAGTACAC	CTCTGCTTCT	1860
AAAACATTGT	TAGAAATCGA	TTTGACTTTC	CTGATCGATT	TGTCCTGTTA	TTATTTCAAT	1920
TTACTATATT	TAAAGCAGGC	TATGCGACAG	CCAACCTATC	AAATTCCTGA	GAGAATGTAT	1980
TTATTTGGAG	AATCCGATCA	TTATTTATGG	TTGCCAAGAG	GTTTGCTGTA	TCCATTGCAA	2040
GATAAATTTA	AGCAGGTATC	TGTGGAAGAT	AGGAGAAAGG	TACAAAGGTC	TATTAGCGTG	2100
GAATTTAAGG	GAGAACTCAC	TTTTGAGCAA	GAGTTAGCCC	TGTCAGATAT	GACTTCTAAA	2160
GAAAATGGTT	TACTTCATGC	GGAGACTGGT	TTTGGAAGA	CCGTTTTAGG	TGCTGCTCTT	2220
ATCTCTGAAC	GGAAAACAAA	AACAATTATT	CTAGTCCATA	ATAAGCAACT	CTTAGACCAA	2280
TGGCTAGATC	GCTTAAACTG	CTTTTTGACT	TTCGAAGAGG	AGGAGGCTAT	CCGTTATACG	2340
GCATCAGGTC	GTGAAAAGGT	AATCGGCTAT	GTTGGGCAGT	ACGGTGGGAC	TAAGAAATGG	2400
CTGAGTAAAC	TGGTTGATGT	CGTTATGATT	CAATCTCTAT	TTAAGTTGGA	AAATAGTCAA	2460
AGTCTTTTGG	ATGAGTATGA	GATGATGATT	GTGGATGAGT	GTCATCATGT	CTCTGCCTTG	2520
ATGTTTGAAA	AAGTTGTTGC	TCAGTTTAGA	GGGAAGTATC	TTTACGGTTT	GACGGCTACG	2580
CCTGAGCGTA	AGAATGGTCA	TGAGCCTATT	GTTTTTCAGA	GAATTGGTGA	GATACTCCAT	2640
ACTGCTGATA	AGAGGGAAAC	GGATTTTAAA	CGGCAATTGC	AATTAAGATT	CACTTCTTTT	2700
GGTCATTTGG	AAATTGAAAA	GACCAAAGCA	AGTAATTTTA	TACAGCTTAG	TGATTGGATT	2760
GCTACTGACT	CAGTGAGGAA	TCAGATGATT	CTCAAGGATA	TTCTAGCCCA	AGTGGCAGAA	2820
GGACGGAATA	TCTTGGTTTT	AGTTAATCGA	ATTCAACAGA	TAGATGTCTT	TGAAAAATTA	2880
TTGAAAGAGA	AAGAGGTTGA	TGACTGTTAC	ATTATTAGCG	GAAAAACCAA	AGTCCGAGAG	2940
AGAACGAGTT	TACTGGAGAC	GTTAGAACAG	TTAGATAAAG	GGTTTGTTTT	GTTGTCTACT	3000
GGAAAATACA	TTGGCGAAGG	TTTTGACTTA	CCTCAGTTGG	ACACGCTTAT	CTTGGCAGCA	3060

1107

CCCTTTTCTT	GGAAAAATAA	TTTGATTCAG	TATGCAGGTC	GGATTCATAG	AAACTACAAG	3120
GATAAGTCTT	TGGTGCGTAT	TTTCGATTAT	GTGGATATTC	ATGTTCCCTTA	TTTAGAAAAG	3180
ATGTTTCAGA	AACGACAAGT	AGCTTATCGA	AAGATGGATT	ATCGTGTCAT	CGAGGGTGAG	3240
GAGAAACAAT	TCGTTTATGT	TGATAGTAGA	TATGAGAAGG	TGTTGAGAGA	GGACTTAGCA	3300
GGGGAAAGAC	AGGAATGTCT	GCTTATTTTA	CCTTATGTGC	ACCAGACAAA	ACTGATGAAT	3360
TTTCTAAAAG	AATTTAGGAT	TAGTCAAATT	GAGATATGTA	TACCAGAGAC	GGTTGCAAAT	3420
AAAGCATGGC	TAGACCAGTT	GAAGAGCCAG	AAAATTAAAG	TGTCTTTTAC	TCAATCAAAA	3480
ATAGTAACGC	CTATTCTTTT	GGTGAATAAG	ACTATTGTTT	GGTATGGTGC	AATGCCATTA	3540
TTAGGGAAGG	TAGATGAGAT	GACCATATTA	CGTTTGGAAT	CAGCTAGTAT	AGTTTCTGAA	3600
CTAGTGGCAG	GTTTACGATA	GAGAAAATTT	TTAAAAATTT	CTATGTATGA	TTTTTCATTC	3660
TTTAGTGAGA	CTGTTGCCAT	TATCACATTC	GAATCACACA	AAATAAAAAA	ATTTTATATA	3720
GTACTTGACA	AATAGATTGA	AATATCATAA	AATAAAAACG	GTTACAGAGT	TATTAATTAT	3780
TTAAGCTTCA	TGTCACCATT	AAAAATTGAA	ATAAAAGGAT	GTTATCACTA	ATACAAGTGA	3840
GCAGGAACCT	ATTTAATCAC	ATCAGAAGAA	GTTTCTTGAT	GTTTTTAAGT	AGGTTCCCTT	3900
TATTTTAAAA	GGGAAATTTT	ATGATCATAA	AACGAATACT	AAACCACAAT	GCCGTAATTG	3960
CGCAAAGTAA	AAAAGATATC	GATATTCTTC	TTTTTGGAAG	GGGAATAGCT	TTTGGAAGAA	4020
AAACTGGAGA	TAAAGTAAAT	CCAATTGATA	TTGAGAAAAG	TTTTTTTCTC	AAAAATAGAG	4080
ATAATATGAC	CCGTTTTTACA	GAGATGTTTA	TTAACGTTCC	TTTGAGATTG	GTGTACATCA	4140
CCGAAAAAAT	AATTAACCTA	GGTAAAATAA	CATTGGGTAA	TAATTTTGAT	GAAATTATCT	4200
ATATTAATTT	AACGGATCAT	ATTTCTTCGA	GCATAGAACG	TTATAAAGAA	GGGATTATTA	4260
TTTCGAATCC	CCTACGCTGG	GAAATATCGA	AATATTATAA	AGAAGAATTT	GAACTTGGGA	4320
AAAGGGCTTT	ACAAATAATA	AAAAAAGAGT	TAGGTATTGA	ACTTCCAATT	GACGAAGCTG	4380
CATTCATAGC	GCTACATTTT	GTTAATGCTA	ATTTAGAAAA	TAATTTTCAA	GAGTCGTATA	4440
AAATCACTGA	AATAATTATG	GGAATTGAGA	AAATCATTCA	AGATTTCTAT	TGTACTGAGT	4500
TTAACCAAGA	TTCTATTGAT	TATTATAGAT	TCATAACTCA	TATGAAATTA	TTTGCCCATC	4560
GCTTGGTTGA	GAATACAACT	TATTGTGACG	ATGATGA			4597

(2) INFORMATION FOR SEQ ID NO: 176:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3984 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

1108

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

CGGCTTATTT ACTACTTGTT CCATCATATA TGGAATATGC ATGAAACCTG CTCTCATATT	60
AGGGAATTTT TTATCCACTA AATAAAGAGC TTGGTACATC AAATGATTGC AAACAAAGGT	120
TCCTGCACTA TTGGATACAA CTGCCGGAAG TCCCTGTTTT TTGATAGCTT GTACCATCGC	180
TTTGATAGGT AAACACTAA AATAGGCCGA TGCTCCATCA ATACGAATCG GTGTATCAAT	240
TGGTTGATTG CCTTCGTTAT CAGGTATGCG AGCATCATCT TGATTAATAG CCACTCGTTC	300
AGGTGTTAAG CCGGTCCTGC CGCCTGCTTG TCCAATACAA AGTACAGCAT CTGGTTGATA	360
TCGTAATATT TCTGCCTCTA AAACCTTCTGA CGACTTATAA AAAACCGTTG GAATTTCTAC	420
CCAGCGAACT TCAGCCCCAT TAATCTCAGA TGGTAATAAT TTTACAGCCT CCAAAGCTGG	480
ATTAATCTTT TCACCTCCAA AAGGATTAAA ACCTGTAACC AATATTTTCA TTTTATTTTC	540
CTTTACTAAA ATGCGAGAAA GTACATTAAG AATATGTGAA TAACAATCAT TACTAGAGCA	600
ACACCTGCTT GAGCCTTTAT AACGCCATTC TGATCTTTCA TATCCATCAA TGCTGCTGGT	660
AGAGCGTTAA AATTAGCAGC CATTTGGGGTC AATAAGGTCC CACAATAACC TGCTGTCATG	720
GCAAGAGCAC CAGCCACAAT TGGATTAGCT CCCAGAGCAA ATACAAAGGG AACTCCAACA	780
CCTGCTGTAA TAACGGTGAA TGCTGCAAAA GCATTTCCCA TAATCATTGT GAATAGAACC	840
ATTCCAAGAA CATAGGCCAA AACTCCTATA AAGCGACTAT CTGAAGGAAC AATACCGCTA	900
ATCAGATGAG AGATAACATC ACCAACACCT GCTACAGTAA AAATAGCCCC CAAAGCCCCCT	960
AATAATTGAG GAACAATCCC ACTTGTTGAA ACTTGCTGAG TCATTCGATT ATTTTCTGAT	1020
AACAGACTCT TAGGGTGAAT ATTGGTAATC ACAAGAACAG AAATTGTAGC AAACAAGGCG	1080
GCAAGGCTAA TCGAAATCTT GCTAAATTCT GGAATCATTT GCGCTAAGAC CAACGCAAGT	1140
ATTGCCATCA GCATAACTGG AATAAAAATT TTATTTTTCA ACCTGTTAGA TTCAATATTG	1200
GCTTTCATTT CATCTAAGGA TGGCAAGGTT CCGATACGGA CTTGCTTAAA CAATGTTAAC	1260
AGCGATAATA GGATTACAAT AATACCAATA CTCATATTTG GCATATAGGA ACCACCTATA	1320
AACGTAATAG ACAATAGAGT CCAAAATGCA GATGTCCCAA GTCGAACTGG GTTTGTTTTA	1380
TCTTTATAAC TACAATAGGC TGTATGGAGA AATTGACAAC CAATCACAAT ATAGGTCAAC	1440
TCTAATAGTT GCTTTGCCAA CTCTGTCATT TTTGTTCTCC TCCCCTAGTC TTTTTTGATA	1500
TCAATTTTTT ATCAAATAAA TAATTATAAA TCCCCACTAC AATAAGTGTT ATAACAGCAA	1560
CAATAATAGA TGTAGAAGCA ATCCCTGCAT AATTGCTTTC ATAGCCTAAC TGATCTAATG	1620

1109

TTCCCCCTAT	CAAGAGGACT	CCCCCAGCAC	CTACAAACGT	ATTTTGAGCA	AAGAAATTC	1680
CAAAATTTTC	ATTGCGAGCC	GCACGCGCTT	TTATTGTCTC	ATCTTCAACC	TCTGTAACT	1740
TTCTACCTAA	TTGAGACTCT	GCAGCTGCTT	CTCCCATAGG	TTGAACCAAA	GGTCTGACAA	1800
ACTGAGGGTG	TCCTCCTAGA	CGAATTGAAA	AGAAACCAGC	TAACTCTCGA	ATAAAGAAAT	1860
AAACTGTATA	GAAGTTTCCA	ACTGTCAGAC	CTTTAATCTT	TCGAATCAAA	TCGATTGATC	1920
GTTGCTTGAG	TCCAAAGGTT	TCTGACAGCC	CCACAAGAGG	CAAGGTAACC	ATAAAAATCG	1980
TGAGCACTCG	CTGATTGCTA	AATTCTTTTC	CCAAAATCTC	CAAAAATTCA	ACGAGAGAAA	2040
CACCTGAAAC	TAAAGCTGTA	ACCAAACCAG	CTAAGACTAC	TGTTGCAATT	GTATCAAATT	2100
TTAAAATAAA	ACCCACAACA	ATGATTGCTA	TTCCTATTAA	TCTAATCCAC	TCCATATCAA	2160
ACTCCTTTAT	ATTCAAAATG	ACAGTATTTT	TAAAATTTTA	TCAAGATCAA	TACCATTCCCT	2220
TATTTAATGT	GTTTTTCTAG	TTCTTTTTTG	TATTTGCTAT	TGGATTCCAA	TTTTTCTTTT	2280
TGCCATTTTT	TAAAAACCTC	GTTATATTCT	TTTGTTGTAA	CAATATCTTT	TTGCAATTTT	2340
ATTCCTTTAA	AGATATATGG	ATCCCCCTTA	ATACCAACTT	GTGAGTATGG	TTTTGAGAAT	2400
GGTACTACGT	TACTTACAAC	TGGAGAACCA	CCAGATGAAG	CTGTTGGCAT	CAATAATGAA	2460
CTATCTGTCT	ACCAAGCTTG	AGCTTTGGCA	TATTTTTTCAT	ATCTTTTCTC	TAGGTCAGTG	2520
GTCTCAGAAA	CAGCATCTTC	TAACAATTTC	TTATATTTAT	CCAAACCAGG	TTTAGCTACA	2580
ACATCCTTAT	CTTTTCCTTT	CGTAATACCA	AGGTGTTTCA	TGGCAGAACC	AGATTTTGGA	2640
TCTATAATAT	TCAAGTGAGA	CGCTGGATCT	TGATAGCTTG	GAGCCCATCC	TGTACTGTTC	2700
AAATCATAGT	CTTTTTGAGA	AGGAGCAACA	TTGCCGTATT	TATCATTTTC	CATCAAACCA	2760
TCAATAACAT	TTCCAATAAC	GTCTGTCCTC	GATGTTGAG	TCGCTATACT	GTAGCCCAAT	2820
GATGCTGGAT	CTACTGCATA	GACATAAGAA	AATGTTGTCG	GTGCATCTGC	TTCTTTATCA	2880
GTTTTTCCAC	AAGCCACTAA	AATAGCTGAC	GTGCTCAGGA	CCACTCCTGC	TGTTAAGAGC	2940
CACTTTTTCT	ATTTCATAAA	GAATCTCCTT	TGGTTTATTT	TAATCTACTT	TTACAATCCA	3000
ACCTTCTGGC	GCTTCAATAT	CGCCAAACTG	AATACCCGTC	AATTCATTAT	ATAATTTACG	3060
CGTCACAGGA	CCTACTTCTG	TTTCACTATA	GAATACATGG	AAATCATCAC	CATGTTGAAT	3120
ACCTCCAATT	GGAGAAATAA	CCGCTGCTGT	ACCACAGGCA	CCTGCCTCTA	CAAAACGGTC	3180
AAGATTATCA	ATTGGAACAT	CACCCTCAAT	AGGAGTTAAT	CCCAAGCGAT	GTTCTGCCAA	3240
ATAAAGCAAG	GAATACTTGG	TAATAGATGG	CAAGATAGAT	GGAATCAATG	GTGTTACAAA	3300
TTCAATTATCA	GCTGTAATTC	CAAAGAAGTT	AGCTGATCCG	ACTTCTTCAA	TCTTTGTATG	3360

1110

AGTTGATGGG TCCAGATAGA TAACATCTGA GAAATGACGT GACTTGGCCA TTTTTCCTGG	3420
TAAGAGACTT GCAGCATAGT TTCCACCAAC CTTAGCCGCA CCTGTACCAT TTGGTGCTGC	3480
ACGGTCGTAC TCATCCTGAA TCAAGAAGTT GGTGTTGGACC AAACCACCTT TAAAGTAATT	3540
TCCAACCTGGC ATAGCAAAGA TGGTGAAAAT GTACTCTTCT GCCGGTTTTA CCCCATAAT	3600
ATCTCCGACA CCAATCAAAA GAGGGCGAAG ATATAAGGTT CCACCTGTTC CGTATGGTGG	3660
TACGTATTCT TCATTCGCAC GGACAACTGC TTTACAAGCT TCTACAAACA TGTCTGTCGG	3720
AACTTGTGGC ATCAAGAGAC GGTCACATGT ACGTTGCAGA CGTTTAGCAT TTTCATCAGG	3780
ACGGAACAGT TGAACACTGC CATCCTTAGT ACGATAAGCT TTCAAACCTT CAAATGCTTG	3840
TTGTCCATAG TGAAGACTTG GAGAAGACTC TGAAATATGC AAAGTTGCAT CCTCTGTAAG	3900
CTCTCCTTGA TCCCATTGTC CATTTTTGAA ATGAGCAAGA TAGCGATAAG GTAATTTTCAT	3960
ATAGGAAAAA CCGAGGTTTT CCGG	3984

(2) INFORMATION FOR SEQ ID NO: 177:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8703 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

TATCTAATTA TTGGTTTTTA TCGCTGACCT TGGCTATTGT TGGGGTTGTT TTACCCTTGT	60
TGCCTACAAC ACCTTTCCTT TTGTTGTCTA TTGCTTGTTT CTCCAGAAGT TCCAAGCGAT	120
TCGAAGATTG GCTTTATCAT ACCAAGCTCT ATCAAGCATA TGTAGCTGAT TTTCGTGAGA	180
CCAAGTCTAT TGC GCGTGAA CGAAAGAAAA AAATCATCGT CTCTATCTAC GTCTTGATGG	240
GAATTTCTAT TTATTTTGCA CCTCTTTTAC CAGTCAAAAT CGGTCTGGGT GCTTTGACCA	300
TCTTTATTAC TTATTATCTC TTCAAGGTCA TTCCAGACAA AGAATAGTTA AAACAGTAGT	360
TATTTGCCTT GATAAAATTG AAAGCATATT CATAACAATA TGATATAATA AAATTGAAGT	420
AATATTCAAG GAGAATCAAA TGATTTACGA ATTTTGTGCT GAAAATGTGA CTTTACTTGA	480
AAAAGCGATG CAGGCTGGAG CTCGTCGGAT TGAACCTCTGT GATAATCTAG CAGTTGGTGG	540
GACAACACCC AGCTATGGAG TGAATAAGGC AGCGGTTGAA CTGGCAGCTA ACTACGATAC	600
AACCATCATG ACCATGATTC GGCCACGTGG TGGTGACTTT GTCTATAATG ACCTAGAAAT	660
TGCTATCATG CTAGAAGACA TTCGTTTGAC TGCTCAGGCT GGAAGTCAAG GGGTTGTATT	720
TGGAGCTTTA ACTGCTGATA AAAAGTTGGA TAAGCCTAAT CTGGAAAAGT TAATTGCTGC	780

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ATCAAAAGGA	ATGGAAATTG	TCTTTCACAT	GGCCTTTGAT	GAAC TAAGTG	ATGAAGATCA	840
AGCGGAAGCT	ATTGACTGGC	TCAGTCAAGC	CGGTGTCACT	CGTATCCTAA	CTCGTGCTGG	900
TGTGTCTGGC	GACTCCTTAG	AAAAACGTTT	TGTTCACTAT	CACAGAATTT	TGGAGTACGC	960
TAAAGGTAAA	ATTGAAATTC	TACCAGGTGG	GGGGATTGAC	CTTGAAAACC	GTCAAACCTT	1020
TATCGACCAG	GTGGGGGTAA	CACAATTGCA	TGGTACTAAG	GTTGTTTTTT	AAAAAATAGA	1080
AAGGAACTGC	TAGCTTTGGG	TAGCAGTTTT	CAC TTATGTT	TGAAATTTTT	AAATCCTATC	1140
AATTTAATCA	AGAAAAGGCT	CATGATTATG	GTTTTATAGA	AAATAGCGAA	GTCTGGACAT	1200
ATAGTTGCCA	GATTTTGCAA	GGTGA CTTG	TCATGACTGT	GTCCATCACT	GCTGATAATG	1260
TGAACTTTCA	AGTCTTTGAC	CAAGAGACTG	GTGACCTCTA	TCCTCACGTT	TATATGGAAA	1320
GCATGAGGGG	AAGTTTTGTC	GGAAATGTCC	GTGAGGCTTG	TCTGGAGATT	CTTTACCAGA	1380
TTCGGAAGGC	TTGTTTTGAT	GTGCAAGATT	TTATCTGTCA	TCAGACTAAG	CGTATCATGA	1440
CTCAAGTTCA	GGAAAAGTAT	GGAAACCAGT	TGGAGTATCT	GTGGGAAAAA	TCGCCTGATA	1500
CAGCTGTATT	GCGCCATGAA	GGCAATCAAA	AGTGGTATGC	CGTCTTGATG	AAAATCTCTT	1560
GGAATAAGCT	GGAAAAGGGC	AGAGAAGGAC	AAGTGGAAGC	AGTCAACCTC	AAGCATGACC	1620
AAGTAGCTAA	TTTGCTTTCA	CAAAAGGGGA	TTTATCCAGC	CTTCCATATG	AGCAAGCGCT	1680
ACTGGATTAG	TGTGTCCCTT	GATGATACTT	TATCAGATGA	AGAAGTACTG	GAATTGATAG	1740
AAAAAAGTTG	GAAC TTAACC	TCTAAAAAAT	GAAATATTTT	AATAATTTTC	ATGAAC TTTT	1800
AATTAGCTAA	ATATTCTTTA	CTGAAGAGAT	TTTTAGAAAA	TATAGGATTT	ACCACACTAG	1860
AGGAATATGG	TGCCATCTTC	AAATACCTGA	TTGAGAATGT	CAAGACGGAT	CGTCAGATCA	1920
TCTATTCGCC	TCACTGTCAT	GATGACCTCG	GAATGGCAGT	GGCAAATAGC	CTTGCTGCTG	1980
TCAAGAATGG	TGCAGGACGT	GTTGAAGGGA	CTATCAATGG	TATTAGGGAG	CGAGCTGAAA	2040
ATGCTGCTTT	GGAAGAAATT	GCAGTGGCTC	TCAATATTCG	CCAAGATTAC	TACCAAGTAG	2100
AAACCAGTAT	TGTCCTAAAT	GAGACCATCA	ATACGTCAGA	AATGGTTTCT	CGCTTCTCTG	2160
GTATTCCAGT	TCCTAAAAAC	AAAGCCGTCG	TTGGTGGCAA	TACCTTCTCC	CACGAATCTG	2220
GTATTCACCA	AGATGGAGTC	CTTAAAAATC	CTCTCACTTA	TGAGATCATC	ACACCTGAAT	2280
TGGTTGGTGT	TAAGATTCTG	CTTGGA AAAAT	TATCTGGTCG	CCATGCTTTT	GTTGAGAAAC	2340
TGAGAGAATT	GGCCCTAGAT	TTTACAGAAG	AGGATATCAA	ACCACTCTTT	GCTAAGTTCA	2400
AGGCACTGGT	CGATAAGAAG	CAAGAAATCA	CAGATGCAGA	TATTCGAGCT	TTGGTAGCTG	2460
GAACCATGGT	TGAAAATCCA	GAAGGCTTCC	ACTTTGATGA	TTTACA ACTT	CAAAC TCATG	2520

1112

CAGATAATGA	CATTGAAGCG	CTCGTTAGCC	TAGCCAATAT	GGATGGTGAG	AAAGTCGAAT	2580
TTAATGCGAC	AGGGCAAGGT	TCCGTTGAAG	CAATCTTTAA	TGCTATCGAT	AAGTTCTTTA	2640
ACCAATCTGT	TCGTTTGGTG	TCCTACACTA	TCGATGCGGT	AACAGATGGA	ATCGATACCC	2700
AGGATCGGGT	TTTGGTCACT	GTTGAAAACA	GAGATACAGA	AACCATCTTT	AATGCAGCAG	2760
GGCTTGATTT	TGATGTGTTG	AAGGCTTCTG	CTATTGTCTA	TATAAACGCT	AATACCTTTG	2820
TTCAAAAAGA	GAATGCAGGT	GAGATGGGAC	GCAGTGTTTC	TTACCACGAT	ATGCCTAGTG	2880
TGTAAAGGAG	AAGGCTATGG	CAAAGAAAAT	AGTAGCTCTA	GCAGGAGACG	GAATTGGCCC	2940
AGAAATCATG	GAGGTTGGTT	TAGAAGTTCT	GGAGGCTCTA	GCTGAAAAAA	CAGGTTTTGA	3000
CTATGAGATT	GACAGACGAC	CGTTCGGAGG	TGCAGATATT	GATGCAGCAT	GACCTCCCTT	3060
ACCTGATGAA	ACCCTTAAGG	CAAGTAGGGA	AGCAGATGCT	ATCCTACTAG	TAGCTATCGG	3120
TAGTCCTCAG	TATGATGGAG	CAGTGGTTCG	CCCTGAACAA	GGCCTGATGG	CTCTCCGTAA	3180
GGAACTCAAT	CTTTACGCTA	ATATTCGTCC	TGTAAAAATC	TTTGACAGTC	TCAAGCATTT	3240
GTCACCACTC	AAACTGGAAC	GAATTGCTGG	TGTAGACTTT	GTCGTGGTGC	GTGAATTGAC	3300
AGGCGGGATT	TACTTTGGAT	ATCATATTCT	TGAAGAGCGC	AATGCGCGTG	ATATCAACGA	3360
CTATAGCTAT	GAGGAAGTGG	AGCGGATTAT	TCGCAAAGCC	TTTGAAATTG	CAAGAAATCG	3420
CAGAAAAATC	GTTACTAGTA	TCGATAAGCA	AAATGTTCTA	GCGACCTCAA	AACTCTGGCG	3480
GAAAGTAGCT	GAGGAAGTCG	CACAGGATTT	CCCAGATGTA	ACCTTGGAAC	ATCAGCTGGT	3540
AGACTCAGCT	GCTATGCTTA	TGATTACCAA	TCCTGCTAAG	TTTGATGTTA	TTGTAACGGA	3600
GAATCTTTTT	GGAGATATTT	TATCTGATGA	ATCAAGCGTC	TTATCTGGTA	CACTTGGGGT	3660
TATGCCATCA	GCCAGTCATT	CTGAAAATGG	ACCAAGTCTC	TATGAACCTA	TTCACGGTTC	3720
AGCACCTGAT	ATTGCAGGTC	AAGGAATTGC	CAATCCTATT	TCCATGATTT	TATCAGTTTC	3780
CATGATGTTG	AGAGATAGTT	TCGGACGTTA	TGAGGATGCA	GAGCGTATCA	AACGTGCTGT	3840
TGAGACAAGT	CTGGCGGCAG	GAATTTTAAC	GAGAGATATA	GGAGGTCAGG	CTTCAACAAA	3900
GGAAATGACG	GAAGCTATTA	TTGCAAGGTT	ATGAAGTTAG	ACGAAAAAAT	TACTCTAGTC	3960
CTTTTGATTT	GGAATGTCAT	CATTTTCTTG	ATTTATGGTA	TTGACAAATC	TAAGGCAAGG	4020
AGAAGAGTTT	GGCGCATCCC	TGAGAAAATC	TTACTTATTT	TAGCCTTTAC	TTTTGGTGGT	4080
TTTGGTGCCT	GGCTAGCAGG	AATCATCTTT	CACCACAAGA	CTCGAAAATG	GTACTTTAAA	4140
ATAGTTTGGT	TTCTTGGGAT	GGTGACCACA	CTAGTAGCCT	TATATTTTAT	TTGGAGGTAA	4200
TGGATGGCAG	GGTCTTCGAG	GGAATACGCT	GCTTGGGCTC	TAGCGGACTA	TGGTTTTAAG	4260
GTCGTGATTG	CAGGATCTTT	CGGTGACATT	CATTACAATA	ATGAACTCAA	TAATGGCATG	4320

1113

TTGCCAATCG	TTCAGCCTAG	AGAGGTTAGA	GAGAACTAG	CCCAGCTAAA	ACCAACCGAC	4380
CAGGTAAGT	TGGACTTGA	ACAACAAAA	ATCATCTCAC	CAGTTGAAGA	ATTCACCTTC	4440
GAGATAGATA	GCGAGTGGA	ACATAAACTC	CTAAATAGTT	TGGATGATAT	CGGTATTACC	4500
TTGCAGTATG	AAGAGTTGAT	TGCTGCTTAT	GAAAAACAAC	GACCAGCCTA	CTGGCAGGAT	4560
TAGAAAAAAT	AGAAAAGGAG	ATATAGTAAA	CTGAAATAAG	ATGTAAACAA	ATGAATTGGA	4620
GCTTAACATC	CATTTCCAGC	AATTTTTTAG	AACTACAGT	GGACTATTCT	GGATTCAACA	4680
CATTATAAAA	TTATGACAAA	ACACATTAC	AAGAAGGCTA	CGACATTTTA	AAAGGTGAGG	4740
GCGGATGTAT	CGTTTGCCCT	ACTAAAGTTG	GTTACATTAT	CATGACCAGT	GACAAGGCAG	4800
GACTTGAGCG	TAAGTTCGCA	GCCAAAGAAC	GTAAGCGTAA	CAAACCAGGT	GTTGTTCTCT	4860
GCGGTAGCAT	GGATGAACTT	TGCGCTTTAG	CGCAACTCAA	CCCAGAAATT	GAAGCATTCT	4920
ACTAAAAACA	TTGGGATGAA	GATATTCTTC	TTGGTTGTAT	CCTTCCTTGG	AAACCAGAAG	4980
CCTTTGAAAA	ACTCAAAGCA	TACGGGGATG	GCCGTGAAGA	ACTTATTACT	GATGTACGTG	5040
GTACTAGCTG	TTTTGTTATC	AAGTTTGGA	AAGCAGGTGA	ACAATTGGCT	GCCAAGCTTT	5100
GGGAAGAAGG	TAAAATGGTC	TACGCCTCAT	CTGCTTCAAT	GACAAAACGA	TTGAAACTCG	5160
CTATGAGCAA	GGTGTAATGG	TGTCTATGGT	CGATAAGGAC	GGCAAACCTCA	TCCCAGAACA	5220
AGGAGGAGCA	CGTTCAACTT	CACCAGCTCC	AGTTGTGATC	CGTAAAGGGC	TTGACATTGA	5280
TAAAATCATG	ATGCACCTGT	CAGATACTTT	TAATCATGG	GACTACCGTC	AGGTTGAGTA	5340
TTATTAGGAT	AGAGAAGAAG	TCTAGTGTTA	TGAGATATTA	AAGCTCCTAA	CACTGGGCTT	5400
TTGTTTAGAA	TTTCTTTTCT	TTTTCTATAG	GATATGGTAT	TCTATGTAGA	AAATATATGT	5460
TAATAAGTAA	TGCCAATATT	TAAACATCAT	TAGTAAAAGG	AGTTAGATTG	ATGAATAAAA	5520
GAAAAGTTAG	TTTAGAAGAT	TTTTATAAAT	GGTATAGTCT	AAATAAAGAA	GAGTTATTAA	5580
ATAAGGCAAC	TGTTGGTGAA	AAGTTTAATG	ATAAATTAAA	AGAAGAGTTT	CTCCAGGAAT	5640
GGCCTTTGGA	TAGGATTTTA	ACAATGTCAA	TCGATGAATA	TGTAATAGGA	AAGGGACAGC	5700
AAAATAAGTC	TTTATGCTAC	GCTCTTGAGA	AGGGAAAATA	CAAAAATCTA	TTTCTTGGA	5760
TTTCTGGTGG	CTCAGCTTCA	AAATTTGGTA	TTTATTGGAA	TAAAAAACA	AACAAATATA	5820
AAGATCAAGC	TAATAATGAG	ATTTACAGAGT	TGGATCAGCG	ATTTTCAAAA	TTAAAATCAG	5880
ATTTGTATGA	AATTATCAAA	GAAGGTATTC	GTTTAACTT	TGAAAATCCT	ATTTTGTATA	5940
TGAAAAGATC	AACAAATGAA	TTTATTGGTC	GTTCTGCTAT	GGTGACAAAA	TTACTTTGTA	6000
TCTATACTGA	GGGAGATCCT	TTCTTTGGTG	TAAATATTAA	TAGTCAGAAA	GAATTTTGGA	6060

1114

ACCACTTTGT	TTCTCAGACA	AATCAAGGTG	GACCTTATCT	GCAAAATCAT	AAAATAATTG	6120
AACTGGTGTC	CAAAACTTAT	CCTGAGTTGG	AGCCATCGAA	ATTAGGAACT	ATGCTTTTTG	6180
AGTATTCTAA	GCTTTTATG	GAAAATAAGG	AAGACAATAG	TACAATGGAT	TCATCAAACA	6240
ATTTTCGTCA	TCAATTAAC	CAATCTCTAT	TAAAGTCTCC	AAACCTCATC	CTCCGCGGTG	6300
CTCCTGGCAC	GGGAAAACT	TATCTTGCTA	AAGAAATTGC	TAAAGAATTA	ACGGATGGCA	6360
ACGAAGATCA	AATCGGATTT	GTACAATTTT	ACCCATCATA	TGATTATACG	GATTTTGTAG	6420
AAGGTTTAAG	ACCAGTATCA	AATGGGGATG	GAGCTATTGA	GTTTAGGCTA	CAGGACGGTA	6480
TTTTTAAAGA	TTTTTGTCAG	AAAGCAAAAG	AAACCCAATT	GATTGGAGGA	CAAGATAATT	6540
TTGATGAGGC	TTGGGATTCT	TACTTAGAAT	ATATAAATGT	TGCTGAAGAA	AAAGAATATA	6600
TAACAAAAAC	ATCTTACTTA	TCTGTTAATA	GTAGACAAAA	TTTGTCAGTA	AATTATGATA	6660
GTGGTGTTCC	AGGATGGTCA	CTACCTAGCA	AATATGTTTA	CGAGTTGTAT	AAAGATAAAA	6720
ATTATAATAA	GCAAGAATAC	TACAAAAGTG	GTGGAAAAAC	TGTCCTAGAA	ACATTGAGAA	6780
AGAGATTGG	TTTGAAAGAC	TATGTTTCCC	CAACAGAAAT	TGATACTGAT	AAGAATTTTG	6840
TCTTCATCAT	CGATGAGATC	AATCGTGGGG	AGATTCTCTAA	GATTTTTGGC	GAACCTTTTT	6900
TCTCTATCGA	CCCCGGCTAT	CGTGGTGAAA	AAGGAAGTGT	TTCTACCCAA	TATGCAAATC	6960
TACACGAAAC	TGATGAAAAG	TTCTATATCC	CCGAAAATGT	TTACATCATC	GGAACATGA	7020
ATGATATTGA	TCGTTCAAGT	GATACCTTTG	ATTTTGCTAT	GCGTCGTCGT	TTTCGTTTTG	7080
TTGAAGTTAC	TGTCGAGGGT	CAAGCTGGCA	TGTTGGATAA	AGAGTTGAAT	ATCCATGCAG	7140
AAGAAGCAAA	AATTCGTCTA	AGAACTTGA	ACGCTGCTAT	CGAAAATATT	CAGGAATTAA	7200
ACAGTCATTA	TCATATTGGA	CCAAGTTATT	TTCTTAAGTT	GAAGGATGTA	GATTTTGACT	7260
ATGAATTACT	CTGGTCTGAT	TATATTAAGC	CTCTCCTAGA	AGACTACTTG	CGAGGTTCTT	7320
ATGATGAGGT	TGAAACTTTG	GAaACTTTGA	AAAAAGCATT	TGATCTGACA	AATAATGAGC	7380
AAAAAGATCA	GGCAGTAGCT	GATGACAATG	AAGGCGATGA	AAACGATGAT	GCGGATTACT	7440
GATAATCAAC	ACAAGATTAT	TAAAGAAAAA	TTTGTTGAAG	AATATCCTAA	ACTAAGCAAT	7500
CCTCTTTTAG	ACAGAACCTT	GGAAAGTCTA	TCCCAAGATG	AACGTATTTT	CATTTTCCA	7560
AATGATTWGA	CTCATACTCC	TGATTTGGAT	AAGGACCAAA	AGATTTTGA	AACAGTCAAT	7620
CAGAAAATCA	AGACAGGGAA	CGTGATTGGT	TTTCTTGGAT	ATGGTCAGGA	AAGATTAACG	7680
ATTCCTCAC	GATTTTCTGA	TGAGAGTAAT	GACCACTTTT	TGCATTATCT	CTTAAACAAG	7740
GTTCTTCATA	TCAATCTCAC	TAGTTTAGAT	GTTGCTTTGT	CTCGTGAAGA	GAGGCTTTAT	7800
CAACTTTTGG	TGTATCTCTT	TCCCAAGTAT	CTACAAGCTG	CTATTGAAA	AGGTCTTTAT	7860

1115

AAGGAATATC ATCGATTTTC TCATAACGAC AGTCATGTTA AGGGAGTGAT TGATGTAAGA	7920
AACCATCTCA AGAAAAATCT TCCTTTCACG GGAAATATTG CCTACGCAAC GAGAGAGTTC	7980
ACCTATGATA ATCCCCTCAT GCAGTTGGTC CGTCACACTA TTGAATACAT TAAGAATCAG	8040
AAAAGCATTG GTCAAGGGGT ACTAGATAAT CTCTCAACTA GTCGTGAAAA CGTATCTGAA	8100
ATCGTGCGTG TAACGCCCTC TTATAAACTA GCTGATCGTG CTAAGATTAT TCGGGGAAAT	8160
CAATCTAAAC CTATACGTCA TGCATACTTT CACGAGTACA GAAACTTACA AGAACTTTGT	8220
CTGATGATCC TAAACCAAGA AAAGCACGGT TTAGGGTATC AAGATCAAAA AATCTATGGT	8280
ATTCTCTTTG ATGTTGCCTG GCTTTGGGAA GAGTATGTTT ACACCTTGTT GCCAAAAGGT	8340
TTTGTACATC CCAGAAATAA GGATAAGACG GATGGAATTT CAGTATTTTC TGTGGGAAA	8400
CGAAAAGTAT ATCCAGATTT TTATGACAGA GAACGAAAGA TTGTTCTAGA TGCAAAATAT	8460
AAAAAAGTGG AATTGACTGA AAAAGGAATC AACCGTGAGG ACTTATTCCA GCTGATTTCC	8520
TATTCTTATA TTTTAAAAGC TGAGAAGGCT GGACTGATTT TTCTTAGTAT GGAGCAGTCA	8580
GTAAATAGTG AAATAGGAAA AGTAGCTGGC TATGGAGCTC AATTGAAGAA GTGGTCTATT	8640
CGAATCCCTC AGAATGCCTC ATTCTATAGT ACATTTTGTA AAATGATGGA AAATTCAGAA	8700
GAG	8703

(2) INFORMATION FOR SEQ ID NO: 178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4854 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

CATCACCAGT TTTAGATGGC TTTAACAGTG AAATTATTGC TTTAATCTT TCTTGTTTCGC	60
CTAATTTAGA ACAAGTACAA ACAATGTTGG AACAGGCATT CAAAGAGAAG CACTACGAGA	120
ATACGATTCT CCATAGTGAC CAAGGCTGGC AATATCAACA CGATTCTTAT CATCGGTTCC	180
TAGAGAGTAA GGAATTCAA GCATCCATGT CACGTAAGGG CAACAGCCAA GACAACGGTA	240
GGATGGAATC TTTCTTTGGC ATTTTAAAAT CCGAAATGTT TTATGGCTAT GAGAAAACAT	300
TTAAATCACT TAACCAATTG GAACAAGCCA TTATAGACTA TATTGATTAT TACAACAATA	360
AGAAAATTAA GATAAACTA AAAGGACTTA GTCCTGTGCA GTACAGAACT AAATCCTTTG	420
GATAAATTAT TTGTCTAACT GTTTGGGGGC AGTACACAAG AAAGCGCTTT AAAACCAGTA	480

1116

GACCTTTTCA	TAAGGTTCGC	TTGATGTACC	AAGATGAGGC	TGGTTTCGGT	AGAATCAGTA	540
AACTGGGATC	TTGTTGGTCT	CCAATAGGAG	TAGGTCCACA	TGTCCATAGT	CACTATATAC	600
GAGAATTTTCG	CTATTGTTAT	GGAGCTGTTG	ATGCCCATAC	AGGCGAATCA	TTTTTCTTAA	660
TAGCTGGTGG	ATGTAATACT	GAGTGGATGA	ACGCCTTTTT	AGAAGAGCTT	TCACAAGCTT	720
ATCCAGATGA	TTATCTTTTA	CTCGTTATGG	ACAATGCTAT	ATGGCATAAA	TCAAGTACCT	780
TAAAGATTCC	GACTAATATT	GGTTTTACCT	TTATTCCTCC	ATACACACCA	GAGATGAACC	840
CATTGAACAA	GTGTGGAAAG	AGATTTCGTAA	ACGTGGATTT	AAGAATAAAG	CCTTTCGAAC	900
TTTGGAAGAT	GTCATGAATC	AACTCCAAGA	TGTCATACAA	GGATTGGAGA	AGGAGGTGAT	960
AAAGTCCATC	GTTAATCGGA	GATGGACTAG	AATGCTTTTT	GAAAACAGAT	GAGTATAAAA	1020
TTGAATTGCT	TATAAAAAAG	CTCCATACAC	TGGATGTGTA	TAGAGCAATG	GGGCTTTATT	1080
TGATATAGAG	TTCTTGGTTT	TTTAGGACAA	TTTCTCGGAT	ACTTGCAAAC	TTTTTAAGTT	1140
TTTTGATTTC	TTCTGGATGA	GTGACGAGAG	TGATAACATA	ACCTTCCTTG	CCCATACGAC	1200
CAGTACGGCC	AGCACGGTGT	GTGTAGGTTT	CGCTATCTCT	AGGAATATCA	AAGTTTACGA	1260
CACATTCTAG	GCTATCGATA	TCAATTCCAC	GAGCCAAAAG	GTCAGTTGCA	AGAAGCAGGG	1320
TTAGTTGGTT	ATCTTTAAAC	TTTTCTAAGA	TGATTTTTCT	AAATTTAACA	TTAACATCAC	1380
TAGCGAGGGA	AACAGCCAAT	ATATCACGAT	ACTGTAGTTT	TTCCTCGGCA	TTCCCAAGGT	1440
CTGACAGGCT	ATTGAAGAAG	ACTAGACCAC	GGAAATCCTC	TACATGAGCC	AGTTTTCGTA	1500
GCATATCCAC	TCGATGACGT	TGGTCTACCT	GCATGTAGAA	ATGCTGGATA	TTGTCCAATT	1560
TTTGATCAGA	GAGATCAATA	GTGCGTGTAT	TCGGCACAAT	CTTTTCTTGG	TCAAACCTGG	1620
TCGTGGCACT	CATGTAGACC	AGTTGGTGGT	CACGAGGTGC	GTAGTGAGTG	ATTTTTTCTA	1680
CAAAGTGAAT	CTGAGAATCA	TCTAGTAATT	GGTCAAATTC	ATCCAGGATG	ATGGTTTCCA	1740
CATTCATCAT	CTTGATTTTT	TTAAGTTTAA	TGAGTTCAAA	GATACGGCCA	GGAGTTCCAA	1800
TCAGAATTTT	TGGCCCCTTT	TTAAGACGTT	CAATTTGTCT	TTTCTGACTT	GAACCTGAAA	1860
GGAAGAGTTG	AGCAGTCAAT	CCGATAGCTT	CTGCCCACGT	TTTACATACA	TCAAAAATCT	1920
GTCCAGCAAG	TTCCGTATTT	GGTGCTAGAA	TCAAGAGTTG	TTGGGCTTTT	TTCTTTTGTA	1980
GTCTGAGAAG	ACTTGGTAGG	AGATACGCTA	GGGTCTTACC	AGTTCCGGTT	TGGCTCACTC	2040
CTAGGAGGTT	TTCTCCAGCA	AGAAGGGGCT	CAAATAGTTG	AGTTTGAATG	GGGGTGAATT	2100
CTTGGAACCC	GAGTTGGTCA	CTCAGTTCTT	GCCATTCAGT	CGGTAGTTTG	GTTTTCATTT	2160
TTCTGCCTCA	AATCTAATGC	CAGCAGTCTG	GCGCATGGTA	TATAGTAGCT	CATGAACAGA	2220
GCCTGCATCA	TACAGCCAAG	TTTGGTAGAG	ATTCAGATCT	GGTTGCTGGA	TCATGTGTGC	2280

1117

AAATGCAGCG	ACTTCCTCAG	TCATCGTATG	AGGAGCCTGT	TGGATAGGAA	GCTGGACTTG	2340
ATTCCTTGG	TGGTCGGTAA	AAATAGCTGA	GCGAATATGC	TCAATCGTGT	TGAGAGTCAA	2400
GGTTCATCT	GTTGTATAAA	TCTCGCAAGG	AAGATTGGAA	GTGATGTTTT	TTCCAGCCTT	2460
GATGTGAACT	TGATAGTCTG	GGTAGAAGAG	GATACCATCT	CCATTTAGGT	CAATGCTATT	2520
GTCAAGCTGT	TGAGCATGGT	AAGTCGCGTC	ATTGGCTTTT	CCAAAAAGAC	GAACAGCAGC	2580
ATAGAGGGGA	TAAATCCCCA	AATCCATGAG	GGCTCCACCA	GCAAAACGGT	CTGAAAAGAC	2640
ATTTGGTGTT	TGTCCAGCCA	ACAAGTCAGG	CATCTTGGAA	GAGTATTTGG	CATAGTTGAA	2700
ATCTGCTCCT	AACACTTGCT	TATCTGCTAA	AAAGTTTTTG	ATAGTAGTAA	AGGCTTTCTC	2760
GTGGTAATTA	CGAGCTGCTT	CAAAGATAAA	ACAGTTATTT	TTTTCAGCTG	TTTGAATCAA	2820
ATCAAACCAT	TCTTGTGGTT	GAGAGACAGC	TGGCTTTTCG	AGAATAACAT	GTTTACCAGC	2880
AGACAAGGCA	GCTTTTGCCT	GAGCAAAATG	TAAGGAGTTT	GGAAGGCGA	TATAGACTAA	2940
ATCAAAAGAA	GATTTGAAGA	AGACTTCTAA	TTGATCGAAT	AGTTGGATAT	TCTGATAGCG	3000
AGAAGCAAAG	GTTGCTGCAG	TTTCTAGTTT	TCTAGAATAG	ATTGCGACCA	GTTGGTATTC	3060
TCCACTGGTA	TGGGCTGCTT	CTATGAAATG	ATGGCTGATA	GCGCCAGTTC	CGATGACACC	3120
TAATTTTAGC	ATAAATACTC	CTTTTCCGAT	TTTAAATCCT	TCTTTCATTA	TAACATAGAT	3180
AGACGGGACT	ATCCAACAGA	GAGGAGAAAA	TTTCAAATAA	GCTATTAGCT	TTCTTTTCCG	3240
AATAAATAGA	TAGAAGCATA	GAATCTAGCA	AACCTAGATT	TAAAAATGTG	CTATAATAGA	3300
AGGAGGAAAA	GGAGGATTCT	CAGACATCTA	GGTATCAGCC	CAACTAATGA	TTTGTCAATT	3360
TATCCGCGAT	ATGCTGGACT	TGCCAGCAAA	AAATGTGACG	ATTTTGGAGG	GAAGTAACAT	3420
TCACGTCTTG	CCTTCCATGC	CCTACTCAGC	GTAAGATTTC	TATACTAGTA	TAGACGTCTT	3480
GGCGGAGTTA	GATAATGGAA	TCCAAGTTAT	CATCGAAATT	CAGGTTTCATC	ATCAGAATTT	3540
TTTCATCAAT	CGCCTATGGC	CTTATCTGTG	CAGTCAGGTT	AATCAAAACC	TAGAAAAAAT	3600
TCGCCAACGT	GAAGGTGATA	CCCACCAGAG	CTACAAACAA	ATCGCACTAG	TATACGCTAT	3660
CGCAATTGTC	GATAGTAATT	ACTTCTCAGA	TGACCTAGCT	TTTCATAGTT	TTATAGTAAA	3720
ATGAAATGAG	AACAGGACAA	ATCGATCAGG	ACAGTCAAAT	CGATTTCTAA	CAATGTTTTA	3780
GAAGTATAGG	TCTACTATTG	TAGCTTCAAT	CTACTAGAAA	TTCCATAGAT	AGAAAACCTAC	3840
ATAATCTCTA	CAGATACGGA	TGTTGGAGTT	GATGTAAGAT	GCTTTGGCTT	GCTAGAGGAA	3900
TTGTGGATTG	CCAAATTGTA	TCATTGAAAT	TATTGCTCAA	ATTTGTTATG	ATATAAATAT	3960
GAATAAAAGT	AGACTAGGAC	GTGGCAGACA	CGGGAAAACG	AGACATGTAT	TATTGGCTTT	4020

1118

GATTGGTATT	TTAGCAATTT	CTATTTGCCT	ATTAGGCGGA	TTTATTGCTT	TTAAGATCTA	4080
CCAGCAAAAA	AGTTTTGAGC	AAAAGATTGA	ATCGCTCAAA	AAAGAGAAAG	ATGATCAATT	4140
GAGTGAGGGA	AATCAGAAGG	AGCATTTTCG	TCAGGGGCAA	GCCGAAGTGA	TTGCCTATTA	4200
TCCTCTCCAA	GGGGAGAAAG	TGATTTCCCTC	TGTTAGGGAG	CTGATAAATC	AAGATGTTAA	4260
GGACAAGCTA	GAAAGTAAGG	ACAATCTTGT	TTTCTACTAT	ACAGAGCAAG	AAGAGTCAGG	4320
TTTAAAGGGA	GTCGTTAATC	GTAATGTGAC	CAAACAAATC	TATGATTTAG	TTGCTTTTAA	4380
GATTGAAGAG	ACTGAAAAGA	CCAGTCTAGG	AAAGGTTTAC	TTAACAGAAG	ATGGGCAACC	4440
TTTTTACACTT	GACCAACTGT	TTTCAGATGC	TAGTAAGGCT	AAGGAACAGC	TGATAAAAGA	4500
GTTGACCTCC	TTCATAGAGG	ATAAAAAAAT	AGAGCAAGAC	CAGAGTGAGC	AGATTGTAAA	4560
AAACTTCTCT	GACCAAGACT	TGTCTGCATG	GAATTTTGAT	TACAAGGATA	GTCAGATTAT	4620
CCTTTATCCA	AGTCCTGTGG	TTGAAAATTT	AGAAGAGATA	GCCTTGCCAG	TATCTGCTTT	4680
CTTTGATGTT	ATCCAATCTT	CGTACTTACT	CGAAAAAGAT	GCGGCCTTGT	ACCAATCTTA	4740
CTTTGATAAG	AAACATCAAA	AAGTTGTCGC	TCTAACCTTT	GATGATGGTC	CAAATCCAGC	4800
AACGACCCCG	CAGGTATTAG	AGACCCTAGC	TAAATATGAT	ATTACAAGCG	GGGT	4854

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

TAAACAGGTG	TTAGGTGCTC	TAAACTATTA	AAATTCTAAG	GAAATAAGGC	TACTTTTTCT	60
GGGTCTTGTT	CATAGTAGGT	GTGGTTCTTT	TTTTCGAGTG	TAGCCCATAG	CTTTGAGCGC	120
ATAGTGGATG	GTAGTTGGAT	GACAGCCAAA	TTCAGAAGCT	ATTTCAAGTCA	AATAAGCATC	180
TGGATTGTCA	GTAAGATAGT	TTTTAAGTCT	ATCTCTATCA	ACTTTTCTTG	GTTTTGTTCC	240
TTTTACTTGG	TGGTTTAGCT	CTCCTGTTTT	CTCTTTTAGC	TTTAACCAGC	CATAAATGGT	300
ATTACGTGAG	ATTTGGAAAA	CGTGTGATGC	TTCTGTTATA	CTACCTGTTT	GCTCACAATA	360
AGAGAGAACT	TTTTTACGAA	AATCTATTGA	ATATGCCATA	AGAAGATTAT	ACCACATTGT	420
GTACTATTTT	TGGTTCATTT	TACTATATTT	CTAAACACTT	AGAAATAATA	AAACAAATTA	480
AATATTATTT	CTAAATATTT	GAAAATAACA	TCTATTTGTA	TTATACTATC	TTTGAGGTAA	540
CTATTATGAA	CTATATCAAA	AGACCACATT	ATTTAGATTT	TTTAAGAAAA	CATCGTGACC	600

1119

GACCAATCAT	CAAAGTTGTG	AGTGGAGTTA	GACGAGCTGG	TAAATCTGTG	CTTTTCAAC	660
TCTATAAAGA	GGAGTTACTA	GCAACTGGGG	TAGACGAGGA	TCAGATTATA	TTCATCAATT	720
TCGAAGATTT	GAGTTACTAT	GATCTGCGAC	ATTTTCAAAC	ATTATTCGCT	TATATAAAAG	780
ATCAATTAGT	TAGCAAGAAA	ACATACTATA	TCTTTTATA	TGAAATTCAA	TATGTTGAAA	840
AATTTGAACT	GGTAGCAGAT	AGTCTATTCA	TCTTAGCAAA	TGTAGACCTC	TATTTGACTG	900
GATCTAACGC	CTACTTTATG	AGTAGCCAAT	TAGCAACAAA	CTTGACTGGT	CGGTATGTTG	960
AGATAGAGGT	TCTTCCTTTG	TCATTTGAAG	AATATCTATC	AGGTCAATCT	CTCACAGAGA	1020
ATCTGAATAC	AACAGAAATT	TTTAACAATT	ATCTCTTTAG	TGCTTCCCT	TACTTATTGC	1080
AAACATCATC	TTACGATGAA	AAAATTGACT	ATCTCAGAGG	AATATATAAC	TCCATACTGT	1140
TAAATGATAT	TGTCACTAGA	TTGGGAAAAC	CAAATCCTAC	TATTATTGAG	CGCATTGTCC	1200
GAACCCCTCT	CAGTAGTACA	GGTAGCTTAA	TATCAACAAA	TAAGATTCGC	AATACCCTAG	1260
TCAGCCAAAA	TGTTTCAATA	TCCCATAATA	CTTTGGAAAA	TTATTTGACA	ACTTTGACAG	1320
ATAGTTTACT	TTTTTATTCC	GTTCCACGTT	TTGATGTAAA	AGGTAGAGCA	TTATTGCAAC	1380
GTTTAGAAAA	ATATTATCCC	GTTGATTTAG	GTTTACGACA	TCTCTTATTA	CCAGACCAGA	1440
AAGAAGACAT	TAGGCATATC	TTGGAAAATA	TGGTATATTT	GGAATTGAGA	CGTAGATATT	1500
CACAAGTATA	TGTTGGTAAT	TTAGATAAGT	ATGAGGTTGA	TTTTGTTGTT	GTAAGTATC	1560
TTGGCCACTA	CGCTTATTAT	CAGGTCAGTG	AAACAACACT	TGCTCCAGAA	ACACTAGAAA	1620
GAGAACTTAG	ACCACTAGAA	GCCATTAAAG	ATCAATTCCC	TAAATATCTA	TTAACAATGG	1680
ATACGATTCA	GCCAACAGCC	AATTACAATG	GAATCGAGAA	GAAAAGCATT	ATAGATTGGT	1740
TACTAGAAAA	ATAGATAAAT	ATAAATCATA	CAGCTAATTA	GATTTGCAAC	AGTCTGTTAT	1800
CAATGATTCT	ACCCAAATCC	TAACAAGATA	TAGTGAATTT	CGAATACGCT	ATATAATACG	1860
GACACTTGAA	AATAGAAATT	GGGGATGAAA	GGGGATCTAT	AATTTCTGGA	AGTACTATCA	1920
AAAATTAATA	TCATAGTCTT	ATTAGAGAAT	AGCATCACCC	ACTTTCTCAA	ATAAGATTAA	1980
ATTGTAAGTG	AATTATAATG	AAAAAGAGAC	TGAGCAATCA	GTCTTTAAAA	TCAGAAAAGC	2040
GCATAGTATC	AGGTATTGAA	CAACCTTGAT	AATATGCGTT	TTATTATGGA	AATATTGCT	2100
TCATTTTCTC	CTGAAATAGA	GCTTTTGCTA	TCCTATTTTT	CTCTATTCT	AATGATTAC	2160
TTCAACTTCT	TACCTCTTGG	GAAAAA				2186

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3236 base pairs

1120

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

GTCACACGTT TGACTTCACG TATTTTCATAA GTATAAACTT TATTTTATC GGTAGATAA	60
ATCTTCATGC CATTTT TAGC ATTATCTAAA GGAGAAAATA ACATTTTATT AGCATTATCA	120
ACACCAAAGA TATGGTGACT AGCTAGACTA TAATTTCCCTT CTCCCATTAC TTGCTCGCGT	180
TTCATTGTAC CAGCTCCGTA GAAGAGATTA ACATTATCAA GTCCTTTAAA AATCGGCAAA	240
TTCATTTCCA ATTCAGGAAT TGCAATTCCC CCAATAACTG GTAATTTTGT AGCATCCCAT	300
TGAGAAGTTA GAACAGCTTC CGAAGAGATA GCTTTGACAG AATCAAAGTC AAAATTGCCT	360
TCTGTATCCT GATTTTCTTC TAATTTTCT TTTGATACCT GGCTAACTTG ATACTTATTG	420
GTATTCCAGA CTATGAAAAT ATTTCGAATT TGAGTATTAA AAATCAAAGC CAGTGACAGT	480
AATATCAGAA ATCCTGCTAG GATATTTGTC AGCAGATTTT TTCGCTTGTT TTTCTTTTTA	540
TTATTTTTTT GAGACATTAT GCTTCACCTT CTGTTTCGTT TTCTGTCCCA ACTTCTTCTT	600
TTTCTGCCAC CGCAACCGTT GTGAAAGTCA CTATCTGAGC ATCTTGATCC AGGCGCATTA	660
CTTTAACTCC CATAGTTGCA CGTCCTGTTT GTGAAATATT GGCAAGATTG GTTCGAATCA	720
TGACACCTGT ATCAGTGATA ATCATCAAAT CCTCATCCCC TTGAACAGTC ATAAGACCGG	780
CCAGCAAGCC ATTTTTTTTCG GTAATTTTAG CTGTCTGCAT TCCCTTACCA CCACGACCTT	840
TTGTTGGGTA TTCAGTAGCG ACTGTACGCT TACCATATCC TTTTCTGTG ATAATAAGAA	900
CCTCATCTTG ATCAGTAATC AAGCTGGCAC CAACAACCTG GTCTCCTTCA CGAAGGTAA	960
CACCTTTCAC ACCAGTGGCG ATACGGCTCA TACCACGAAC GGCTGATTGA TTAAAGCGAA	1020
CTGCATAACC AACTTTGGTA CCAATGATAA TATCCATATC TCCTTCTGCC AACAAGACAT	1080
TGATTAACTC ATCTTCATCC TTTAAATTCA GCGCTTTGAG ACCATTTTGA CGAATATTGG	1140
CAAACCTCCTT AACACTGGTT CTCTTCACAA TACCGTGACG GGTTGTAAAG AAGAGATAAG	1200
CATCATCACT GCGATCAGAC TCAACATTGA TAACCGTCTG AATACTTTTCG TCTTCATCCA	1260
ATTTCAAGAG ATTGACTACT GGTAGCCCTT TGGCAGTCCG ACCATACTCA GGAATTTTCAT	1320
AACCTTTAAG ACGATAGACA CGTCCCTTGT TTGTGAAGAA GAGCAGATGA TCATGGGTGC	1380
TAGTTGACAC TAACTCACGA ACAAAGTCAT CATCTTTCAC TCCCGTTCCT TGGACACCAC	1440
GACCCCCACG TTTTGTAGCA GTGAACTCGT CCTGATCCAA ACGCTTAATG TAGCCTCTGT	1500
TAGAAAGGGT AATCAAGACA TCCGATTCTT CAATCAAGTC CTCATCCTCG AGACTCAAGA	1560

1121

CCTGTCCAAT	CATCAACTCT	GTACGGCGCT	TATCAGAAAA	TTTACGTTTA	ACTTCATCCA	1620
ATTCTCTTT	GATAATTTGA	GAAACACGTT	CAGGCTTAGC	AAGAATATCT	GCTAAATCCG	1680
CAATCAGAGC	CAAGAGGTCA	TCATACTCAG	ATTGAATCTT	ATCGCGTTCC	AAACCTGTCA	1740
AACGACGAAG	ACGCATATCA	AGGATAGCTT	GACTTTGACG	TTCAGAAAGC	TTAAACTTGC	1800
TCATCAACTC	AGCTTGAGcT	TCCGCATcCG	tTTCACTAGC	ACGGATGATA	CGAATCAyTC	1860
GTCGATATGG	TCTAGCGCAA	TCAAGAGACC	TTCTAAGATA	TGAGCGCGCG	CTTCCGCTTT	1920
TTCCTTATCA	AAACGTGTAC	GACGAACAAC	CACTTCTTTT	TGGTGCTCGA	TATAAGCATC	1980
CAAAATCTGA	CGAAGAGACA	AAATTTTCGG	TATACCATTT	TGGATAGCGA	GCATATTGAA	2040
ACCAAAATTG	GTTTGCATTT	GGGTCATTTT	GAAGAGGTTA	TTGAGAATAA	CATTGGCTGA	2100
GGCGTCGCGC	TTGACTTCAA	TAACAAATCG	AACACCTTCA	CGGTTTGACT	CATCACGTAC	2160
TGCTGTGATA	CCCTCAATGC	GTTTTTCCTG	AACCAAGCGA	ACAATATGCT	CATGCACCTT	2220
GGTTTTATTG	ACCATGTAAG	GAAATTCTGT	TACAACGATA	CGCTCACGAC	CAGTCTTAGT	2280
CGTTTCAATC	TCTGTACGAG	AACGTAGGAC	AATCGAACCT	TTACCTGTTT	CATAAGCCTT	2340
ATGGATACCT	GATTTCCCCA	TGACAAGAGC	ACCAGTTGGA	AAATCTGGTC	CAGGCAAGAC	2400
TTCCATCAAG	TCCTTGGTAG	TCACTTCAGG	ATTATCCATG	ACCAACTTCA	CTGCATCAAT	2460
gGTTTCACCC	AGATTATGAG	GTGGAATATT	GGTTGCCATC	CCAACCGCGA	TACCAGTTGC	2520
TCCATTAACC	AAAAGGTTTG	GAAAACGCGC	TGGCAAGACC	AAGGGTTCCC	GTTTCATTGGC	2580
ATCATAGTTA	TCAACGAAAT	CAACTGTATT	TTTGTTGATA	TCACGAAGCA	TTTCAGAGC	2640
AATCTTGCTC	ATACGTGCCT	CGGTATAACG	TTGAGCGGCA	GCACTATCTC	CATCCATGGA	2700
ACCAAAATTC	CCATGACCAT	CTACAAGCAT	GTAACGGTAG	CTCCACCATT	GAGCCATACG	2760
GACCATGGCT	TCATAAATAG	AGGAATCCCC	GTGTGGGTGA	TATTTACCCA	TGACATCCCC	2820
TGTAATACGA	GCAGATTTTT	TATGGGGTTT	GTCTGGGGTC	ACACCCAATT	CATTCAATCC	2880
GTAGAGAATG	CGACGGTGAA	CAGGTTTTAA	GCCATCTCGA	ACATCAGGAA	GAGCTCGCGC	2940
TACGATAACA	CTCATGGCGT	AGTCGATAAA	ACTTGCCTTC	ATCTCCTTTG	TCAGATTGAC	3000
ATTCACTAAA	TTTTTATCCT	GCATTAATAA	ATGCCTCATT	TCACAATTAG	TAAGTAACAA	3060
CATTATACCA	TAAATTCCCA	TCTATTTTCA	CCTCTAAACC	ACTAAAACGT	TTACATCGAG	3120
AACTATAAGG	CATATTCGTG	ACAAAGTTTT	TTAAAAGTGA	TAGAATGAAG	TTGTCTAGGG	3180
AAAACCCCTA	ATAGAATAAG	GAGATGGTTA	nACAATGACT	CTGACTAACA	CACAAA	3236

(2) INFORMATION FOR SEQ ID NO: 181:

1122

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8651 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

AGGTCCTGAA GTATTGGAAC AGGAAGGTCA AGAGTTTTTG GAACATTTCA AAAA	ACTCTT	60
GGAGTCAGTT GAAGTAGTAG CCATCTCAGG TAGTCTGCCA GCTGGCCTTC CAGTTGATTA		120
CTATGCGAGC TTGGTAGAAC TTGCTAATCA AGCTGGCAAG CATGTAGTCT TGGACTGCTC		180
AGGTGCAGCA CTTCAGGCTG TTCTTGAATC ACCCCATAAA CCAACAGTCA TCAAACCAA		240
TAATGAAGAA TTGTCTCAGC TTCTTGGAAG AGAAGTTTCT GAGGATTTGG ATGAATTAAA		300
AGAAGTACTT CAAGAACCTT TGTTTGCAGG GATTGAATGG ATTATCGTTT CACTTGGTGC		360
CAACGGTACT TTTGCCAAAC ATGGTGACAC TTTCTACAAG GTAGATATTC CTAGAATTCA		420
GGTGGTAAAT CCTGTTGGAT CTGGAGACTC TACTGTGGCA GGAATTTCTT CAGGACTTCT		480
TCACAAAGAA TCGGATGCAG AATTACTCAT CAAGGCAAAT GTCCTTGGTA TGCTCAATGC		540
TCAAGAAAAA ATGACTGGTC ATGTCAACAT GGCCAACTAT CAAGCTCTAT ATGATCAATT		600
AATAGTAAAA GAGGTATAAA ATGGCTTTAA CAGAACAAAA ACGTGTACGC TTAGAAAAAC		660
TTTCTGATGA AAATGGTATC ATCTCAGCTC TTGCATTTGA CCAACGTGGT GCTTTGAAAC		720
GCCTCATGGT TAAACACCAA ACAGAAGAAC CAACTGTGGC CCAAATGGAA GAACTTAAAG		780
TCTTGGTAGC AGATGAATTG ACTAAATATG CTTCATCTAT GCTTCTTGAC CCTGAGTATG		840
GACTTCCAGC AACTAAAGCT CTTGATGAAA AAGCTGGTCT TCTCCTTGCT TATGAAAAAA		900
CAGGTTATGA CACAACAAGC ACAAACGCT TGCCAGACTG CTTGGATGTT TGGTCTGCAA		960
AACGTATTAA AGAAGAAGGT GCAGATGCAG TTAAATTCTT GCTTTACTAT GATGTAGATA		1020
GCTCAGACGA ACTCAATCAA GAAAAACAAG CCTACATCGA ACGCATCGGT TCTGAGTGTG		1080
TGGCTGAAGA TATCCCATTC TTCCTTGAAA TCCTTGCTTA CGATGAAAAA ATTGCGGATG		1140
CAGGTTCTGT AGAATACGCT AAAGTAAAAC CACACAAAGT TATCGGCGCT ATGAAAGTCT		1200
TTTCAGACCC ACGCTTTAAC ATTGATGTTT TGAAAGTTGA AGTTCCTGTT AACATTAAAT		1260
ATGTTGAAGc KTCGCTGAAG GTGAAGTAGT TTATACACGT GAAGAAGCAG CAGCCTTCTT		1320
CAAAGCGCAA GATGAAGCAA CGAACTTGCC ATACATCTAC TTGAGTGCTG GTGTATCAGC		1380
TAAACTCTTC CAAGATACTC TTGTATTTGC TCATGAATCA GGTGCGAACT TTAACGGAGT		1440
TCTTTGTGGC CGTGCTACAT GGGCAGGATC AGTTGAAGCT TACATCAAAG ATGGTGAAGC		1500

1123

AGCAGCTCGC	GAATGGtCGC	ACAACTGGAT	TTGAAAACAT	TGACGAACTC	AACAAAGTTC	1560
TTCAAAGAAC	AGCAACTTCA	TGGAAAGAAC	GCGTGTAAGA	AAGTCCTCCT	AGTTTAGGAA	1620
CATGAATCTA	AAAAAATTTA	AAAAAAGTTG	TATGTAAAGG	CTTACAAAAT	AACTTACTTG	1680
TGCTATACTT	AAATCACAAG	TTAATATGAA	TTAGAAAGTA	ACTATATGAA	GTATAATAAA	1740
AATAGGATAT	AGTTTATTTT	ACGAGCTAGG	AAGGAAAAAT	ACGGAAACAA	TATTGCCAGA	1800
ATAAACTATA	TTTAGATGCA	CATTTCAATC	ATTGTTTTAT	AAAAGGAGAA	GATAAACGGC	1860
TACTAAAAAG	AGTTTTTAAAG	CGTTAGTTGT	AGGACTAGGT	ATTGTTTCAA	TATTCTTATC	1920
AGCCTTACCT	ATGGTTAGTG	GTTCTGTATT	TGCAGATAGT	GCCCTAACTA	CAGTAGATAA	1980
AGCAAATGAT	ATTGTTTTGA	ATGTTGATGG	GAATAAATTT	TATAATGTTT	CGGTTTCAGA	2040
AGATATTGTA	AATGCTGGTC	AAATTTTGGG	AGATTATTTT	TATGTAGATA	AATTTGGAAA	2100
TATAAATTTA	AAAGGCACTC	CTGAAGAGTT	AGCAAAAAAT	ATTGGTATTT	CTGTACAAGA	2160
AGCAAGTTTG	ATGTATGGAG	CTGTAAAAGA	GTTACCCAAC	GTTTACGAAA	GAGGTCCTGT	2220
AGGTTTTTCGT	TTCAATCTTG	GTCCTCAAGT	GAGGGGGATG	GGTGGCTGGG	CTGCTGGAGC	2280
TTTCGCTACT	GGATATGCTG	GATGGCATT	GAAACAATTT	GCGGTTAATC	CTGTTACATC	2340
TGGATTTGTT	GCTGTAATAA	GTGGTGCGAT	TGGCTGGGCT	GTAAAACTG	CTGTAGAAAA	2400
TTATTGGACA	GTTGCTGTAG	CTACAGTAGA	AGTGCCGTTT	GTGAACCTTG	TTTACACCAT	2460
AGATTTACCT	TAGAGGTTAT	TTCTTTATGA	ATCATTCTTT	TAAAAAATA	ACTGTATTTT	2520
GTTTTATAGT	TTCTTGTTGTT	CTTTGTTTAT	TAGACTTAAT	GAATTTTAAA	AATGTAGCTA	2580
CTTTTTTATT	TTTCTGTCTT	CCTGTTTTTG	TTTTGATTTA	CAAAAATAAA	TAAAAACAGA	2640
GCCTCTGTTT	GATGAATTTT	AGAACATAGT	TAAGTTTTAA	AAAAAGTTGT	ATGTAAAGGT	2700
TTACAAAATA	ACTTACTTGT	GCTATACTTA	AATCACAAGT	TAATACAAGG	TGAGTGTTAC	2760
TAAGTAATAT	TAGGCATGAT	CACAGGTGAA	TTAGAAATCA	GCTGATTTTC	TAGTTCATTT	2820
GTGGTCATTT	TTTGTAATTA	TATACCTTTA	AGATATAAAA	GGAGGTTGAC	ATGTATCGAA	2880
TTCTAAATCC	AATGAATCAC	AATGTCTCGC	TTGTCAGAAA	TGATAAGGGA	GAAGAGGTGA	2940
TTGTAATTGG	TAAGGGAATT	GCATTTCGGG	AGAAGAAGGG	GGATTTGATT	GCTGAAAATC	3000
AGGTTGAGAA	AATCTTTTCGG	ATGAAGACCG	AAGAGTCCAG	AGAAAACTTT	ATGGCTCTTC	3060
TCAAAGATGT	TCCGCTTGAT	TTTATCACAG	TGACCTATGA	AATCATTGAT	AAGCTATCAA	3120
AGAAATATCA	TTATCCGATT	CAAGAGTATC	TCTATGTAAC	CTTGACAGAT	CATATTTACT	3180
GTTCTTATCA	AGCTCTAACT	CAAGGAAGGT	ACAAGGATAG	TAATCTGCCA	GATATTTCCG	3240

1124						
CTAAGTATCC	TGTCGCTTTT	CAAATCGCAA	ATGAAGCTTT	TGAAATTTAC	CGTCAGAAGC	3300
TAGCAGATCA	TTTTCCTGAG	GACGAAATTA	TTCGGATTGC	TTATCATTTT	ATTAATGCTG	3360
AAGGTGAAAA	TGAAGTGGA	CTTGTGGAGT	CGATTGATAA	GAGGAAAGAA	ATTCTCAGGA	3420
ATGTTGAAGA	AGTTTTAACG	GACTATGCAA	TTCAACGAAC	TAAAAAGAAT	AACCATTTCT	3480
ATGATCGCTT	TATGATCCAT	TTGAATTATT	TCTTGGATTA	TTAGACAGA	TCTAGAGATG	3540
ATAACCAATC	ACTTCTGGAT	ATGGAAGATC	ATATTAAACA	ATCCTATCCA	AAAGCCTTCG	3600
AGATTGGTTC	CAAGATCTAT	GATGTGATTA	CGCAACATAC	GGGTCTTGAT	TTGTATAAAA	3660
GTGAACGAGT	TTATCTAGTT	CTACATATCC	AACGTTTATT	GTCATAAAAA	TTTATTTAAA	3720
ACTATATAAG	GAGAATTCTA	TCATGAATAG	AGAAGAAGTA	ACATTGTTAG	GTTTTGAAAT	3780
CGTAGCCTAT	GCTGGCGATG	CTCGTTCAAA	ACTATTGGAA	GCCTTGAAGG	CTGCTGAAGC	3840
TGGTGATTTT	GAAAAAGCGG	ACGCTCTGGT	AGAGGAAGCT	GGTAGCTGTA	TTGCAGAGGC	3900
TCACCACGCG	CAAACAAGTC	TATTGACTAA	GGAAGCTTCA	GGTGAGGACT	TGGCTTATAG	3960
TGTAACCATG	ATGCATGGCC	AAGACCACTT	AATGACAAC	ATCTTGTTAA	AAGATTTGAT	4020
GCATCATTTA	ATTGAACTCT	ACAAGAGAGG	AGTTCAATAA	TGAATAAACT	AATTGCATTT	4080
ATCGAGAAAG	GAAAGCCTTT	CTTTGAAAAA	CTATCTCGTA	ATATCTATCT	TCGTGCTATT	4140
CGTGATGGTT	TCATTGCAGG	TATGCCTGTT	ATTCTCTTCT	CAAGTATCTT	TATCTTGATT	4200
GCCTTTGTAC	CAAACATCATG	GGGCTTTAAA	TGGTCTGATG	AAGTTGTAGC	CTTTCTGATG	4260
AAACCTTATA	GCTATTCTAT	GGGTATTCTG	GCTCTCTTGG	TAGCTGGTAC	AACAGCTAAG	4320
TCATTGACTG	ACTCAGTAAA	CCGAGCATG	GAAAAAACCA	ATCAAATCAA	GTATATGTCA	4380
ACATTGTTGG	CAGCAATTGT	TGGTTTGTGG	ATGTTGGCAG	CTGATCCTAT	CGAAAGTGGT	4440
CTAGCTACTG	GATTCTTGGG	GACAAAAGGT	TTGCTTTCAG	CCTTCCTTGC	TGCCTTTGTT	4500
ACTGTAGCCA	TCTATAAGGT	TTGTGTAAAG	AACAACGTCA	CTATTCGTAT	GCCTGACGAA	4560
GTTCCACCAA	ATATCTCACA	AGTCTTTAAA	GATGTGATTC	CATTCACCTT	ATCTGTTGTT	4620
TCTCTTTATG	CTCTTGACTT	ATTAGCACGT	TATTTTGTGG	GTTCTAGTGT	GGCAGAATCA	4680
ATCGGTAAAT	TCTTCGCACC	ACTCTTCTCA	GCAGCAGACG	GATACCTTGG	TATTACCATT	4740
ATCTTTGGTG	CCTTTGCCTT	CTTCTGGTTT	GTTGGGATTC	ATGGTCCATC	TATCGTTGAA	4800
CCAGCTATCG	CAGCTATTAC	CTATGCCAAT	GCCGAAGTTA	ACTTGAACCT	TCTCCAACAA	4860
GGGATGCATG	CAGACAAGAT	TCTTACTTCT	GGTACACAAA	TGTTTATCGT	TACCATGGGT	4920
GGTACAGGTG	CGACATTGGT	CGTTCCATTT	ATGTTTCATGT	GGTTGACAAA	ATCGAAACGT	4980
AACCGTGCAA	TCGGACGTGC	TTCAGTAGTT	CCTACCTTCT	TCGGTGTA	TGAACCAATC	5040

1125

TTGTTTGGTG	CACCTCTTGT	TTTGAATCCA	ATCTTCTTCA	TTCCATTTAT	CTTTGCTCCA	5100
ATTGCAAACG	TATGGATTTT	CAAATTCTTT	ATTGAAACTC	TTGGAATGAA	CTCATTCACT	5160
GCTAATCTAC	CATGGACAAC	TCCAGCTCCA	CTAGGTCTAG	TTCTTGGAAC	TAACTTCCAA	5220
GTGCTATCAT	TCATTCTTGC	TGCCCTTCTA	ATCGTGGTTG	ACGTTGTCAT	TTACTATCCA	5280
TTCCCTTAAGG	TCTATGATGA	ACAAATTCTT	GAAGAAGAAC	G TTCAGGTAA	GTCTAATGAT	5340
GAATTGAAAG	AAAAAGTTGC	TGCAAACTTC	AACACTGCAA	AAGCGGATGC	TATTCTTGAA	5400
AAAGCGGGTG	TCGATGCAGC	ACAAAATACC	ATCACTGAAG	AAACAAATGT	CCTCGTTCTC	5460
TGTGCAGGTG	GAGGAACAAG	TGGTCTCCTT	GCAAATGCCT	TGAATAAGGC	AGCAGCAGAA	5520
TACAATGTCC	CTGTGAAAGC	AGCAGCAGGC	GGCTATGGTG	CTCACCGTGA	AATGTTACCA	5580
GAGTTTGATC	TTGTTATCCT	TGCCCCTCAA	GTTGCTTCAA	ACTTTGAAGA	TATGAAAGCA	5640
GAAACAGATA	AGCTCGGTAT	TAAACTAGCG	AAAACAGAAG	GCGCTCAATA	CATCAAATTA	5700
ACTCGTGATG	GAAAAGGTGC	TCTTGCAATC	GTACAAGCGC	AATTCGATTA	AGGCTAGAGA	5760
CTCTGAAATA	GTCTCCCATC	GTTACGGAAA	TCGCTATGGC	GAATTTCTTA	TTATTAATTC	5820
GTCGGTAAAA	AGATATCGTT	TTTACCTCCT	CATGTCACAA	TTCCGGTGA	TGGTACAAGA	5880
AGTGAGATGG	AGAAGGATGG	CTCACTGACT	CCTCTCCTCT	CACTTTTACT	TTATTTAAAT	5940
CAAGAAATAG	GTGAAAAAAA	TGACAAAAAC	ACTTCCAAAA	GACTTTATTT	TTGGTGGCGC	6000
AACAGCTGCT	TATCAAGCAG	AAGGTGCTAC	ACATACTGAT	GGAAAAGGAC	CAGTTGCTTG	6060
GGATAAATAT	CTTGAGGATA	ACTACTGGTA	CACTGCCGAA	CCAGCTAGTG	ATTTTACAA	6120
TCGATATCCA	GTTGACCTCA	AGCTAGCAGA	AGAGTATGGT	GTCAATGGTA	TTCGAATTTT	6180
TATTGCTTGG	TCACGTATTT	TCCCGACTGG	TTACGGCCAA	GTAAATGCTA	AAGGTGTTGA	6240
GTTTTATCAT	AATTTATTTG	CAGAGTGTC	CAAACGTCAT	GTTGAGCCTT	TTGTAACTCT	6300
TCATCACTTT	GACACGCCAG	AAGCTCTCCA	CTCAAATGGA	GACTTCTTAA	ACCGTGAAAA	6360
TATCGAACAT	TTTGTAGACT	ACGCTGCCTT	CTGTTTTGAA	GAATTTCCAG	AAGTAAACTA	6420
TTGGACAACC	TTTAATGAAA	TTGGACCAAT	CGGTGATGGT	CAATATTTGG	TTGGGAAATT	6480
CCCTCCAGGT	ATCCAGTACG	ACCTTGCCAA	AGTCTTTCAA	TCACACCACA	ATATGATGGT	6540
GTCTCATGCA	CGCGCGGTAA	AATTGTACAA	AGAGAAAGGC	TATAAAGGGG	AAATTGGTGT	6600
TGTTACAGCC	CTGCCAACTA	AATATCCTCT	AGATCCTGAA	AATCCAGCAG	ATGTTCTGTC	6660
AGCTGAGTTG	GAAGATATCA	TCCACAATAA	ATTCATCTTA	GACGCAACTT	ATCTAGGTCT	6720
CTATTCAGCT	GAAACCATGG	AAGGTGTCAA	CCATATCTTA	TTAGTCAATG	GTGGTAGTTT	6780

1126

GGATCTTCGT	GAAGAAGATT	TTACAGCATT	AGAAGCTGCA	AAAGACTTGA	ATGATTTTCCT	6840
AGGAATCAAC	TACTATATGA	GTGACTGGAT	GGAAGCCTTT	GATGGAGAAA	CTGAAATTAT	6900
CCATAATGGT	AAAGGTGAAA	AAGGAAGCTC	TAAGTATCAA	ATCAAAGGTG	TTGGTCGTCC	6960
TGTAGCTCCT	GACTATGTAC	CACGCACGGA	TTGGGATTGG	ATTATCTACC	CTCAAGGTTT	7020
GTATGACCAA	ATCATGCGTG	TGAAGAAAGA	TTATCCTAAC	TACAAGAAGA	TTTACATCAC	7080
TGAAAATGGT	CTCGGCTATA	AAGATGAGTT	CGTTGATAAC	ACTGTTTACG	ATGATGGTCG	7140
TATTGATTAC	GTGAAGCAAC	ACTTGGAGGT	TTTATCTGAT	GCGATTGCAG	ATGGAGCTAA	7200
TGTAAAAGGT	TACTTCATTT	GGTCATTAAT	GGATGTCTTC	TCATGGTCAA	ACGGTTATGA	7260
GAAACGTTAT	GGTCTCTTCT	ACGTAGATTT	TGAAACTCAA	GAACGTTATC	CTAAGAAATC	7320
AGCTCACTGG	TACAAGAAAG	TAGCGGAAAC	TCAGATTATA	GACTAGTAGA	ATTAGTCATT	7380
AGATATAGAA	TTTTAGTGAG	TCAAAAAGAT	GTTCAAAGAT	TTTATCCAAT	CTATTTATGA	7440
AAAAAAGTTT	ATATTATAAA	TTTCGAAAAA	TGCTCTCAAA	TACCGTGTTT	GACGAGTGAA	7500
GAATTGAAAA	GTCTTGAAAA	ATGGTATGTC	TCGACTGGTA	AAGAATGGAT	TTGTCATTCA	7560
GATGATGAGC	TGGAAGAATT	TAAAAATCTA	TTTTTTAAATT	TTATCAATCC	TGAAGAATGG	7620
GATACTATCT	CCTTTGATTC	AGATTTTATG	CCGTTTCAAC	AATCGTAACC	AATTTCTCAA	7680
AAAAGTTAAA	TCTTATATTT	AGTACTCTGT	AAAACCTCTA	TCTAATCACG	TTGCTTATAC	7740
TCAATGAAAA	TCAAAGAGCA	ACTTTAAACT	AGGAAGCGAG	TCGCAGATTT	CTCAATGCAT	7800
AGCTTTGAGG	AATTGGGCAA	AAAGTCTTTG	ATATAGAAAA	ACGCATAGTA	TCAGGTGTTT	7860
CAACACCTGA	TACTATGCGT	TTTATTGTGG	GAAGATTTAC	TTTTTTTCTT	CTGAAATTGA	7920
GTTGTTACCC	AGGCTCTTTC	AGTTTATTAA	GGCTTGATGA	CTTTAATGTG	TTTAGATAGC	7980
TTAAAAAGGA	TTGAATCACT	TAGTTTAGAA	TCTGAAACAA	TAGTATCAAG	ATTTGATACA	8040
TTATAAAAAG	TATAAAAATC	AAACTTATTG	AACTTGCTAT	GATCTGCGAG	TAAATATTTT	8100
TTATTAGAAT	TATTTAAAGC	GATGCGTTGA	GCCTCTCCCT	CTTCCTCGCT	AAAAGTAGCT	8160
AGAGCTCCGT	TTTGAATACC	ATTACAGCTA	ACGAAAGCTT	TAGAAAATTG	GAGATTAGAG	8220
AGATTTTGTA	GGGTCAATGT	ACCAACAAAA	GCACCTGTAA	TATCGCGATA	ATTTCCACCT	8280
ATTAAAATCA	AATCTGTTAA	TTTTCGTTTC	CTTAAAATCA	GAAAAACAGG	TAGACTGTTG	8340
GTTACGACGC	GGATATTGTC	AATAGGCAAC	TCACGCGCAA	AAAACCTCTA	TGTTGTTTCCT	8400
GGTCCAATGA	AAATAGTTTC	TCTTTCTTCT	ACTAGACTGC	CTGCAAAATG	GGCTATTTCT	8460
TGTTTTTCTG	CCGTTTGGAG	GGCTTGTTTT	TCAATATTTG	ATCGCTCATT	AGTCAAAAGG	8520
GAGTTGGTTC	GAAGTTTTTC	AGCTCCACCA	TGCACACGAA	TCAGCAAATC	TTTATCAGCT	8580

1127

AATTCCTGTA AATAGCGCCT TGCAGTCATA TCTGAAACGG CTATTTTCGTC CATAATCTGT 8640
TTAACTGTTA T 8651

(2) INFORMATION FOR SEQ ID NO: 182:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3786 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

AATCTCCAAT CAGTGCCACT TCAGCTACAA AGAAGAGGAG GATAATAACT CCGTTCACAA 60
 GGACAGACAA GAATAATTGA TAGAAGGAGT CGGTTTCACT TGCTTGACTT GGTCTTGTA 120
 TGATWTGGAG ACTGGCAAGC AGAATGATTC CAATGCTAAT CACACACAAG AGGGCTGTAA 180
 ATCGTAGGCT ATCAAAGAAA GCAAAGAAAC TAGCAATAGC AGTGAGGAmG ATTGGAATTG 240
 CCAAGAGTTG ACTATATTGT TGGAGAACCT TGTCTAGCGT CCAGTCCTTT TCCTGGTGGA 300
 TAAATCGTCT CACAACGAAA CTACCCAAGA GGAATGAAAA GAAGAAGAGT GTTGTCGCTA 360
 CTAGGATAGA GATGATAGAA AAAAGAGTTA AAGGAGCTAG CTGCTCAGGG AAGCGACTGT 420
 TAATGCTTGC TATATGTCCA TAGTAAGCAT GTTTGATGTG ATAGATACTA AAGAAAAAGG 480
 AAGATGCAGA AAACAGAATG AGCAAGAGAA AGGCTGTGTA ACTGTGTGTG AACTTGTTT 540
 CCAACTTACT TGTAGGAGAT TTGATCGCTT CCACTAGCCA AGACCAAAAA TCAAGCACTT 600
 GCTCTTTCCA TTTATCCCTA GATTTTGGAG CTTGGTCGGG GATATAAGGA CTTTCTAAAG 660
 ATTTACTGAT AAGAAGTGGC TCTTTCGTGG TTGCTTTTTG CTGAGGAAGA GCTTCTTGGC 720
 TCTCTTCAGC TATAGTGA CT TTTTCTGTTT CTTTAGAAAG GTCTGGCTCT TCTTCAGTAG 780
 AATTAGATGC CTTCTTTTCT TCTATTTCTG TTCTCGCTTC ACTGTCTTCA GGAGCTTCAA 840
 TTTTCTCTTC TTGCTGGCTT TCCAATTCGA CTTCAGCTTG AGGGACTTCC TCCTCTAACT 900
 GAGTATTTTT TTCAATTGGT GTATCGAGAT CGGCTATCGT TTCTTCAGCC TTGTCTGCAA 960
 CCTCTTGAGC TTGCTCTTCA GGCTTGTTCT TGCTTGTTGT TTTTACAAAA TCATTACTTT 1020
 CAAACCATTC TTGTTTCATG GTAGAACCTC CTTTTTAGTT AGATAAATAT GTTTCCATAG 1080
 TAGCAAATGT AAGCGTTTTT GTCAACGTCT GCTTGGTGTG GATATTAGAT CAATATTATC 1140
 ATCAGATCTC GCAATGAGTT GATCCTTGAC ATCGGTTTTT TCAGTTTGT AAGGGTTGCT 1200
 TAATTCGTA CCTCTTGATT CAGGCTTTTC TCTTGTGAAT TGGAAGATAG AACCATAGTT 1260

1128

GCTTGAGATG	TCCCAGTTAA	TTCGTTGGCT	TTCTTTCTGG	TCTAGGATGA	TTCTGAGATA	1320
ATCTTTGGCA	GTCAGTTCAA	CCTTGCCATG	GACTTGGATA	TTTTCAGCGT	GGAAGTGATT	1380
CTCTGTTGAC	TCTAGCTGAC	TATCTGTAAG	AACTGTATCA	AAGATATTAA	CGATATTGGG	1440
CGTTGTGAGT	TTACTGTTTT	TGATACGACT	TCCTTCAATT	CGGAGGATAT	AGCTGTTTGT	1500
ATTGAGGGTC	GCATTTTCAA	GGCTAGCATT	TATGATGGTG	GTTTGTCCGC	GATTGGCTGA	1560
GATGTTGATC	CCTTTTAGAG	TTCTCCCTTT	TGGTAGTCGG	AGAATAACTT	CTTCAAAACG	1620
ACTAGAGTAG	CTACTTGCGA	TATGAAGAAT	CCCACCAATT	CCAGAAGAGA	GAAACGGAGT	1680
TTCAGACAGT	TTCTTATCAG	TGAGACTCAG	AGTTCTATCG	TTCTGATTGG	TGATAAGATC	1740
ATGGTGAGCA	GAAAGAGATG	GATGGTAAGA	AATGTGGATT	TGATCATCGA	AAGAGTCTGT	1800
GATGGTGAGC	GTGTGTTGGT	GGAGAGTAAT	TTCTAGGTTT	TCGACTTCCT	TGCCAAAGGT	1860
TAGCTTTTCC	GTACGGCTAT	CATAGACAGG	TTCTTTGGAC	ATGGAAAGTA	GGCTCTTAAt	1920
CCCGTCAGAT	TGGATACCTA	CAAAAAGCAG	GATAAAGCCG	ATAACGGTAG	TCACCACACC	1980
AAAGATGAGA	AATCCTTTTG	TCCATTTACG	CATGCTGATT	ACCTCTCTTT	CCTTTTTTTAA	2040
GAACAAATTG	TACCAGACGA	ACAATGAGTA	GACCGAAGAA	GCGAGTTGCA	TAGGAAATGC	2100
CAAGTAAAC	TAGCGAAGAA	GCACCGATAG	CCAGTAAACC	AGAACCAGAA	ATCAAGATAA	2160
AGGCTGATTT	GGCTTGGGCG	AGGACAGTGA	AACTTTCAAC	TAAAAATAGG	AATCCGCCGA	2220
TGATACCCAG	TATGGAAACT	GCAAAGAAAG	CCAGAAATGAC	AGTCAAAGCG	GCTACAAGAA	2280
TTGCGAACAG	GGTCACGAGG	ATGGCGATTC	CCAGAGGAAT	GCCGATAGGT	GCTGCAAGGA	2340
GGGCTAACAA	GGCGATATGT	AAAATTTGTC	GGTTATTTTT	TTGAGCGGGT	GCTTCATTGA	2400
TTTTTTTATC	GAGAAGATTG	GATAGAACTT	CGTGGGCCGC	TTCTTTGGGA	GTTCCCAAAC	2460
TAGCGATGAG	TTCTTCTTCT	CCTTCGACTC	CAGCATCGTC	AAAGAGCTCT	CTGAAATAGT	2520
CCATGGCTTC	GATACGGTCA	GCTTCAGGTA	GTTTCTTGAG	ATAGAGTTCT	AGCTGAGTCA	2580
GGTATTCAGT	TCTTGTCATG	GCGGATACTC	CCTTCTATGA	TGCCATTGAT	GGTGTCTGTA	2640
TAGAGTGCCC	ATTCATCTTT	TAGGGTCAAG	AGCTGCTCTA	TACCACCGTT	TGTCAAGGAG	2700
TAGTATTTGC	GCATGCGACC	TTGGAACCTC	CTAGAAATAGG	TTGTCAGAAA	GCTATTGCCT	2760
TCCAATTTTT	TGAGAATGGG	ATAGAGTGTG	GATTCTTTGA	TATTAGCGAT	CAGCTTAATG	2820
GTTTGGCTAA	TCTCATAACC	ATAAGAATCA	CCCTGCTCCA	GTACAGCCAA	GATGAGAAAT	2880
TCAATCAAGG	CAGAGGATGT	TGGAAAAGTAC	ATGGGAAACC	TCCTTTTCTA	ATGTGTAAGA	2940
TTTTTATATA	TAATTTTCT	ACACATACAT	TGTACATCTA	AAAGAAAGCC	CTGTCAAGAG	3000
AAATGTGTAA	AATTTTATA	TATAAAAAAC	TTCTAGCTAA	AACTAGAAGT	TTAAAGGATC	3060

1129

TTATCCGCTC TGTCCACTGT AAAGAGGGCC ACAGTCATCA GGATATCGAT GAGCAAGAGG	3120
GCAGCTACAG ATGGTACCCA AGAGTGGAAC AGGTCAAAAC TGTAACCAAA GAGGGTTGGC	3180
CCAAAGGCTG CTAGGATATA GCCTCCTGTT TGAGATAGGC CGGACAATTG GGCTGTCTTT	3240
TCAGGGGCGC TTGTCTTGAG TGAAAAGTTG ACCATGAGAT AAGGGAAGAG GGCCTGGTT	3300
GCGGTTCCGA TGAGGAGATG GATGGCAAGC CAGTAAATGA AATTATTGAT TGGGAAAAG	3360
AGCATGGAAA TGCCGACCAC ACCAGCTAGT GAAACCAGAG TGAGCATGAG CTGACGGTTG	3420
CGAGTAGATA AACTGGTTGT CAGGCTTGGG ATGGTCATTG AAAAAGGAAT GCTAATCAGA	3480
GATAAGATAG AAGTCAGCAA GCCAGCTTCG TGACTGGATA GACCTGCATG GATAGACATG	3540
GTAGGTAACC AGGTCATGAC GGTGTAAAAG ATCAAGGATT GAAAACCTGA AAAGATAATA	3600
ATTGCCCAAA CCTGTTTATT ACGCATGACC TTTATTTGAC TTTTGTGTTT GGTGTGTGGA	3660
GCTAGTCTAT GATTATAGCG GTGATTTGGG AGCCAGACCA AAAAAGTTGC TAGACAGAGT	3720
AACGTGAGGA GAAGGATAAG TCCTTTCCAA GAACTGGCTT GTGTAATGGG CACAGCTAGA	3780
TAGGAA	3786

(2) INFORMATION FOR SEQ ID NO: 183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3054 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

TCAGCTAAAA AACATTGCTA AATTGATTGA AGCTGGTGCT ACACATTCCG ATTCAACTTC	60
TCACACGGCG ACCACCAAGA ACAAGGTGAG CGTATGGCAA CTGTTAAACT TGCGGAAAAA	120
ATTGCAGGTA AAAAAGTTGG TTTCTTCTT GATACAAAAG GACCTGAAAT CCGTACAGAA	180
TTGTTTGAAG GTGAAGCTAA AGAATATTCA TACAAAACCTG GTGAAAAAAT TCGTGTGCA	240
ACTAAACAAG GAATCAAATC AACTCGTGAA GTGATTGCGT TGAACGTTGC TGGTGCTCTT	300
GATATCTATG ATGATGTTGA AGTTGGTCGT CAAGTTTGG TTGACGATGG TAAACTTGGT	360
CTTCGTGTGG TTGCTAAAGA TGATGCAACT CGTGAATTTG AAGTTGAAGT TGAAAACGAT	420
GGTATCATCG CTAAACAAAA AGGTGTGAAC ATCCCTAACA CTAAAATTCC TTTCCCAGCT	480
CTTGCTGAAC GCGATAACGA CGATATCCGT TTCGGTCTTG AACAAAGTAT CAACTTCATC	540
GCAATTCAT TCGTACGTAC TGCAAAAGAT GTGAACGAAG TTCGTGCAAT CTGTGAAGAA	600

1130

ACTGGAAACG	GACATGTTCA	ATTGTTTCGCT	AAAATCGAAA	ACCAACAAGG	TATCGATAAC	660
TTAGATGAAA	TCATCGAAGC	AGCTGATGGT	ATTATGATTG	CTCGTGGTGA	TATGGGTATC	720
GAAGTACCGT	TCGAAATGGT	TCCAGTTTAT	CAAAAAATGA	TTATCAAGAA	AGTCAATGCT	780
GCAGGTAAAG	TTGTTATCAC	TGCAACAAAC	ATGCTTGAAA	CAATGACTGA	AAAACCACGT	840
GCAACTCGTT	CAGAAGTATC	AGATGTATTC	AACGCTGTTA	TCGACGGAAC	TGACGCTACA	900
ATGTTGTCAG	GCGAGTCTGC	AAACGGTAAA	TACCCACTCG	AGTCAGTAAC	TACAATGGCT	960
ACAATCGACA	AGAACGCTCA	AGCTCTTCTT	AATGAATACG	GACGTCTTGA	TTCAGATTCA	1020
TTTGAGCGTA	ACTCTAAGAC	AGAAGTAATG	GCTTCTGCTG	TTAAAGATGC	TACTAGCTCA	1080
ATGGATATCA	AATTGGTTGT	AACTCTTACT	AAGACAGGTC	ATACTGCACG	TTTGATTTCT	1140
AAATACCGTC	CAAATGCTGA	CATCTTAGCA	TTGACATTTG	ACGAATTGAC	AGAACGTGGC	1200
TTGATGTTGA	ACTGGGGTGT	TATCCCAATG	TTGACAGATG	CTCCATCTTC	AACTGACGAT	1260
ATGTTCGAAA	TCGCTGAACG	TAAAGCGGTA	GAAGCAGGTC	TCGTTGAGTC	AGGCGATGAT	1320
ATCGTTATCG	TTGCTGGTGT	GCCAGTAGGA	GAAGCTGTTC	GCACAAACAC	AATGCGTATC	1380
CGCACAGTAC	GTTAAGAAAA	ATATAAAAAC	CTATCATATC	CAGCTTTAGA	GCTTGTGTGA	1440
TAGGCTTTTT	GTATAGAGGG	TAAGAAATAG	GCAAACTTTT	CATAATGGAT	TGATACTCTT	1500
CGAAAATCTC	TTCAAACCAC	GTCAGCGTCG	CCTTACCGTA	TATATGTTAC	TgACTTCGTC	1560
AGTTCTATCT	ACAACCTCAA	AGCAGTGCTT	TGAGCAACTG	CGGCTAGCTT	CCTAGTTTGC	1620
TCTTTGATTT	TCATTGAGTA	TGAAATAAGA	TATGCACAAA	TTGATTAGAA	AGTCAAATGA	1680
ATTTCTACAA	ATGTTTTAGC	AATCGTAATG	TACTTGCTCTA	GATTCGATCT	GATATATTTT	1740
CGATTTAATG	ATATGGTATT	TAAAACCTCC	AAAGTAGCTT	ACTCCATTCT	TTTACTTACG	1800
TGAGTGTAGA	TGTTATTTAC	TGTTTTAGCG	TTTTTGTGTT	CCACTCTAAC	CATTATAGCA	1860
TTCTTCTCAG	CTAGTGTAAT	AAGGAGTGTG	TGCCTGAAAA	TATGGGAACT	AAGGGGCTGG	1920
TTTATCGGTT	TCTCTAGTTT	AGTATTTGCC	TTTTGCAAAG	TGATCTTAAA	TGCCTTTCTC	1980
TAAATTTACA	TATCACTATT	GTTTAACAAA	ATCTAATCTA	TTTTAGGTCA	CTTATTCCTT	2040
TTTTGAAATG	TAGAATGAAC	TTTTTCAAAG	TTTTTCGAAT	CTTTTAAAAT	CTGTTTGCTT	2100
TATATCGCCA	TTCTCCCCC	TTTTTTAATT	CTCCCTATAT	AGCCTGACAG	CTTTCCCGAT	2160
GGTACGAATA	TGGTTGCTTT	CGTCTAGGTG	GATGTCGGGG	TATTCGGGAT	TGAGTTTTTT	2220
TGAGGCAGCC	TTGGCGGAGT	TTCTTGACAT	AGTTAGTGCC	GTCTACTTGG	AAGATGCCGA	2280
TGGTATTATA	GTCAATCTGT	GGGGTATTCT	TGATAAATAG	GTAGTCGCTG	TTTCTTATCT	2340
TTGGCTCCAT	GGAATTGCTG	ACGACATAAG	CGATTGGGTC	GTAGTCGTCT	GGGATAATGG	2400

1131

AAACTCCATA TCTAAATCGT TGTCCTGCAT CGAGCGGCTA CCTGCAGAGA TAAACTACCT	2460
AACACGAGAG TAAGTAGTCT GTCTGTAGTC GTCCAGTCTG ATGATTTTTA CGATACTTCG	2520
TTTTTCTGAT CATAAGTTG CCTCTCGGCA TAGGTCAGAA CTTTACCTTG TCTGGGTGGT	2580
TCCCGTTGGT CGTAGATAGA TTGGATATCG CTAGGAGAAT CCTTTTGAAC TGGAGGAAAG	2640
AGGGCATCGA TCAAGCTACT GAATACTTTA ACTAAGTCAA ATATAGTATT TTTCTTAGTA	2700
GACCTAACCC TTTTTTCATA ATTTCTAATG GTGTTTTTAC TTATACCTAT CTTAGTACCC	2760
AATTCTTATT GAGTCCAACC ATTACTAGTC TATATTGTTT TATAGTTGAT TGAGTTTGGA	2820
ATAGTACGCT GTAGCTGCTA AAACATTTCT AGAAATTAAT TTGACTTTCC TAATAGAGTT	2880
GTTCATATCT TATTTCAATC TATTATGTTT TTCACCTCTA ACAATCGCAA TCTCTTCTTT	2940
ATCCATGAAT GAAATCGCTT TCTATTTTGT TAAGTAAAGC ATAACACGAA ATCCACGAAA	3000
ATGAAAACCT TTGTTGTGTT TTCGTAAAAA ATTTGTTGAC AGAGCACGAA ACGC	3054

(2) INFORMATION FOR SEQ ID NO: 184:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1590 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

TGTGATTTTC yGAAAATTTG GTAAAATATA TCTTAATCAT TTTCAGGAGG AAAAAATTT	60
GACAAGATAT CAGAATTTAG TAAATGGAAA ATGGAAATCA TCTGAACAAG AAATTACGAT	120
TTATTCACCA ATCAATCAAG AAGAATTGGG TACAGTTCCA GCCATGACTC AGACTGAAGC	180
TGATGAGGCT ATGCAAGCTG CGCGTGCAGC CCTGCCAGCA TGGCGAGCTT TATCAGCAGT	240
TGAACGTGCG GCTTATTTGC ATAAAACAGC AGCTATTTTA GAACGCGATA AGGAAGAAAT	300
TGGTACTATC CTTGCCAAAG AAGTAGCAAA AGGGATTAAA GCAGCAATTG GAGAAGTAGT	360
GCGTACAGCA GACTTGATTG GTTATGCTGC TGAGGAAGGT CTCCGTATCA CTGGACAAGC	420
AATGGAAGGT GGTGGTTTTG AGGCAACAAG TAAAAACAAA CTGGCTGTTG TCCGTCGTGA	480
ACCAGTTGGT ATCGTGCTAG CGATTGCTCC CTTTAATTAT CCAGTTAATT TATCTGCTTC	540
TAAAATTGCA CCTGCCTTGA TTGCAGGGAA TGTGGTCATG TTAAAGCCAC CAACACAAGG	600
TTCCATTTCT GGACTCTTGT TGGCTAAAGC ATTTGAAGAA GCAGGGATTC CGGCAGGTGT	660
TTTCAACACC ATTACAGGTC GTGGTTCAGA AATTGGGGAT TATATCATTG AGCACAAAGA	720

1132

AGTCAACTTC ATCAACTTTA CAGGTTCAAC TCCTATTGGA GAACGTATTG GTCGTTTAGC	780
TGGTATGCGT CCTATCATGT TGGAACCTGG TGGGAAAGAT GCAGCTCTTG TACTAGAAGA	840
TGCAGATTTG GAACATGCTG CCAAGCAAAT TGTTGCGGGA GCCTTTAGCT ACTCAGGACA	900
ACGTTGCACG GCCATTAAAC GTGTCATTGT TCTCGAAAGT GTAGCAGATA AATTAGCTAC	960
TTTGCTTCAG GAAGAAGTTT CTAAATTAAC AGTTGGTGAT CCATTTGACA ATGCTGATAT	1020
TACACCTGTT ATTGACAATG CTTCAGCCGA CTTCATTTGG GGCTTGATTG AGGATGCACA	1080
AGAAAAAGAA GCTCAGGCTC TTACACCAAT CAAACGTGAG GGCAATCTTC TCTGGCCAGT	1140
GCTTTTTGAC CAAGTTACAA AAGATATGAA AGTGGCATGG GAAGAGCCAT TTGGTCCTGT	1200
TTTACCAATC ATTCGTGTGG CTAGTGTAGA GGAAGCTATT GCCTTTGCCA ACGAATCTGA	1260
ATTCGGCCTT CAATCATCAG TCTTTACAAA TGATTTCAAA AAAGCCTTTG AAATTGCTGA	1320
AAAACCTGAA GTAGGTACAG TCCACATTAA TAATAAAACC CAGCGTGGTC CAGATAATTT	1380
CCCATTCCCTT GGTGTCAAAG GTTCTGGAGC TGGAGTGCAA GGAATTAAAT ATAGCATTGA	1440
AGCGATGACA AATGTCAAAT CCATTGTTTT TGATGTGAAA TAACGTGTAA AACCAGGAAA	1500
TTGTTTTCTT GGTTTTATTT TTTTGCTATA AAATAATAAT AATTATAGAA AAAATACGAA	1560
CTTTTTGGTA TTATAATAGA TTGAAACCGG	1590

(2) INFORMATION FOR SEQ ID NO: 185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4848 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

CCTGCAGTTG TCAGACCTGT AATTTTCTTT TTATCTGTAA TAAGAATCGT TCCAGCGCCT	60
AGAAAACCCA CACCTGATAT AACTTGAGCT CCTAATCGTG TAGGATCTCC TGTCCCAAAT	120
TTATAAGATA CGTATTCATT CGTCATCATA ATCAAACATG CAGCTAGACA AACAATACTA	180
TAAGTTGCGA TGCCTGCAGG CTGGGATTTG CTCCCTCTCT CTAAACCAAT TATACTACCA	240
ATGACTACTG ATAAAACAAT CCTGACAACT ATTTCAATAT TTGATAACCC AAGACTAGTG	300
GCTGTCATGA TTATTTCTTT ACTTTACGCC CCGGTCTTTG TGTGAAGTAT AATACCGTTC	360
CAGAAATAAT CATCAGAACA ATTGTATAAA CAAATACCAG AGCTTGTCGA TTAGATGTTG	420
CTGTTTCATC ACCTGCAGAT CGAATCGTAA TACCTAATGG TTGAGCTAGG GGATGGTAAA	480
GGAATACAGA TAAGTCGAAG TCAGTTAATA AAGAGTTAAA GTTTAAAGCA ATAACAGAGA	540

1133

GAACAACCGG	TAAAATAAAT	GGAATGATAA	CCTTCATCAT	AGTATAAAAA	GGTGAAGCAC	600
CCATACTTCT	TGCTGCATCT	TCCATCTCAT	CATCAACACT	AAATAAAAATA	GCACGTACCA	660
TTCTATAAGA	AAATGGGATT	TTTACAACATA	TATATGCAAT	AAGTAGAATT	ACCAAACACTAC	720
CTACCAAAAT	CTGATTCAAG	ACAAGAAATT	GTGGCTGATT	AAAAGTAAAT	AATAAACTTA	780
CTGCTAAAAG	TGTACTTGGT	AGTAACCAAG	GAAGTAGAGC	ACCATATTCA	AATAAGAAAT	840
CAAAACGAGA	TTTATGTTTT	CTGACAACAC	GAGCAAATAC	AACTGCGAGA	ATTGTTGCTG	900
TTGTCGCAGC	AATAATAGAA	TAAATAAAGC	TGACCAAGAA	TGGAGAGAAT	GCCGCACTAT	960
TACTAAAGAA	TAAGCGATAA	TTTTCTAAAG	TAAAGTTTGA	TAATGTTAAG	TTACCTGTTT	1020
GAATTGCAAC	TGGATCTGTA	AATGAGTATA	ATACTATAAA	AATTAGTGGA	AGCATGAAAA	1080
CTGTGAACAA	TCCATATGCT	ACAATGTGAG	CAATGATATT	CCAAGGCTTA	GACGCAATTT	1140
TTTGTTTTTT	AAGAGGCGCT	TTAGTCTTAG	AGATAGAAAT	ATAATTTCCA	CCTTTTTCTA	1200
TCTTATTCAT	GATAGTAAGC	AAAATTGTAG	TTGCAATACC	TAAAATAAAT	GCAAGTAGGG	1260
CAGCTAAATC	ACGAGAATTC	CCCATCCCTG	CAAATGTAAT	AATCATTGGA	TTTATAGTTT	1320
GAAATTCTTT	ACCACCAACA	ATCATGGGTG	CTGCTACTGC	AGATAAACCA	CTAAGAAAAA	1380
CCATAATAGT	AAGTGCAAAT	AGAGTTGGAA	TTAAGGTTGG	TAACACTACT	TTTCGGAAAA	1440
CAGTAAATGG	TTTGTCTCCC	ATATTTGAG	CAGCCTCAAT	AGTGTGATAG	TCAACGCTTC	1500
GAATTGTATT	TGTTAAAAAC	AATGTATGAT	TAGCAGTTCC	TGAAAATGTC	ATAATGAATA	1560
AGACTGCACC	ATACCCAATA	AACCAGTTAG	GGTCTAAAGA	AGGGATAACA	TTTTGTAAAA	1620
ATTTTGTAAT	CAATCCATAA	GGACCATAGA	CAAATTTATA	TCCAGTCGCT	AAAACCACTC	1680
CTCCATAAAT	TAAAGAGGTC	ATATAACCTA	ATTTTAAAAT	TTTAGCACCT	TTAATATCAA	1740
AGTACTCTGT	AAATAGAACA	CAAAGAATAC	CTACGACATT	AACTGTAATA	ATGAGTGAAA	1800
ATGCTAACTT	AAAACGTGTC	ATAATACTCT	GAAGTGCCCT	CTGAGATTTT	AGAACACGAT	1860
GTACAGCATC	AAGGGAAAAT	TCTCCTCCTT	TTACAAATAC	ATTCACACT	AGATCAAAGT	1920
TTGGATAAAT	AATAAATGTT	ACTAAGAACC	AGATTAACCC	TAAACGAATA	AGCCAATCTT	1980
TTAAATTTAA	TTTATGACGC	ATACTGCACC	TCCTTAAAAT	TGCAGAACGT	CTGATGGTGT	2040
GATAAATAAT	TCCACACTTT	CTCCGACAGA	TCTAATAGCA	GCCTGACTAT	CAATACTTGT	2100
TACATTAAGA	ATCTGACTTT	CAGAACTTT	TATTGTATAG	TGAATTGTAA	CTCCAGAAAA	2160
CTCAACATCA	ATAATTGTCC	CTTTTAGAAT	AAAATCTTGT	TCAGTTTCAC	GATTGAATCG	2220
AACTTCTCT	AATCGAATGT	ATCCTTTTTT	ATCCTCTAAG	AAAACGCTTG	TATTTTTCAA	2280

1134

TAATACTTCG	TGGACTGTTT	CATCGGTCAA	AACATTAATA	TCTCCAATAA	AATCACATAC	2340
AAATTCAGTT	TGAGAATTAT	GATAAATCTC	TACTGGTGTA	CCGACCTGTT	CGATGTATCC	2400
ATTGTTAAAG	ACTGCAATTC	TATCAGATAA	AGTCAAGGCT	TCCTCTTGAT	CATGAGTAAC	2460
ATATAAAGTA	GTAATACCTA	ACTCTTTTTG	AAGTCTTTTC	AACTCTTTTC	TCAAATCTAC	2520
ACGTAATTTT	GCGTCAAGGT	TTGACAATGG	TTCATCTAGA	CAAAGAATTT	TAGGTTCAAG	2580
AACCAGAGCA	CGAGCCAATG	CTACCCTTTG	TTGTTGACCC	CCAGATAAAT	CTGATACATT	2640
ACGCTGTAAC	TGTTGATCAG	AGATCTTAAT	TTTTGCTGCC	ACTGCTGATA	CTTTAGCTTT	2700
AATAACATCT	GGAGCTACCT	TCTTAACTTT	TAAACCAAAT	GCAATATTAT	CAAAAACAGT	2760
CATAGTTGGA	AATAGCGCAT	AAGATTGAAA	TACAATACCA	ATTCCACGCT	TTTCAGGTTC	2820
CAAATGAGTG	ACATCTGTTC	CATTAACCTC	AATACTTCCT	GATGATGGAT	CTAGAAAACC	2880
TACCAATGCT	CTCAAAGTAG	TTGATTTACC	ACATCCTGAA	GGCCCAAGAA	ATGTAAAAAA	2940
TTCCCCTTCA	TGTATATCTA	AATTCAGATT	ATCAATTGCA	ACAAAATCAC	CATATTTAAT	3000
TTGAATATTA	TCAAATTTAA	TCATCTCACT	AACTCCCTCT	ATTACTAAAC	CAAAGCCTC	3060
TCTTTATTTT	TTCCATAAAT	TTAGAAATAA	TAGAGAGACT	TGGACATAAA	AATTAACCTC	3120
TATTTCTTAT	TGTACGTATT	CTAATTCAGC	TTTTTCTACC	CATTCATCCA	AATGCTTTCC	3180
AACAGCTTCC	CAGTCAATAT	TTTGTGGTTT	CACTTGATCA	ACAAATTTCT	TCGTATCTTC	3240
AGGTAGATCT	TTGAGGGCAT	CTTTATTTGC	AGGAATAGAT	CCAAAGTTCT	TACTATATTC	3300
TACTTGAATT	TCTGATTGAC	CAAACCAATC	AATAAATTCT	TTAGCTAACG	CTTGTTTTTT	3360
ACTAGTGCTT	AAAACCATAG	TTTGTTTCAGT	TACAAATGGT	ACACCAATCT	CAGGAGTCAT	3420
AACTTTGAAA	ACAACATTTT	GTTCTTTTTG	TCCAATAAAT	GCACCAGAAC	CCCACATCAT	3480
TCCATATTGT	ATTGGATCTT	CTTTGTCTAA	CATCTTAACA	ATTGAACTTT	CTCCCTTTTG	3540
AAGAGTGTAT	GCATTTTTCA	AATATTCTTT	TGCTACTTCC	CAACCTTTTT	CGGAAACACC	3600
TAATTCACCT	TTATCATCAA	GGTATCGAAC	TAAGATACTT	GCTAGAATTG	CCCGTCCTGT	3660
ACCTCCTTGA	AGACCAGAAA	TTGAATATTT	ACCTTTATAC	TTACTACCTA	ATTCAGTCCA	3720
ATCTTTAGGC	ATTTCTTTTA	CATCAGGCGC	CCCAATTAAA	ACTAATGGTT	GAACAATCAC	3780
AGGATTATAA	TAATTATCTT	TATCTGATAA	AGATTGATCA	ATTTTATCTA	ACCATTTAGG	3840
CTTGTAAGT	ACTAGTAATT	TTTGATCTCT	AATTTTATTT	GAATCAACAG	CACCAATTCC	3900
AAATACCATA	TCTGCAACTG	CATTATTCTT	CTCAGCAATA	ACACGGTCTG	CTAATTGAGC	3960
GCCAGCGATA	TCAACCATTT	TTATATTAAA	ACCAGCTTCT	TTTGCTTTAG	CAGTTAACCA	4020
ATCACCACGA	CCATTTGAGA	CTGAGTTCGA	ATAGATAACT	AATTCCTGAC	TTTTATCAGC	4080

1135

TTTTTCTTCA	GATGAAGAAG	CAGTCGTAGA	ATTTGAACCT	CCAGAGCAAG	CAGCAAGTGT	4140
AGTAAgAGCA	ACTCCCGTTG	CAAGTACAGT	AGACCAAACCT	TTCATTTTTT	TCATGATAAG	4200
TTCTCCTTTT	TTATTATTTT	ATTTAAATTT	TTCGTGATAT	GGAACAAATT	GTCTCATATC	4260
TTCAAATACA	GTATAGTCAA	TACGGTTTAC	AGTAATAGTT	GGAATCTTCT	CTAATAAAAT	4320
TTCAGTTAAT	TCTGCTCTGA	CTTTAGTAAA	CTCTTCTTCC	TCCTCTTCGG	TTAGAGGAAT	4380
CCGAAGATAC	CCAATTGAAA	TATGGAATTG	ATATCTATCA	TGATTAGGGA	AACAAACACC	4440
TGCTTTTTCT	GAGACATAAG	TACGAATTTT	TTCTAATCTC	TTTGCAGAAG	CTTCATCTGC	4500
AGGTTCAACT	AGTATGTTTT	GTTTTCCCAT	TTCAGTTATA	CGCATATGAA	TTTCTTCATC	4560
CAACAATGGA	AAAATTTCAA	GTTGTTTAGC	AAAGTAATCA	TGTATTTCCCT	GTAAAGGTGT	4620
ATCTAGAGGA	AGATTACTGC	TCCAAAACCTC	gtTCACGATT	TTCATGGCAC	AACAATTCAA	4680
TTACAGTCAT	GTGAATAGAA	TTCTTGAGAG	TTAAAGTAAA	CTTATCGATA	AATGGTAATT	4740
CTCTATAACG	TGATTGAATA	ATATCAACAA	CTTCCATCAA	ATCTTGTTTA	GTATAAAGAT	4800
TTGCTACAAC	TGTATTCCCA	GGGAAATGAT	TAAATTCCCC	ATTCTCGG		4848

(2) INFORMATION FOR SEQ ID NO: 186:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3763 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

GTTATAAGCA	ACACCTTCTT	GCTTGCCATA	AGTTGTGAAA	TGGGTAGAAT	CGATATCTAC	60
AATGAGTTGG	TTTAGCTGGT	GAAACTGTAA	AAAGAATTCG	ACCAATTCAA	GGTTGAGGCA	120
TCGCAAACTA	TGGACTGTTT	CCTCGTCAGT	TCTGGAAAGA	AAACGGGATA	AGGTTGGCTG	180
TGAAGCAAGC	TGCCCTCCTT	CCAATAATTT	TGGAAAGTAG	GCATCAGCTG	ACAATTCTTT	240
ACAAGCATAG	TCCGTTCCAT	AACCTGTTAA	CAGTTGAAAG	AGGAACTGGA	CAAGGATATC	300
TGAATCCGAA	TAACGACAGT	AGCGGCGTTG	GTCATTCGTT	ACTAAATACT	TAGAAATCCG	360
CTCTTTTAGT	TTCAACTGGG	AAAAAAGTTC	CTGAAAAAAG	ATAAGACCAC	CATACTGGGT	420
TAAATGACCT	CCATCGAAAG	ATAGTTGGTA	AAAAGACTTG	TTTTGGAAGT	GATGATTTGG	480
TAAACTGTTC	ATGTGAGTTT	CCTTTCTTTT	TGTGTTTTTT	TCTACACTTA	TACCATAAAG	540
GGGAAACTCT	TTTTTGTCTA	GTAAAAAACA	CCCATTTGGGT	GAAAAAAGAA	ACCATCCAGG	600

1136

ATCTAAGCTA	AGGCAAGGAT	TCTGGATGGT	TTTTAGATTT	GGGGTGAATA	ATTGGGGATT	660
TAGGAGAAAT	GATGGTATCT	TCCAAATCAA	AATCAACTTC	ACTCCATAGT	CTCAACTGAT	720
TGATTTTCCC	ATCTTGATAG	GTCACATCCT	TGTCAAGGAT	AAACTGAGTC	AACACCTCAT	780
GTTGACCTTG	ACACCTGATG	TCATCTACCA	AGAGCCAGAC	ATCCTCTACC	AACATGAGGA	840
TTTTTCTCCT	GTGAAGATAA	GGCAAATCAG	GTTCTGCTGA	CCAATAAGCC	CCCTCAATAT	900
AATGCACTCC	CTCCCTTTCT	TTATGGTGAC	AAAACAGGGA	GTGAGGATAG	TATTCATATT	960
CCCAGGATCC	CGTGATTCTT	TCCGGAGCTT	TCCCATCTAC	AATGCAGGTC	GAATGACTCC	1020
AAGCACTCTT	TAAGAGATAA	CGTTCATATA	TCTCCCGATA	AGAATAACGC	CCAGCATCTA	1080
TGAAAATAGG	TTGGCCTTGA	TACTGTAAGC	AAAAACTATT	CTCGTCACTA	TGACTATGGG	1140
CACTTCCTAG	CGGACCATTT	TTGAAAAATA	GATAACGATG	TTCATCCTTA	ATGCAGACAT	1200
GTCCAGAGTC	TTCAAAGATC	ATGGACTTAG	GCTGCCAAGC	TCTCTTTTCA	AATTCCTGCA	1260
GTCGCTTGAC	CTTTTCTCGC	CCCAGGAACA	AGAGGCTAAG	CAAATCAACT	TTAACATCCA	1320
GACCGTTAAG	AAGGTCTTCC	TGGTTCAAAA	CCACAGCAGA	CAGGCTCAAA	ATTTCTGTCTG	1380
TTTCTGTAGA	ATCGCTATCA	CCAAAAGCCA	AAGTCCGTCC	ATCTAAGCCT	GTCATCATTT	1440
GAATATAGGT	CGCCATCTTT	TCCAGCAACT	CTTGCTAACT	ATCTTGCAAG	TCTGGAAGCA	1500
AGAGACACAA	ATCCAGCAAG	GCTTTATAAA	CCTCTACATG	ATAGAGAATC	GA CTGTTCAA	1560
ACTGGCTTCC	ATCTCCTAAA	ATCTGTGTCT	CAATTTGCTG	TTTCAACTCC	TCTGAAGCAA	1620
AATGGTAAGC	TTCTTCTAGA	TCCATCTTAT	CTGAAAAGAA	ATGATAGATA	GCAAGCATCG	1680
GAATTGTTTG	TAAAATCCCC	CAGTTACTAA	GGGTGTACTT	GGCGCGATAG	TAGCTTTTCA	1740
TAAAGTCAAT	CTGCTTTTCT	AGACTGACCA	AAATTTTCTC	TAGTTCTTTC	TCCTCTAGCA	1800
AGTCAAATTT	CAAGAGGAGC	AAGAGTAGTT	TCAACCAAGT	AAAGGAACGA	ATACCCGTAT	1860
CCAAGGTTCT	AGTCATCAAG	GATTGAGGAG	AAAATTCTCT	CACCTGCTCA	ATCCAATCAA	1920
ATAGAAAGAA	CTTGCACTTT	TGAATATAGT	CCTTATCTCC	TTCTACCAGA	TACCCTATCA	1980
TAAACTGCAA	GAGATATTCT	TGTCGATTGA	GCATATAAGA	CCATTCTGGA	TCATCTTCAA	2040
ATACTTGATC	CCATACCATC	GGCTGGATTT	GATGGATTTT	TGAACAAGGC	TCCATATCCC	2100
AAGGACTATC	AAACATAAAA	CGATTGTCCA	TCAAGCGTTC	AAGGGAAC TC	TTGACTTTCT	2160
CATAGTCTTT	TGAACAGTGC	GACAAGATAT	AATCACGACA	TTGATTTCCA	TCGACTCTTT	2220
CAAAAAATTG	TCTTCTTTCT	TCTTTCATTA	TCTATTACCA	GAAAAAGAAC	TACTTAAAAA	2280
GCAGTTCTTT	TGTCTTTCCC	ATTACACTTT	CCTTTTCTAC	ATGGATGACC	ACACCTTTTG	2340
CAATCTGCAA	GGAGACCAAG	TCATCTTGGA	TAGAAATGAT	TTTTCCATGA	ATTCCAGACA	2400

1137

ATAACAACAC TTCATCACCA AATGTTAAAG AAGCTAAATA CTCTTGTCGT TGCTCCATCT	2460
GTTTGCGAAG CAACTTTTGC TGACGAATAG AATGAAAGCT TGACAGTAAA AGGGGACTCA	2520
CTGCCAAGAC AATCACTATT CCATAAAACA ATGTTGTATC CATTAAGCTA TAATCTTAAG	2580
CCAGCTTCCG ATAATTCCGA TGATAACTGT TAAAATAACG AGTTTATATG TTGTCCATTT	2640
CTTTTCTTTG ATCAAGTAGT AACTAAAAG TGTAAATAGG GCTGGTAGAA GAGCTGGAGC	2700
AACCTTATCA AGCATTC CCT GAATACTTAC GATACTTTGT TTAGCGTCTG CTTTAACTTC	2760
CCCTGCAGCA AAGGTAATCG GCACCATAAT CTTAACAGAT GTCGCTGCCA AACCAGCAAT	2820
TACGtTACAC CGATAATATT GGCAATACGA GAAATCGTTG CCATCTGTTC GCTTAGTTTA	2880
TCAATCACAG TTGTTCCTAG TTTGTATCCA TACAGACCAG TTGACAATTT AATCGCTGTT	2940
AAAATCGTAT TCATCGCAAG GAAGAACAAG ATTGGACCGA CAACCAAGCC TTCTTGAGCA	3000
AACGAAGCTG CGATGGTTGA GAACAATGGA GCTAAACAGA ATTGAGAAAG AGAATCCCCA	3060
ATACCTGCCA ATGGTCCCAT CAAGGCCATC TTGATGCTAC GTGTTTCTTT TGCCGGACGG	3120
CCATTTTCCA ACATTACAAG ATGCAAGCTG GTAATAAAAG GCAGGAAGTG TGGGTTGGTA	3180
TTATAGAATT CACAGTTTTC TTCCAAGGCT TGGTAGAAAC CTTCTTGATC CTCTCCATAG	3240
TGTTTTTTCA AAGCAGGATA CATCACATTG GCATATCCCA ACCCTTGATA GTTACTATAG	3300
TTAAATCCAT TTTGACAAAA GAATGCCCCG AAAGACGTTT TAAGATAATC ACGTTTTGTT	3360
AATTTGTTAG ATCCAGTCAT CGTGTGCTTC CTCCTCTACC ACATGATCCG CTGTTTTTGG	3420
CTTGTTATAA AATTCAATCA AAGCAAAGAT AGTACCTACA ATTGCAATAC CAATTGTTGG	3480
GATGTTTAGA TAAGCTGCAC AAACATATCC CAACAAGACA AAGGGAATCA ACTCTTCTT	3540
AGCCATCACT GACAAGATCA TCGCAAAACC GATAGCTGGG AGCATTTTAC CAGCAACTGT	3600
CAAACCTGTA AGTAATACCG GTGGAATGTA GTCTACGAGT TTCAACAAGG TATCCATTGA	3660
AAGGGCACCA AGCAACCCAA GGTAAATCCA ATAAAGGCAA ACAACCAAAT TGTTGCATTT	3720
AGAGTGAAC TAAATTTCTT CAAATTATGG TTTTCAAGT GCT	3763

(2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5053 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

1138

CAATCTCTGA	GTATGTGCGG	TCAATACTAw	CAAAGGGAAT	yCCTGACGTC	AAGTAATGTT	60
CAATTGGmCT	ATAGGTAATG	GCAACCACTC	CATCAACTTT	ATTATGACGC	AACATCTCCA	120
GATAGTCTTG	CTCTCTATTT	GTACCATTGA	TAGAACATAA	GAGTAATTTG	TTATTTCTCT	180
TATAGACTTC	ATTTTCCACA	TGCATAGCAA	ATTCTGAAAA	GAAGGGATGC	CAGATACTTG	240
GTACAATGAT	TGCAATCGTT	TCTGTTCGAT	TTTTTTTCAT	TCCTCTAGCG	TAGTAATCTG	300
GAATGTAATT	CAAAGTTTTA	ATCGCTTGTT	CCACTTTTTT	CAAAGTTACT	TCTTTAATGC	360
CTTTTTCTTT	ATTAATTACA	CGTGAAACAG	TTCCAACACT	AACCTCTGCT	TCTAAAGCAA	420
CATCTTTCAT	GGTAATTGAT	TTTCTTTGTT	CTACCATATT	ATCACCTCCT	TTCAATATAT	480
AGTATCATGC	AAATGCTTTT	TAAGCAACTA	TTTCTCAATC	ATTTTTGGCC	AGATCATTTA	540
TCCCATCATG	AATAAAATCA	CTCCAATTAG	CTTTTGAAAA	TACTTCAATT	TTCATGTGTA	600
AACATCTACA	TAAAACAGGA	AAAGCCTTGG	TTTCATGGCT	TTTTTCGTAT	CTTCTATAAA	660
AAAAGCAAGA	GTTTtagatG	GCTATAAATC	TAGATGTACA	TTTTGCTTAA	ATGATTGAAG	720
GTCTTTTCTT	AACAAAAACA	CCCCCAAAT	TAGACTTTTT	CTGTCTAACT	TTTGAGGTAC	780
AGTCAAACG	CGAAATAGCG	TTTTTTTGTT	ATTTTTGGTT	ACTCATCTAA	TCGAATAAAC	840
ATCATGGCAT	TTAACAAGTA	TATGAGTGAG	ACCGTGTTTA	TATTATTTGA	ATAGATGAGT	900
CTCTTATTTT	CAATAGGAGG	AATAATAAAA	TTAGAAATAA	TGATATCATA	AGGTGAATCT	960
TCTAAAGATT	CCTTTGATAA	TTCTAATTCA	GTCCAAACTT	CCAGTTCAAA	ATTATTGCTA	1020
CAATAATAAG	AAAGTGTCTC	TGCAACGAAT	TTTGCATGAT	ACTGATCAAA	ATTACTCATA	1080
ACTAAAACCT	TTAGTTTAGG	CTGATTTTGT	AGCAAATTAA	TCACCAAATG	TTTGGTATGA	1140
GTGATGAAGG	TATAAGATAG	ATGATTTACC	ATCATTGAAC	TAGAACAAAC	CTCAAGAGTC	1200
TCTAAATAGT	GAGAAAGCTC	TTTTTTTATA	TCTGAAACAA	ATTTTGAAAA	AATATTTTGA	1260
AAGTTCCTGA	TTGTATTCCC	TTTTTGATCA	AATAAAATAA	ACTCAGTAAA	CAACTCTTGA	1320
CGATACAGAT	GTGCGGTATT	ATGCAGATGC	CAAATCAGAT	TATCCTTATT	CTCCATTTCA	1380
ATCTGATACT	TGACTGAAAT	CTGATCAATA	AAATCACTCA	ATAGATGGTA	AGATTTTTCA	1440
ACATAACTAT	CCTTTTTTAC	GCATTTTCATA	AAGAGACTTT	CATCTATGAA	AAACATTTTT	1500
TGAAAGTAAG	ACACAAATAA	TTGGCAAACA	ACTTCTTCAT	CTAAAGAGAT	ATTGTATTCT	1560
GATTCAAAAC	TCTGAGCAAC	ACCTTCTATT	CCTTCTGCCT	GCATTAAAAA	ATCCAAACTT	1620
TGGTCGTTAA	AAGAATCTTT	ATCTACTTCC	ATAAAATGAC	CAAACTTTAT	TCTATATAGG	1680
TTCGTAACTA	GGAGCAACTT	TAGCATTTCTA	TGCGTTGACA	AATTCATTGG	AAAGCTTGTT	1740
TCCTTATAAA	CCAATTCTAA	CAATTGAGAT	AGTGGCTCTG	ATGAAAAATT	TTCAAATGGC	1800

1139

CATTCTAGGA	AATAATATTT	TTCTGAAAAA	TATTGTGCAA	AAAAGTAACG	AATGTCTCTC	1860
TCATTTCCAA	TGATTTGAAC	AGGGGTCAGA	CTAACTTCAA	ATTGAAATTG	CCTTTTAATC	1920
ACTTTATTGA	TTTGGCTAAT	AATACGATAG	AGCGAAGATG	AACTGATATA	AAATTCTTTA	1980
CAAATACTCT	CAGCTTGACA	ACCTTCATTA	AAGAAGATGA	ATTCTAAAAT	CGAAAAATGA	2040
GTTGAATGTT	TAAAGAAATG	ATGGTAAACC	ATTTCAATAT	CACTATCATC	GGTATTAATA	2100
ATGCGTATAC	CATTAGTAGA	AGAATGAAAA	ATCAAGTCAG	GAAAAGCAGA	TTTAACATGG	2160
GATAGATCAT	CTTTGACTGC	ACGTTCTGTA	CAATTTAATA	ACTCTGCTAG	TTCAGAACGA	2220
TGAAACCAAC	GTTTATGTTC	AAATAATAAT	TCTAATAATT	CTAATTGCCT	ATGACTTTTT	2280
TTAGATAATA	AATCTCTCAT	GAATATCTTT	CTCTCTTTAT	AAATTATCGG	ATTAAACCTC	2340
TTGCAATTAT	ACCACAAAGA	ATAGGTATAG	CATGATATAA	CGACTTTTCC	TAAAATCTTT	2400
TATTTTCGTAT	AATAACACTA	CGGAGACAAT	ATATAAACAA	TTTTCTTATT	TTACCGTCTA	2460
TTGAGGGCGT	GAATACAGAA	TCAAATTCAA	GTCTAAAGAT	TATATTTTTA	ATTTTAAAAA	2520
TTATATAATA	GCAACAATTA	AAGAATTTGA	TTTTTTAAAA	TTATATAATA	ATAACAATCG	2580
AAATAATTGA	CTTTTCTATA	TTAAAGTTAT	ATAATAGTAA	TAATCAAAGA	AATTGATTTT	2640
TTGATATTAA	AATAAAAAAG	GAGGGTAGGC	AGTGTTGTGA	TCAATTATTG	CTGGAGGTCT	2700
TATTGGTCTC	TTGGCAGGTA	AAATCACTAA	AAAAGTAGTT	CTATGGGAAT	CATCGCAAAT	2760
GTATTCGCTG	GTTTAGTCGG	GGCATATGCA	GGACAATCTC	TTTTAGGTAG	TTGGGGTCCA	2820
GCAATCGCTG	GAATGGCTTT	GCTCCCATCT	ATTGTAGGTG	CAGCGATTGT	GATTACTGTA	2880
GTGTCATTCT	TTACAGGTAG	AAAGTAAACT	TTTCGCCAGT	AAAGTTAGCA	AACTATTTTT	2940
AAATCAATGA	CGGGAAAAAT	AGTTTAAATG	TTAAATCGAA	AGGATTGTAT	ATGTCAAAAG	3000
CAAAGAAAAT	ATGTTTCATT	ATTTTCTGTA	TTTTAATCTT	GACAATTTTC	CTTCCTGTTT	3060
TGATAGATTA	TCATCAAGTT	AGTGATCTAG	GTATTCATCT	ACTTAGCTGG	AGACAGAACT	3120
CCGTAGTTGA	ATTCTATCTT	GCTAGATATG	TCTTTTGGGG	GACAGTGGTT	CTATCAACTT	3180
TAGTTTTATT	ATCCATTTTA	GTTGTGATGT	TTTATCCTAA	ACGTTACTTG	GAAATCCAAC	3240
TTGAAACTAA	AAACGATACA	TTAAAATTAA	AGAATTCGGC	AATCGAAGGT	TTTGTTAGAA	3300
GTTTGGTGAG	TGATCATAGA	TTGATCAAGA	ACCCAAGTGT	TCATGTAAAT	TTACGAAAAA	3360
ATAAATGTTT	CGTTCATGTA	GAAGGTAAAA	TTCTTCCTTC	AGACAACATC	GCTGACAGAT	3420
GCCAAATAAT	TCAAAATGAA	ATAACTAATG	GATTGAAGCA	GTTTTTTGGT	ATTGAGCGTC	3480
AAGTAAACT	TGAAGTTGCA	GTAAAAAATT	ACCAACCAAA	ACCTCAAAAC	AAAAAGACTG	3540

1140

TTAGTCGTGT GAAGTAAGGA AGTAAAAAAT GGAATGGCTT AAACAATATC GATATCCAAT	3600
TATCGCTGGT CTCATAGGCG TATTTCTGGC TTGTTTGATT GTCTCCTTTG GCTTCTTCAA	3660
AACAATATTT GTATTGATTT TAGGAGCACT GGGAGTTGCA GCTGGATTAT ATATCGAAAA	3720
AAACTATATA GATAAATAAA AAAATAAAAA TTAATAATTT AATTAAAGGA GTTTCATATG	3780
TCAAACGAAA AAAACACAAA CACTAACGTA GAAAAGAAAG ATGCTACTGT TGTAGCTCAC	3840
GAAATCAAAG GGGAACTTAC TTACGAAGAT AAAGTTATCC AAAAAATCAT TGGTCTTTCA	3900
CTAGAAAACG TTTCAGGTCT TTTGGGAATC GATGGTGGTT TCTTCTCAA TCTTAAAGAA	3960
AAAATCGTTA ACAGCGATGA CGTAACAAGT GGTGTTAACG TAGAAGTTGG TAAAACACAA	4020
GTTGCAGTTG ACTTAAACGT TATTGTTGAG TACCAAAAAA ATGTTCCAGC TTTATATTCA	4080
GAAATCAGAG AAATCGTATC TTCAGAAGTT GCTAAAATGA CTGACTTGGA AATTGTTGAA	4140
ATCAACGTAA ACGTTGTCGA CATCAAACT AAAGAACAGC ATGAAGCAGA CTCAGTAAGC	4200
CTTCAAGATC GCGTATCTGA CGTTGCTGAA TCAACAGGAG AATTCAC TTC AGAACAATTC	4260
GAAAAAGCTA AATCTGGTCT TGGATCTGGT TTCTCAACTG TTCAAGAAAA AGTTAGCGAA	4320
GGTGTAGAAG CTGTTAAAGG TGCAGCAAAT GGTGTAGTAT CTCACGAAAA CACTCGTGTA	4380
AACTAAGATA AAATAAATAT AACAGGAGAA ATTATCATGT CAGTAGAAGA AAAATTAAAT	4440
CAAGCTAAAG GTTCTATTAA AGAAGGTGTT GGGAAAGCCA TCGGTGATGA AAAAATGGAA	4500
AAAGAAGGTG CAGCTGAAAA AGTTGTTTCT AAAGTAAAAG AAGTTGCCGA AGACGCTAAA	4560
GACGCTGTAG AAGGTGCTGT AGAAGGTGTT AAAAACATGT TGAGTGCGCA CGATAAATAA	4620
GGTTAAAAGT TACTTTATCT TTTTAGTAAT ATTAGTCAAA AGAGTCTGAG TCAAGATGAT	4680
TCTCAGAAAA CAAAAAGCTA GAGATTCCCA ATTGCGGAAC TCTAGCTTTT TAATTTTGCC	4740
TCTTTCTCTT ATTATATTTT AGCAGGTTGT TGGCCATGAG TACGAATCCC ATGTCAATTC	4800
TCACCTGACG CTTACCTCTC AGATGACATC TCTTATAACC CAAACAAACC TTTATCTGCC	4860
CAAAGACAGA TTTTCATATCA ATCTTACGTT TAGCGAAAAT TTGTCTACCC TTGGAAGATA	4920
AAAGTGCCTG ATATTCTTTA GTTTTTAAAC ACTGGTAACG TTCATTCATA TACAGTCTCT	4980
TTTGAGGGGC TGATTCAGGT TCATAATCGC AGTCAACATT GATTTCAGG CTGTTTGCTT	5040
TCTATCTCCC CGG	5053

(2) INFORMATION FOR SEQ ID NO: 188:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

AATTCTCTTT TTTCCAACAA AATGTATGAC CTGCACTTGA ATACTTCTCA TTGTTTGTAC	60
ATTCATCTAC TTTCATATAA TCTTTTACAA AATCATAATA TGACATAACA CACTATCCCT	120
TTTAGACAAT ATTCCAATTA GCCTTATTAA TTCAAAACTA TTGTATTAGT AATTATAACA	180
GATGTATAAT AGAAAAGCAA TGATAGATAT TATCAATTAA GCGAATTTAT ATCTAAAAGG	240
GATATTAAAG AAAGGAGATA TGCTTATGAA GATTTACAAA AAAC TATTG CTTATGTCCA	300
AGATAAGAAA TATCTTGGGG TTTTGGCCAT AATTTTTTCT GCTATATCTG CTGCACTTAC	360
AGTATATGGA TATTATTTAA TCTACAAATT TCTAGATAAG TTAATAATTA ATTCAAAC TT	420
ATCCGGTGCA GAGAGTATAG CATTAAAATC TGTTATTACA CTAACAAGTG GAGCGATATT	480
TTATTTTGTC TCAGGAATGT TTTCACATAT CTTGGGATTC AGGCTTGAAA CAAATTTAAG	540
AAAAAGGGaA TCGATGGTCT GGAAAAAGCA AGTTTTAGGT TCTTTGACTT AAATCCATCT	600
GGTCAAATAA GAAAGATTAT AGATGACAAT GCTGCACAAA CTCATCAGGT GGTAGCACAC	660
ATGATTCCCG ATAGTTCTCA GGCAATAATC ACACCCGTAC TTGTACTTGC ACTTGGCTTT	720
ATAGTAAGTA TAAGAGTTGG CATAATTTTG CTTGCTCTTA CTATAATTGG TGGCTTAATT	780
TTAGGGGCAA TGATGGGCGA GCAAGAATTT ATGAAGATAT ACCAAGAATC CCTATCTAAA	840
CTAAGTGCTG AAAC TGTGTA GTACGTGAGA GGAATGCAAG TTGTAAAAAT ATTTAAAGCA	900
AATGTAGAGT CTTTTAAAAG CTTTTATAAG GCGATAAAAG ATTACTCAA GTATGCTTAT	960
GATTATTCCC TATCTTGTA AAGGCCTTAT GTTTTGTATC AATGGTTATT TTTTGGACTG	1020
ATTGCAATTT TAATTATTCC TATAGTTTAT TTTATGACTA GCTTAGCTAG CGCAAAGGTG	1080
ATTTTACTTG AGCTTATCAT GATTTTATTT TTATCAGGAG TTCTCTTTGT TTCATTCATG	1140
AGAATGATGT GtACTCCATG TATATTTCTC AAGGAAATTA TGCAGTAGAT ACTTTAGAGG	1200
CGCTTTACGA AGATATGCAA AAAGACAAAT TAGTGCATGG TAATGTCAAT AATTTTAAAA	1260
ACTATAATAT AGAATTTGAG AATGTTAGCT TTGCTTATAA TGATAAAGCT GTCATTGAAA	1320
ATTTATCCTT TAATTTAGAA GAAGGAAAGT CCTACGCACT TGTCGGTTCA TCTGGATCAG	1380
GCAAATCAAC AGTAGCAAAA CTTATATCAG GTTTTTACAA TGTTAATAAA GGAAGCATAA	1440
AGATAGGCGG GATAGCAATA AGTGAATATT CTGACGAAGC CTTAATTAAA GCCATTTCCCT	1500
TTGTTTTTCA AGATTCAAAA TTATTCAAGA AGAGCATTTA TGATAATGTA GCGTTAGCTA	1560
ATAAAGATGC GACGAAAGAT GACGTTATGA GAGCCTTAAA ATTAGCAGGA TGCGATTTAA	1620

1142

TATTAGACAA	ATTCCCAGAA	AGAGAAAATA	CAATCATAGG	CTCAAAAGGT	GTTTATTTAT	1680
CCGGTGGAGA	AAAACAAAGA	ATTGCAATTG	CTAGAGCAAT	TTTAAAGGAT	TCCAAAATTA	1740
TTATTATGGA	TGAAGCATCA	GCATCTATTG	ACCCAGATAA	CGAGTTTGAA	TTGCAAAAAG	1800
CTTTTAAAAA	TCTTATGAAG	GATAAAACAG	TTATCATGAT	TGCACACAGG	CTATCTACAA	1860
TTAAAGACCT	TGATGAAATT	ATTGTCATGG	ATAGTGGAAG	AATTATAGAA	AGAGGGTCTG	1920
ACAAAGAATT	AATGTCAAAA	GATACAAGGT	ATAAGAGCCT	GCAAGAGATG	TTTAACAGTG	1980
CGAATGAATG	GAGGGTTTCA	AATGAAAGAG	TTTTATAAAA	AAAGATTTGC	TCTTACAGAT	2040
GGAGGAGCAA	GAAATTTAAG	TAAAGCAACA	CTGGCTTCAT	TTTTCGTTTA	TTGTATAAAC	2100
ATGCTTCCTG	CCATATTACT	TATGATTTTT	GCTCAGGAAG	TTTTGGAAAA	TATGGGCAAA	2160
AGCAATGGCT	TTTATATAGT	ATTCTCAGTT	TTGATTTTGA	TAGCAATGTA	TATTTTGCTT	2220
TCTATCGAAT	ACGATAAATT	ATATAACACA	ACCTATCAAG	AAAGTGCAGA	TTTAAGAATA	2280
AGGACAGCGG	AGAATTTATC	AAAATTACCT	CTATCTTACT	TTTCTAAACA	TGACATTTCC	2340
GACATTTTAC	AAACAATCAT	GGCTGATATT	GAAGGCATAG	AGCATGCAAT	GAGCCACTCA	2400
ATACCAAAGG	TGGGCGGCAT	GGTACTGTTT	TTCCCATTA	TATCTGTAAT	GATGCTAGCG	2460
GGCAATGTCA	AGATGGGTTT	AGCTGTAATT	ATTCCATCTA	TTTTAAGCTT	TATATTTATA	2520
CCTTTATCTA	AAAAATATCA	GGTTAATGGA	CAGAATAGAT	ATTATGATGT	CTTAAGAAAA	2580
AACTCAGAAA	GCTTTCAAGA	AAATATCGAA	ATGCAAATGG	AGATTAAAGC	ATATAATTTA	2640
TCGAAGGATA	TTAAAGATGA	CTTATATAAA	AAAATGGAAG	ATAGTGAGAA	AGTACACTTA	2700
AAGGCGGAAG	TAAC TACAAT	TTTAACTTTG	TCTATATCTT	CAATATTTAG	CTTTATATCT	2760
CTTGCTGTTG	TGATATTTGT	CGGCGTAAAT	CTAATTATTA	ATAAAGAGAT	AAATTCTCTC	2820
TACCTTATAG	GATATTTACT	AGCTGCTATG	AAGATAACAG	ACTCTTTAGA	TGCATCTAAA	2880
GAGGGCTTGA	TGGAAATATT	TTATTTATCG	CCCAAATAG	AAAGATTAAA	AGAAATTCAA	2940
AATCAAGATT	TACAAGAAGG	CGATGACTAT	AGCTTAAAAA	AATTTGATAT	TGATCTAAAA	3000
GATGTTGAGT	TTGCCTACAA	TAAAGACGCA	AAAGTTTTAA	ATGGTGTAAG	TTTTAAAGCT	3060
AAGCAGGGAG	AGGTCACTGC	TTTGGTAGGT	GCAAGTGGCT	GCGGTAAAAC	AACTATCTTG	3120
AACTTATAT	CAAGACTTTA	TGATTATGAC	AAGGGACAAA	TCTTAATCGA	TGGCAAAGAT	3180
ATAAAGGAAA	TATCAACAGA	ATCCCTTTTT	GATAAGGTGT	CTATTGTTTT	CCAAGATGTG	3240
GTTCTCTTTA	ATCAAAGCGT	TATGGAAAAT	ATTAGAATCG	GTAAGCAAGA	TGCAAGTGAC	3300
GAAGAGGTTA	AAAGAGCAGC	AAAAC TTGCA	AATTGCACAG	ATTTTATAGA	AAAAATGGAT	3360
AAAGGTTTCG	ATACAGTTAT	TGGTGAAAAC	GGAGCTGAGC	TATCAGGAGG	AGAAAGACAA	3420

1143

AGATTATCAA	TAGCCAGAGC	CTTCTTAAAA	GATGCGCCGA	TATTGATCTT	AGATGAGATA	3480
ACAGCAAGCC	TTGATGTTAA	CAACGAGAAA	AAGATTCAAG	AGTCTTTAAA	TAATTTAGTT	3540
AAAGATAAAA	CTGTTGTAAT	CATTTACAT	AGAATGAAAT	CCATAGAAAA	TGCAGACAAG	3600
ATAGTAGTTC	TTCAAAACGG	AAGAGTAGAA	AGCGAAGGTA	AGCATGAAGA	GCTTTTACAA	3660
AAATCAAAAA	TTTACAAAA	TTTAATAGAA	AAGACAAAA	TGGCAGAAGA	ATTTATTTAT	3720
TAGGAGGACT	ACAATGGATA	ATAAAAAATT	AAAAGTAAAA	GATTTAGTAA	GCATCGGTGT	3780
TTTTGGCGTA	ATTTATTTTG	CCTTCATGTT	TGGAGTTGGT	ATGATGGGCT	TGATTCCAAT	3840
ATTGTTCTTA	ATATACCCGA	CAGTATTAGC	CATAGTTGCA	GGAAGTGTG	TTATGTTATT	3900
TATGGCTAAG	GTTCAAAAGC	CATGGGCACT	ATTTATATTT	GGTATGATAT	CACCACTTGT	3960
GATGTTTGCA	GCTGGTCATA	CCTACGTAGT	TGTGGTTTTA	TCACCTATAG	TAATGATAAT	4020
AGCAGAATTA	ATTAGAAAGA	TTGGTAATTA	TAATTCATTT	AAATACAATA	TGCTTTCTTA	4080
TGCAATCTTC	AGCACATgGA	TATGTAGCTC	TTTAATGCAA	ATGCTTTTAG	CAAAGAAAA	4140
ATATATGGAG	TGGTCTTTGA	TGACTATGGG	AAAAGATTAT	GTTGATGTAT	TAGAAAAGTT	4200
AATAACTTAT	CCTCACATGG	CTTTAGTAGC	CTTAGGTGCT	TTCTTAGGAG	GAATTCTTGG	4260
AGCATATATA	GGCAAGGCTC	TATTGAAAA	ACACTTTTCA	AATGGATTAT	ATTGTGTGGG	4320
ATACTTTACT	CCTTGCCTAA	TTTTATGGTG	CTATCTGAAT	TAAACCCTAT	AGTTAAGATG	4380
TTTTTGAGTA	TACCTATTGT	TATTAGAATG	TTTATTTTAC	CATTTATGGC	AGCAAGCTTT	4440
ATGATAAAGA	CCTCGGATGT	AGGCGCAATA	ATTTTCATCGA	TGGATAAGCT	TAAGATTTCA	4500
AAGAATGTAT	CCATACCTAT	TGCGGTTATG	TTTAGATTCT	TCCCATCTTT	TAAGGAGGAG	4560
AAGAAAAACA	TCAAAATGGC	TATGAGAGTA	AGAGGGATAA	ATTTTAAAAA	CCCAGTCAAA	4620
TATCTTGAAT	ATGTTTCTGT	GCCACTACTC	ATTATATCAT	CTAATATATC	AGATGACATT	4680
GCAAAAGCGG	CAGAAACAAA	GGCAATAGAA	AATCCAATTG	CCAAGACCAG	ATACATTCCG	4740
GTAAAGATAC	AGCTAATTGA	TTTTGTTTAT	GTTTTAGCGG	TTGCTGGACT	TATTGTGGGA	4800
GGCTTAATAT	GGTTGAAATA	AAAAATTTAA	GTCTTGATTA	TGGTGAAGAG	CATATATTAG	4860
ATGATATATC	ACTATCCATA	GCCGAGGGAG	AGTGCCTGCT	ATTTACAGGA	AAAAGTGGAA	4920
ATGGTAAGTC	ATCTTTAATA	AATCAATCA	ATGGACTAGC	TGTAAGGTAT	GATAACGCAA	4980
AGACAAAGGG	CGAAATAATT	ATTGATGGTA	AGAATATAAA	AAATTTGGAA	CTTTATCAAA	5040
TCTCAATGCT	TGTTTCAACT	GTTTTTCAAA	ATCCTAAGAC	ATATTTTTTT	AATGTCAATA	5100
CGACATTAGA	ATTATTATTT	TATTTGGAAA	ATATCGGTCT	TGCAAGAGAA	GAGATGGACA	5160

1144

GGCGTTTGAA GGATATACTT GAGATATTCC CGATAAAAAA TCTTTTGAAC AGAAATATAT	5220
TTAATCTATC CGGCGGTGAA AAACAAATTC TTTGCATTGC AGCTTCTTAT ATAGCAGGTA	5280
CAAAGATTAT AGTTATGGAT GAGCCTTCAT CGAATTTAGA TATTAAAAGC ATAAGTGTTT	5340
TGGCAAAGAT GCTAAAGATA TTAAAAGAGA AAGGCATAAG CATAATTGTT GCAGAGCATA	5400
GAATTTATTA TTTGATGGAC ATAGTTGACC GTGTATTTTT AATAGATAAA GGAAAGCTTA	5460
AAAAAACTTA TACTAGAAGT GAATTTTTTAA AGCTAGATAA AAATGAATTA AATGCTTTAA	5520
GTTTAAGAGA TAAAGAATTA AGTAAATTAA AAGTTCCTTA TTTAAAAGAA GGTGGAGAGT	5580
ATCAGATAAA AAATCTTAGT TACAAATTTA CTGATGATGA GTGTTTAAGC TTAAAAGATA	5640
TTTCGTTCAA GCTTGGGAAA ATTTATGGCA TAATAGGATC CAACGGACGA GGAAAATCAA	5700
CGCTTTTAAG ATGTTTAATA GGTCTTGAGA AAAAATCAAA AGAAGAAATT TATTTTAAGG	5760
GAGAGAAGCT ATCTAAAAAA GAAAGACTCA AAAACTCTTC ACTTGTTATG CAAGATGTAA	5820
ATCATCAATT ATTCACAGAT GAAGTATTCA ACGAGCTTAG ATTAGGAGTA AAGAATTTTG	5880
ATGAAGAAAA GGCGAAAATC ATTTTAAACC CCAATTATTC ACCCCAAATC TAAAAACCAT	5940
CCAGAATCCT TGCCTTAGCT TAGATCCTGG ATGGTTTCTT TTTTCACCCA ATGGGTGTTT	6000
TTTACTAGAC AAAAAGAGT TTCCCCTTTA TGGTATAAGT GTAGAAAAAA ACACAAAAG	6060
AAAGGAAACT CACATGAACA GTTTACCAA TCATCACTTC CAAAACAAGT CTTTTTACCA	6120
ACTATCTTTC GATGGAGGTC ATTTAACCCA GTATGGTGGT CTTATCTTTT TTCAGGAACT	6180
TTTTTCCCAG TTGAAACTAA AAGAGCGGAT TTCTAAGTAT TTAGTAACGA ATGACCAACG	6240
CCGCTACTGT CGTTATTCGG ATTCAGATAT CCTTGTCAG CTTCTCTTTC AACTGTTAAC	6300
AGGTTATGGA ACGGACTATG CTTGTAAAGA ATTGTCAGCT GATGCCTACT TTCCAAAATT	6360
GTTGGAAGGA GGGCAGCTTG TTCACAGCCA ACCTTATCCC GTTTTCTTTC CAGAACTGAC	6420
GAGGAAACAG TCCATAGTTT GCGATGCCTC AACCTTGAAT TGGTCGAATT CTTTTTACAT	6480
G TTCACCAGC TG	6492

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

AACTGAAGGT AAAGGCTTCG ACGCAGAACG TGACGCTGCC CAAGCTGCC TTGATGACCT 60

1145

TAAGAAAGCT	CAAGAAGACA	ACAACTTGGA	CGACATGAAA	ACAAAACCTTG	AAGCATTGAA	120
CGAAAAAGCT	CAAGGACTTG	CTGTTAAACT	CTACGAACAA	GCCGCAGCAG	CGCAACAAGC	180
TCAAGAAGGA	GCAGAAGGCG	CACAAGCAAC	AGGGAACGCA	GGCGATGACG	TCGTAGACGG	240
AGAGTTTACG	GAAAAGTAAG	ATGAGTGTAT	TGGATGAAGA	GSTATCTAAAA	AATACACGAA	300
AAGTTTATAA	TGATTTTTGT	AATCAAGCTG	ATAACTATAG	AACATCAAAA	GATTTTATTG	360
ATAATATTCC	AATAGAATAT	TTAGCTAGAT	ATAGAGAATT	ATATTAGCTG	AACATGATAG	420
TTGTATCAAA	AATGATGAAG	CGGTAAGGAA	TTTTGTTACC	TCAGTATTGT	TGTCTGCATT	480
TGTATCGGCG	ATGGTACCAG	CTATGATATC	ATTAGAAATA	CAAACATATA	AATTTGTAAT	540
ACCGTTCATA	ATTGGTATGA	TTTGGACAGT	AGTTGTATTT	CTTATGATCA	ATTGGAATTA	600
TATAGGCAAA	TACTAAGAAG	AGACAAAAAT	ATATAAATAT	TTCTGTACTT	ATAGGATATT	660
TAAAATCAAA	ATAAAGTTAA	TTTACTTATT	TGCAGAGGTT	GCAACCCAGC	CTCTGTTTTT	720
CGATAAAAAG	GGACGGAATC	TCATTTGTTT	GGGTTTTGTC	TCATCAATAG	AAAGGAACAA	780
AGAGTGTTTC	TAAGTGAACA	CGGGTTTCAG	AATTTCTTAC	TAAATATAAA	AGAAAGGAAT	840
TGAACCCGAC	CTAAATGGTG	GTTTCGATTCA	GAACATCAAT	AGAAAGGAAT	AAGGGTGTTT	900
GTAAGTGAAC	ACGGGCTATG	GACTGTGCCA	AAAAGATAGT	TTTTTCTAGG	ACGTAAGCGT	960
CCGTCGTCAA	AAGTCTTAGA	TGGCTGTGTC	CGTTTGACGC	CCTTTGTATC	TTGAATTATG	1020
AACAATACTG	AATTTTATGA	TCGTCTGGGG	GTATCCAAAA	ACGCTTCGGC	AGACGAAATC	1080
AAAAAGGCTT	ATCGTAAGCT	TTCCAAAAAA	TATCACCAG	ATATCAACAA	GGAGCCTGGT	1140
GCTGAGGACA	AGTACAAGGA	AGTTCAAGAA	GCCTATGAGA	CTTTGAGTGA	CGACCAAAAA	1200
CGTGCTGCCT	ATGACCAGTA	TGGTGCTGCA	GGCGCCAATG	GTGGTTTTGG	TGGAGCTGGT	1260
GGTTTCGGCG	GTTTCAATGG	GGCAGGTGGC	TTCGGTGTTT	TTGAGGATAT	TTTCTCAAGT	1320
TTCTTCGGCG	GAGGCGGTTT	TTCGCGCAAT	CCAAACGCTC	CTCGCCAAGG	AGATGATCTC	1380
CAGTATCGTG	TCAATTTGAC	CTTTGAAGAA	GCTATCTTCG	GAAGTGAAG	GGAAGTTAAG	1440
TATCATCGTG	AAGCTGGCTG	TCGTACATGT	AATGGATCTG	GTGCTAAGCC	AGGGACAAGT	1500
CCAGTCACTT	GTGGACGCTG	TCATGGCGCT	GGTGTCATTA	ACGTCGATAC	GCAGACTCCT	1560
CTTGGTATGA	TGCGTCGCCA	AGTAACCTGT	GATGTCTGTC	ACGGTCGAGG	AAAAGAAATC	1620
AAATATCCAT	GTACAACCTG	TCATGGAACA	GGTCATGAGA	AACAAGCTCA	TAGCGTACAT	1680
GTGAAAATCC	CTGCTGGTGT	GGAAACAGGT	CAACAAATTC	GCCTCGCTGG	TCAAGGTGAA	1740
GCAGGCTTTA	ACGGTGGACC	TTATGGTGAC	TTGTATGTAG	TAGTTTCTGT	GGAAGCTAGC	1800

1146						
GACAAGTTTG	AACGTGAAGG	AACGACTATC	TTCTACAATC	TCAACCTCAA	CTTTGTCCAA	1860
GCGGCTCTTG	GTGATACAGT	AGATATTCCA	ACTGTTACAG	GTGATGTTGA	ATTGGTTATT	1920
CCAGAGGGAA	CTCAGACTGG	TAAGAAGTTC	CGCCTACGTA	GTAAGGGGGC	ACCGAGCCTT	1980
CGTGGCGGTG	CAGTTGGTGA	CCAATACGTT	ACTGTTAATG	TCGTAACACC	GACAGGCTTG	2040
AACGACCGCC	AAAAAGTAGC	CTTGAAAGAA	TTCGCGGCTG	CTGGTGACTT	GAAAGTAAAT	2100
CCAAAGAAAA	AAGGCTTCTT	TGACCATATT	AAAGATGCCT	TTGATGGAGA	ATAATACTCT	2160
TCGAAAATCT	CTTCAAACCA	CGTCAGCGTT	GCCTTGCCGT	ATATATGTGA	CTGACTTCGT	2220
CAGTCGTATC	TACAACCTCA	AAACAGTGTT	TTGAGCAGCC	CGTGGCTAGT	TTCTAGTTT	2280
GCTTTTTACT	TTATAGATTT	TTTAAGACTT	TCCTAAGTAA	TGACGGACGG	TAGTGACCTC	2340
CTTCGAAGTT	CCATACCTAA	ACTTTGAACC	TAAGTTTTAA	AGTTTCCGGA	CAGCTGAAAC	2400
CAAGCTGTTT	CAGGTGTTTT	CATTACGGCA	GAAAGTCTTC	GATTTAGTTG	TGAAATGGTG	2460
AATGATACTC	TTCAAAAATT	TCTTCAAACC	ACGTCAGCGT	CGGCTTGTC	TGGGTATGGT	2520
TACTGACTTC	GTCAGTTCTA	TCCACAACCT	CAAAACAGTG	TTTGAGCTGA	CTTCGTCAGT	2580
TCTATCCACA	ACCTTAAAAC	GGTGTTTTGA	GCAGTCTGTG	CCTAGCTTTC	TAGTTTGCTT	2640
TTTGATTTTT	ATTGAGTATG	AATTACCTAA	ATTATGATGC	ATAGTTGATG	GGATATATAT	2700
AATAGATTGA	AATAGAATAT	GAACAAATTG	ATAAGAGGAT	TTTAAAGTAA	TCTCTAACAA	2760
TGCTTTAGAA	ACTATGGTGT	GCTATTCTAA	ATTCAATTCA	CTATAACTTG	TTTACGTTTT	2820
AAAAAAGAGC	CGTCGGGCTC	TTTTTACTTA	TCTTCAGTTC	CCTGCATTTT	TTTTATCACA	2880
GCTAGTCTAG	TCTGGATATC	CTTTTCCAAG	ACCTTAAACT	TGTAAGTCAA	GTCTTCTTGG	2940
TATTCCTTGA	TAAGTTCTTT	TTGCTGGTTA	ATGATTTGCA	GGCTGTTTTG	GATAATATCC	3000
ACATCGTCCT	TGATAGCTTG	AACGCGGTCA	GTGGTATTCA	AGACTTCATC	TGTGATGGTT	3060
TGGCGATTTT	TTGTAACCAG	ATAACTTCCG	GCTGCAGCTC	CTGCAAATAG	CAGTAGGTTG	3120
GATAATTTCA	TAGCAACTCC	TTAAGCGTTT	TTGATGGTTT	CAGCGACTTG	AGCAAGTTTG	3180
TCAAAGTCTG	GTTTCGTGGC	GATAAAATCA	ATCTTGAGGT	CATCGTCAGC	ACTGTAGCGA	3240
GGCACAAGGT	GAACGTGAGT	ATGAAAAACT	GTTTGACCAG	CGACTTCTTC	ACAGTTGGAA	3300
ATGATATTCA	TACCAGCAGC	CTTAGTGACT	TTCATGACTT	TTTGAGCTAC	TTTTGGTACT	3360
TGGGCAAAGA	GTTGGcTGGC	GCTCGTAGCA	TCCATCTCCA	AAAGATTGCG	ATAGTGTTCT	3420
TTTGGCACGA	CCAAGGTGTG	TCCTAGTGTT	ACTTGAGAGA	TATCAAGAAA	GGCAAGGACC	3480
TGCTCATCTT	CATATACTTT	TGAAGCAGGA	ATTTCCCCTG	CGATGATTTT	ACAAAAAATG	3540
CAATCTGACA	TAAAATCTAC	CTCTACTGTA	CTGAATTTTG	ATATAATATA	GCTACATTAT	3600

1147

ACCAGATTTG	GAGAAAATAT	GTTAGAAATT	AAAAACCTGA	CAGGTGGCTA	TGTTTCATGTT	3660
CCTGTTTTGA	AAGATGTGTC	CTTTACTGTT	GAAAGTGGGC	AGTTGGTCGG	TTTGATTGGT	3720
CTCAATGGTG	CTGGGAAATC	AACGACGATC	AATGAGATTA	TCGGTCTGTT	GGCACCTTAT	3780
AGTGGCTCCA	TCAATATCAA	TGGCCTGACT	CTGCAAGGAG	ATGCGACTAG	CTACCGCAAG	3840
CAGATTGGCT	ACATTCCTGA	GACGCCTAGT	CTGTATGAGG	AATTGACCCT	CAGAGAGCAT	3900
ATCGAAACGG	TTGCTATGGC	TTACGGTATT	GAGCAAAAAG	TGGCTTTCTGA	ACGAGTAGAG	3960
CCCTTGTTAA	AAATGTTCCG	TTTGGAACAG	AAATTAGACT	GGTCCCTGT	TCATTTTTCA	4020
AAAGGGATGA	AGCAGAAGGT	CATGATTATC	TGTGCTTTTG	TGGTGGATCC	AAGTCTTTTC	4080
ATCGTGGATG	AGCCTTTCCT	TGGTCTTGAT	CCGCTGGCTA	TTTCTGATTT	GATTCAGCTT	4140
TTGGAAGTGG	AGAAGCAAAA	GGGCAAGTCT	ATTCTCATGA	GTACCCACGT	GCTGGATTCTG	4200
GCGGAGAAGA	TGTGTGATGC	CTTTGTTCATT	CTTCACAAGG	GAGAGGTGCG	TTCCAAAGGC	4260
AATCTCCTGC	AACTACGTGA	AGCCTTTGAT	ATGCCTGAGG	CTAGTTTGAA	TGATATTTAC	4320
TTGGCTCTGA	CCAAAGAGGA	GGATCTATGA	AAGACTTGTT	TTTAAAGAGA	AAGCAGGCCT	4380
TTCGTAAGGA	GTGTCTTGGT	TATCTGCGCT	ATGTGCTCAA	TGACCACTTT	GTCTTGTTCC	4440
TGCTTGTCCT	GTTGGGCTTT	CTAGCCTACC	AGTACAGTCA	ACTCTTACAA	CATTTTCCTG	4500
AAAATCATTG	GCCTATCCTT	TTGTTTGTAG	GAATTACGTC	TGTTTTACTT	TTACTTTGGG	4560
GAGGAACTGC	CACCTATATG	GAGGCTCCAG	ACAAGCTCTT	TCTCTTAGTT	GGAGAAGAGG	4620
AAATTAAGCT	CCATCTCAAG	CGTCAAACCTG	GCATTTCCCT	AGTCTTTTGG	CTCTTTGTAC	4680
AGACCCTTTT	CTTGCTGTTA	TTTGCGCCTT	TATTTTGTAGC	AATGGGTTAT	GGCTTGCCAG	4740
TTTTTCTGCT	CTATGTGCTT	TTATTGGGGG	TAGGAAAATA	TTTCCACTTT	TGTCAAAAGG	4800
CCAGCAAATT	TTTCACTGAA	ACTGGACTGG	ACTGGGACTA	TGTTATTTCT	CAAGAAAGCA	4860
AGCGTAAGCA	AGTCTTGCTT	CGTTTCTTTG	CCCTCTTTAC	GCAGGTCAAG	GGAATTTCAA	4920
ACAGCGTTAA	GCGTCGTGCC	TATCTGGACT	TTATTTTAAA	GGCTGTTCAG	AAGGTGCCTG	4980
GGAAGATTTG	GCAAAATCTC	TATCTGCGTT	CTTATCTGCG	AAATGGCGAC	CTCTTTGCTC	5040
TCAGTCTTCG	TCTTCTCTTG	CTTTCCTTGC	TGGCGCAGGT	TTTTATCGAG	CAAGCTTGGA	5100
TTGCGACAGC	AGTGGTAGTT	CTCTTTAACT	ACCTCTTGCT	CTTCCAGTTG	CTGGCCCTCT	5160
ATCATGCCTT	TGACTACCAG	TATTTGACCC	AACTCTTTCC	GCTGGACAAG	GGGCAAAAGG	5220
AAAAAGGCTT	ACAGGAGGTA	GTTTCGAGGAT	TGACCAGTTT	TGTTTTACTT	GTGGAATTAG	5280
TTGTTGGGTT	GATTACCTTC	CAAGAAAAAC	TAGCCCTTCT	AGCCTTACTA	GGAGCTGGTT	5340

1148

TGGTTTTACT	AGTCTTGTAT	TTGCCTTATC	AGGTAAAACG	TCAGATGCAG	GACTAACATT	5400
GCTGATACGA	CACTAAAAAA	GAAGTTGAGT	TCAGTCTGTC	TCAACTTCTT	TTTTGTTACT	5460
ACAGGATAAT	GGTTGGTCCG	TAGAGACTTA	TACTCTTCGA	AAATCTCTTC	AAACCACGTC	5520
AGCGTCGTCT	TACCGTACTC	AAGTACAGCT	TGCGGCTAGC	TTCCTAGTTT	GCTCTTTGAT	5580
TTTCATTGAG	TATTAAC TTG	GTCTTGACTT	GGTCAAAGTG	GAAGCGGTCA	TAGGCCCCGCC	5640
AAGCGGCGCG	AGTTGGAGCA	TCTGGATCAA	GAGCGCTGAG	TCCCATGAGA	AGACTGGAAG	5700
TCTGGTAAAA	TTTTTCTAGT	TCAATCAAGA	ATCGATTATC	CACTGTTTCA	GCCTTGGCTA	5760
GAAAACCAAG	AATAGAGTTT	AATTGCTCCT	GAAAGCGGAC	GTCGTCAGCG	CTTGCCTGTT	5820
TGCATGCTTG	GTAGGCTTTG	TTTAAGTCAG	TAATCAAAGT	ATGAGCTCTT	TTGATGGGGT	5880
CTGTATCTGT	CATGGGAATG	CCTCCTTTAA	TCTGGGTGCC	AGTCTTACTT	CTGGCAACTG	5940
TGTTTTGATA	CTGTTAGTTT	ATCACTTTTA	ATTCTTTT TT	TTTATTCAAA	TCTTTAATTG	6000
TCATTGAAAT	GTCTTGAAAT	GCGCTGAGTG	AATTTTATGA	TAAAATAGTT	GTAAGCTCAT	6060
CATGATGTTG	TAGAAAATAA	TCCTTTTAGG	AGTTTTCAAA	GACTGTTTAG	GATTGGGTGT	6120
GCTTGGGCTA	GACCTTTTCT	GTTATTCTTT	TCTTAGGAGG	AGAATCCAAT	GAAATATATG	6180
ATTATTCAGA	CGCAGAAAAC	AGTCTATAAA	GTAAACATCG	ACGATATCTA	CTATATCCAA	6240
ACACATCCAA	CTAAAGCCCA	TACCGTACAG	ATTGTTACAG	AAGAAGCTAG	TTTTAATATG	6300
CTTCAAAATT	TAAGTAATCT	TGAGAACCAA	TGTGGGGAAA	CCTTGATGAG	ATGTCATCGA	6360
AATTGTTTGG	TTAATCTTGA	TAAATTAAAA	TCGATTGATT	TTCAAGAAAG	AATCCTTTTT	6420
CTCGGAGAAG	AAGGTCAATA	CGCTGTCAAG	TATGCCAGAC	GTCGCTATAG	AGAAATTCGT	6480
CAAAAATGGT	TGAAAGAGGG	AGAGTAAGAA	GATGAGAATA	TTTGTTTTAG	AGGATGATTT	6540
TTCCCAACAG	ACTAGAATTG	AAACGACGAT	TGAGAAACTT	TTGAAAGCAC	ATCATATCAT	6600
TCCTAGCTCT	TTTGAGGTAT	TTGGCAAGCC	GGACCAACTG	CTGGCTGAAG	TGCATGAGAA	6660
GGGGGCCCAT	CAGCTATTCT	TTTTGGATAT	TGAGATTCGA	AATGAAGAGA	TGAAGGGACT	6720
GGAAGTGGCT	AGAAAGATTC	GGGATCGGGA	TCCTTATGCC	CTGATTGTCT	TTGTGACGAC	6780
TCACTCGGAG	TTTATGCCCC	TGTCTTTTCG	CTACCAAGTG	TCTGCTTTGG	ACTACATTGA	6840
TAAGGCCTTG	TCAGCAGAGG	AGTTTGAATC	TCGGATCGAG	ACAGCCCTCC	TCTATGCCAA	6900
TAGTCAAGAT	AGTAAAAGTC	TGGCGGAAGA	TTGCTTTTAC	TTTAAATCAA	AATTTGCCCA	6960
ATTTCAGTAT	CCTTTTAAAG	AGGTTTACTA	TCTCGAAACG	TCGCCCAGAG	CCCATCGTGT	7020
TATTCTCTAT	ACCAAGACAG	ACAGGCTGGA	ATTTACAGCG	AGTTTAGAGG	AGGTTTTCOA	7080
GCAGGAGCCC	CGTCTCTTGC	AGTGCCACCG	CTCTTTTCTC	ATCAATCCTG	CAAATGTGGT	7140

1149

GCATTTGGAT AAGAAAGAAA AACTGCTTTT CTTT

7174

(2) INFORMATION FOR SEQ ID NO: 190:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

CCACCAGGGA AAATCATTGA AGTTGGTAGT CACCAAGAGT TAATGCAGGC GCAAAGTTTC	60
TACCATCATC TATTCAATAA ATAAGGAGAA TGTCATGAAT CCTAATCTTT TTAGAAGCGT	120
CGAGTTTAT CAGAGACGTT ACCATAACTA TGCGACAGTG TTAATTATAC CTCTTTCATT	180
ACTATTTACT TTCATCTTGA TTTTCTCCCT TGTTGCCACA AAAGAAATTA CTGTTACTTC	240
CCAAGGAGAA ATCGCCCCTA CAGTGTCATT GCCTCCATTC AGTCAACCAG TGATAATCCT	300
ATCCTAGCTA ATCATTTAGT GGCAAATCAA GTAGTTGAAA AAGGGGACTT ACTCATCAAA	360
TACTCTGAAA CAATGGAAGA AAGTCAGAAA ACTGCCTTAG CAACTCAATT ACAAAGACTT	420
GAGAAGCAAA AAGAAGGACT TGGAATTTTG AAACAAAGCT TAGAAAAAGC GACTGATCTT	480
TTTTCTGGCG AGGATGAATT TGGCTACCAT AATACCTTTA TGAATTTTAC TAAACAATCC	540
CATGATATTG AACTGGGTAT CACAAAGACT AACACCGAAG TTTCAAATCA AGCTAATCTT	600
TCCAATAGCA GTTCATCAGC TATTGAACAA GAAATTACAA AAGTTCAACA ACAAATTGGA	660
GAATATCAAG AGTTGAGAGA TGCTATCATA AATAACAGAG CACGCTTACC AACTGGCAAT	720
CCGCACCAGT CAATTTTGAA TCGTTATCTT GTAGCCTCAC AAGGACAAAC ACAAGGAACT	780
GCAGAGGAGC CATTTTATC TCAAATTAAT CAAAGTATTG CAGGTCTTGA ATCATCTATC	840
GCAAGCCTCA AAATTCAGCA AGCTGGTATC GGAAGTGTAG CAACTTATGA TAACAGTTTA	900
GCAACCAAAA TTGAAGTACT CCGCACTCAG TTTTACAGA CAGCCTCACA GCAACAATA	960
ACTGTGGAGA ATCAATTAAC AGAATTAATA GTACAACAGT ATCAAGCCAC ACAGCGTTTG	1020
GAAAACAATA CCTTAACCTC CCAAGTAAA GGTATCGTTC ATCTGAACAG CGAATTTGAA	1080
GGTAAAAATA GAATTCCAAC TGGTACAGAA ATTGCTCAAA TATTCCCTGT CATCACAGAT	1140
ACAAGAGAAG TACTAATCAC TTACTACGTA TCTTCTGACT ATCTACCTCT ACTAGATAAA	1200
GGACAACTG TAAGATTAAA ACTGGAGAAG ATTGGAAATC ACGGCACCAC CATCATCGGC	1260
CAACTTCAGA CAATTGATCA AACTCCTACC AGAACAGAGC AAGGAAATCT CTTTAAATTA	1320

1150

ACCGCTCTTG	CAAAACTATC	TAACGAGGAT	AGTAAACTCA	TCCAATATGG	CTTACAAGGT	1380
CGCGTCACTA	GTGTAACACTAC	AAAGAAAACA	TATTTTGATT	ATTTCAAAGA	TAAAATTTTA	1440
ACACATTCTG	ATTAATTTTC	AGATAACACT	CTATAACTAT	TTATTATCTT	ATCAAAAAGG	1500
AGAATCATAA	CATGGATAAG	AAACAAAACC	TAAC TTCATT	TCAAGAACTA	ACAACTACCG	1560
AACTCAATCA	AATTACAGGT	GGAGGATTGT	GGGAAGATTT	ATTATATAAC	ATTAATAGAT	1620
ATGCTCATTA	CATCACATAA	GAAC TTCATC	ATCCAATACA	ACTATAAAAA	AATAAGACCG	1680
AGAAACAAGT	ACTCTCGGTC	TTATTTTTC	TCATTCTGTA	TGTATCACAG	TAAGTACCTG	1740
ACGAAAGACT	TGATTTTGAC	AGGTGGTATT	TAGACTGGTA	TTAGGATGGC	TTTCCACAAT	1800
CTTCATGACG	GTATAGAGAC	CAACTCCTCT	CTCCTCCCCCT	TTAGAACTGG	CTCCAAAGGA	1860
GAAGATTTCA	GAAATATCGA	TGCCCTCTTC	TTTGATGGAG	TTTTTCGATGA	TAAAGGTCTC	1920
CTGTGCTCCA	TTTTTTAAAA	AGGCGATTGA	AACATGAGGT	TGACTAGCTT	CCACACTGGC	1980
TTCAATAGCA	TTGTCACAAA	GGATAGACAC	AATGGTTAGA	AAATCAAGTA	GACTCATCCC	2040
CTCGACCTGA	ATCTCCTCAG	GAAC TTCGAC	ATTAAAGACA	ATGTTCTTAT	CTCTGGCTTT	2100
TAAAATTTTC	CCTGCTAGAA	GAC TTTTGAG	GGCTTTATCA	CGAATATTTA	CCAATCTGCC	2160
CAGGTCATAT	TTATTGTTCT	GCAATTTCTG	ACTGGAATCC	TTTAAGACGG	AGCCATAGAC	2220
CTCTTTTATC	TGCTCCATAT	CCTCCTCTTC	AATGCCCAGA	CGTAAGCTAG	TCAAGAGGTT	2280
GGTATAATCA	TGACGAAAGC	TCCGTACTTC	CTTGTAAGC	TCCTCTATAT	GCCGACTATA	2340
GCGTTCCATA	TCTCTATAGC	GCAGGGCCTG	CTCTTGTTCC	AATCTCTCAT	AGAGTTTTTC	2400
CTTCAAATAG	GTATCCAATT	TCTTGATAAC	CCCCATAAAA	AAGAGTAGGT	AAAAGACTAG	2460
GATGAGATGG	CGAACAGTCT	TTGATTGAAT	ACTTTGTTCA	TATTCAAAAA	AAGACAGACT	2520
TTCCATGACT	AGATAGTAGC	CACCCATTAT	CCAGTTAATC	TGAGTCAGGG	ACTTTTGAAA	2580
GGCTTTATCG	AGAATCTCCT	TTCTCAAGCT	AGTAAAATCG	TAGTCCAACC	ATTTCAAAAA	2640
AGCTAGAGAA	ATGAAGAAAT	TGAAAATTAT	TATACATAAC	CCAGTAAATG	AGTAGCCATC	2700
ATATACTTGC	CCTTGTCCTA	AAAATGGAAG	CACAAAATAG	GAGACTCCTC	TATAAAAGAG	2760
ATTCACCAAT	ATCATTGGAA	AGAGACCATA	AAAGAAAAGG	AGTTTTTTTAG	GAAGCCCTCT	2820
CAATAATAAG	AAAGATAAGC	CTATGCCGTA	CAAGGGTTCC	ATAAAATAAG	ATAGGTAAAC	2880
ATTTCCCTACT	ATATAGCTAA	TCATCACAAA	AACAAAGGCC	AACAGTATCT	TCAAAAGAAA	2940
GGCCTTAAAA	ATCCTCTCGA	AAGTAAGATC	AATTCCATCC	ACCTTAAAGA	AGATGACAAT	3000
TTCTAGTCCA	TTAGTAACAA	GTGTATACAA	CAATATCCAA	GCAATGTTCA	TAAATTCTCC	3060
TAGCTCAGTG	TAATTTATTG	ATGGCCTCAG	ACACTTCCCT	GACCTTATAA	CGGGCGATTA	3120

1151

GACAACTTCC ACCATTGGGA GAGAAGAGCA GTTTTTCTTT CTTATCCAAA TGCACCACAT 3180
TTGCAGGATT GATGAGAAAA GAGCGGT 3207

(2) INFORMATION FOR SEQ ID NO: 191:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

CTGAATCAAG TGTACTGCAC CAGTTCGTGC ATCAGGCATA ACAACATCTA CAGATATAAT 60
ATTGTTTTCT GAGTCCGCCT CATAAGTTAA AATCATAAAT TTTTCGATAT TCGAATTTTTT 120
AGTAGCTTGT TCAATTTCTT GAATCATTTT ATCAGAAACT AACTCCATCT GAATTGGAAA 180
GGAATGACTA TTTTCATCAT TTTTGTAGGA AGAATGTTGA TTAAGATAAA GTGTATTCAT 240
CTGAGCATAT TCAAATAAGT AGCCACTCTT ATTTTTTTGT ACCAAAGGAA ATTGGTTTGT 300
AAGTCGCTTC TTACCCTTTA TAATTAACAA TACTTTCCCA TATTTTCTG TATTTGTTTC 360
AAATTCTAAA TATCCCAAG TCTGTCCTGC TAATTGTAAT TTATACTCAA ACAAATCTGC 420
TGATGCAAAT GCAGTATCAA TATGATTAGG TCGCGTCCAT GCATAACCAT TCGACACTAT 480
CATGTCTCT CTTTTTCTA GACGTTTCATC TACATAATCT TTTTGCCCTT TCATCAAAGT 540
ATCTACAATT TTTTGTGCCT CAAGCGAATC AAAGAGATCC TGATTCAACA TAATTCTTCC 600
TCCTCCAAAT ACTTTTTAAT GAATTATACC ATTTTCTTAA AGAAATTACT ACAATAATTA 660
TCTTTTTCTT AAAGTTCTGT GTCAGAGTAA TTTAGAAAAT TATATCTTCT ATAGTAAAAT 720
CAATTAAAAA CTGAACAAAT TTATTGGGAA ATTCAAATCG CTTTCTGAAA ATATTTTAGG 780
AACCGTAGTG TAATATTCCA GATTCAATTC ACTATAAAAC TGACCTTTCT CCTGCAAAAG 840
AAAAAGGAAA GACTTCCTTT CGTGCCTTTC CTCTTACTTG CTACTTGTTT GATTATTTTT 900
GGTAAGCTAC TGCTTGTCTG ATAAAATCCT GAATCGGCTC TCCTTGGTGG AGAGCTTTTA 960
CTATTTTCGA ACCGACGATA ACACCATCTG ACACCGCATT GAAGCGTTCC AGATCGGCTT 1020
GACTAGATAC ACCAAAACCT GTCAAGACTG GGATGTCGGC CACTTGATGA AGTTGCGCCA 1080
AGTGCTTGTC CAAATCTGCA CGGTAATTGC CTGATTTCCC TGTCACCTCA TTGATGGCAA 1140
CGGCATAGAT GAATCCCTCC GCCCCTTCAA TCAACTCTTT CTGGCGCTCA ATTCCTGTGG 1200
TCAAGCTTAC TAAAGGAATC AAGGCGATAT CTGTATTTGC CAAAATGGT TCTACAAAGT 1260

1152

TGGCATGTTC	ATGAGGCAGG	TCTGGGATAA	TCAAGCCCTT	CACAGCTGTA	TCAGCCAGAT	1320
CTTTGACAAA	GTTCTCCACA	CCGTACTGAA	AGAGGGGGTT	GAAGTAGGTC	ATGATGACCA	1380
GTGGAATCTC	TGTTTCAATG	GTTTTCAAGG	TTTCAACTAA	AGCCTGGGTA	GAGGTCCCGT	1440
GGGCTAAACT	GCGCAAGCCA	GCTTCTTCGA	TAACAGGTCC	ATCTGCAACA	GGGTCTGAAA	1500
AGGGAATACC	CACTTCAATT	GCAGAGACAC	CCAAATCTTC	TAAAAAGTGA	ATTGTTTCAG	1560
CAAGACCGTC	CAAACCTTTC	TCGTGGTCAC	CAGCCATGAT	ATAGGGAACA	AAAATTCCCTT	1620
TTCCAGCTGC	TTTAATAGCA	TTTAATTTTT	CTGTTAGTGT	CTTAGGCATG	AGCTTCTCCC	1680
TTCTTTGCTG	CATCTGCTTC	CAAGCGGTCC	TTGACTTGAA	CCACATCCTT	GTCCCCACGA	1740
CCTGATAGGC	AGACAATCAT	AGACTTTTCT	GGTCCAAGTT	CTTTGGCCAA	TTTCACCGCA	1800
AAGGCGATAG	CATGGCTAGA	TTCCAAGGCT	GGGATAATCC	CTTCCACACG	AGACAAGAGT	1860
TGGAATCCTT	CCAAGGCTTC	TTCGTCTGTC	ACAGGGACAT	AGCTGGCACG	TTTAATATCG	1920
TGGTAGTGAG	AATGCTCTGG	ACCGATACCA	GGATAGTCCA	AACCTGCTGA	GATAGAGAAG	1980
GCTTCAAGAA	TTTGACCATG	GGCATCTTGG	AGCACATCCA	TGAGGGAACC	GTGAAGGACA	2040
CCTGGACGAC	CCTTGGTCAA	GGTAGCTGCG	TGGTGCTCTG	TATCCACACC	AAGCCCTGCT	2100
GCTTCAGTTC	CATACATAGC	TACTGACTCA	TCTTCTACAA	AGGGATGGAA	GAGCCCGATA	2160
GCATTCGACC	CACCACCAAC	ACAGGCTACT	AGGGCATCTG	GCAGATCTCG	ACCTGTCAAG	2220
TCACGGTACT	GTTGTTTAGC	CTCTCGACCG	ATGACACTTT	GGAAGTCACG	AACGATTTCT	2280
GGAAATGGAT	GAGGCCCCAA	GGCAGAACCA	AGGATATAGT	GGGTATCGTC	GATATTAGCC	2340
ACCCATGAAC	GAAGGGCTGC	ATTGACCGCA	TCCTTGAGCA	CGCGCGAACC	ATCTGTTACA	2400
GCCTCGACCT	TGGCTCCCAA	AAGCTCCATG	CGGAAGACAT	TGAGGGCTTG	GCGTTTGACA	2460
TCTTCCTCAC	CCATGTAGAT	GGTACATTCC	ATGTTAAAGA	GGGCTGCAGC	AGTTGCAGTT	2520
GCCACACCGT	GCTGACCAGC	ACCCGTTTCT	GCGATAATTT	TCTTTTTTACC	CATGCGTTTG	2580
GCAAGCCAAA	CTTGTCCTAA	GGCATTGTTA	ATCTTGTTGG	CTCCTGTATG	GTTAAGGTCT	2640
TCCCGTTTGA	GATAAATCTT	GGCTCCGCCA	ATATGCTGGG	TCAAGTTTTT	TGCGTAATAA	2700
AGAGGAGTTT	CACGTCCTAC	GTAAGGCGC	AAAAGCTGGT	TTAATTCCTC	TTGGAAACTT	2760
GGGTCTGCCT	GACTTTCACG	GTAGGCCTTC	TCCAACCTCA	AAACTGCTGT	CATCAATGTT	2820
TCTGGGACAA	AACGTCCGCC	GAATTTTCCG	TAAAATCCAT	CTTTATTTGG	TTCCTGATAT	2880
GCCATGCTTT	ACCCTCTCTA	TAAATCTTCT	AATCTTTTCA	TGATCTTTTT	GTCCATCTGT	2940
CTCCACTCCG	CTCGATACAT	CTACTGCATA	GGGAGTAAAG	TGTTGAATTG	CTTTTACTAC	3000
ATTATCTTCA	TTAAGGCCAC	CTGCGATAAA	GAAGGGCTGT	GCTAGTCCAG	TCGTATCCAG	3060

1153

TTGACCCCAA	TCAAAGGGCT	GGCCACTTCC	TGCCACAGGG	GCATCAAAGA	G TAGATAATC	3120
TGCCTGAGAA	TTGGGGACAT	GCCCATTTC	ATCTACCTGC	ACAGCCTGAA	TACTGGCACA	3180
AGGCAAATTC	TCAAATAAAT	CATCTGCCAC	CTGACCGTGA	ACTTGAACCA	AGTCCAAGCC	3240
AACTTTGTCA	ATCGCTTCCA	GCAGTTCTAC	CCGACTTGGT	GAAACAAATA	CTCCAACCTT	3300
TTTCACATCT	GCAGGAATAA	GCTTTGCCAA	CTCAGCTGCC	TCTTCTAAAG	TCACCTGTCT	3360
TTTACTAGGT	GCAAAGACAA	AACCGATATA	GTCGGCTCCT	GCTGAAACGG	CTGTTTCCAC	3420
CGCTTCTTTG	GTCGATAGTC	CACAAATTTT	AACCTTTGTC	AATCTGCAAC	TCCTTGATTC	3480
TCTGGGCCAC	ATTTTCTGCC	TGCATAAGAG	CTGTCCCTAC	CAAAATTCCG	TTAAAGTATG	3540
GGGCTAGTCG	TTCCGCATCC	TGCCCTGTGA	AAATGGCAGA	TTCAGAAATG	TAATAGCGAC	3600
CTTCCTCAAA	GTAAGGGGCT	AAATCTACAC	TGGTCTGCAA	GTCGACCTCA	AAGGTAGTCA	3660
AGTTGCGGTT	GTTGACCCCG	ATAATCTCAG	CACCAAGTCT	GTGGGCTACC	TCTAGTTCAG	3720
CTAGATTGTG	AGTCTCCACT	AAGACTTCCA	GACCAAGCTC	TGTCGCGTAG	TCATACAGTT	3780
CCTTGAGGCG	TTCTTCGGAC	AAGGCTGCCA	CAATGAGCAA	GATAACTGTC	GCACCTGCAT	3840
TGCGAGCGCG	GATGATTTGC	TTTTCATCGA	TGATAAAGTC	TTTGTGAGC	GTCGGAATCT	3900
CTACCTGACT	GGAAATTTCC	CGTAGATAAT	CCAAATGCCC	TTTAAAGAAA	ACCTCATCTG	3960
TCAACACCGA	AATCATCACT	GCTCCGTTTT	CTTCATAAGT	CTGGGCCTGT	TGCACAATAT	4020
CCACATCGAG	ATTGATATCT	CCCAAAGTAG	GGCTAGCTTT	CTTGACCTCA	GCGATTACCT	4080
GCAAGCGGTC	CTGATGATTC	TTCAAAAATT	CTGCCAAGCG	ATAGGTCTGG	CGCAGAGGCT	4140
GGATTTGCTC	CAGCTTCATC	TGCTCCACCT	CACGCGCCTT	CTGCTCTAAG	ATTCGTGCTA	4200
AAAATTCCTG	ACTCATTTTT	GGTACTCCTG	TAACAGTCTG	AGTTTTTTCAA	GGGCCTTGCC	4260
TCTAGCAATC	ACTTGACGGG	CCAAGGCAAC	CCCTTCCTTG	ATGCTATCAA	TCTTACCATT	4320
AGCATAGAAA	CCAAGACCAG	CATTCAAGAC	TGTCGTTTCC	AAGAATGGAC	TTGCTTCGTT	4380
TTTCAGAACG	CTAAGCAAAA	TTTCTGCATT	TTCTTGAGCA	TTCCCACCAC	GAATATCTTC	4440
CATAGCATAG	CCTTCCATTC	CCAAATCCTC	TGGAGTAAAG	CTTGACAAGC	TGATTTCGCC	4500
ATTTTCAAGA	AGTGCAATCT	TGGTTGTTCC	GTTCAAGCCA	GCTTCATCCA	ACCCTTCTGG	4560
TCCAGCAACC	ACGATGGCAC	GTTTGCGACC	CATATTTTTT	AAAACCTGAG	CTGTACTTTC	4620
TAGGAGTTCT	GGACGACTAA	TTCCAAGAAG	CTGTGTTTCT	AAAGCCATTG	GATGAATCAG	4680
TGGACCAGTC	AAGTTCATAA	TCGTTGGAAT	TCCAATTTCC	AAACGAGCTG	GCATGATGTA	4740
TTTCATAGCT	GGGTGCATAT	TTT TAGCGAA	GAGAAAGACG	ATTCCAGTTT	TATCAAAGAC	4800

1154

CTTACCTAGT	TCAGCTGGTT	TGAGGTCAAG	ATTGATTCCC	AAGGCTTCGA	GGACATCTGC	4860
GGAACCAGAT	TTAGAAGATA	TCGAGCGGTT	ACCGTGTTTG	GCCATGTGAA	TACCGCCACC	4920
AGCCAAGACA	AAGGCTGCAG	TTGTGGAAAT	ATTAAAACTG	AAAGACTTGT	CCCCACCTGT	4980
ACCACAGTTG	TCCATGGCAT	CATGAATCTC	AGTTGGAATA	TGCTGGGCAT	GTCCTCTCAT	5040
GACTTGGGCA	ATGGCTGTGC	GTTCTTCAGG	TGTTTCCCCC	TTCATCTTAA	GAGCTAAGAG	5100
GAGAGAAGCA	ATCTGCGCTT	CAGTTACACG	CCCAGTTACG	ATACGCTCAA	TGACATCCGT	5160
CATTTCCACA	CCTGATAAAT	TTTCAAATTT	TGCTAGTTTT	TCAATAATCT	CTTTCATCCT	5220
AGTTTCCTCA	CTTTACAACC	TCCTCGATAA	AATTCCGAAT	AGAAGACAAG	CCGTCTGGCG	5280
TTCCAATGCT	CTCTGGATGG	TACTGGAAGC	CATAAATCGG	TAGGTTTTTA	TGTTGAATCC	5340
CCATGATGGC	TTGGTCATCA	GTCGAACGAG	CTGTCACTTC	AAAGTCTTCT	GGCATTTCCT	5400
CAATCAAAAT	ACTGTGATAA	CGCATGACCG	CACGGCCATC	CTCAATACCT	TGATACAAAA	5460
CAGATGGCGC	TTCAAAGTTG	ATATTGCTCT	GTTTCCCATG	CATGACTTTT	GGAGCCAAAC	5520
CTAGCTTACC	ACCAAAGACT	TCTGCAATGG	CTTGGTGGCC	CAAACAAATC	CCAAGAATCG	5580
GCTTCTTGCC	TGCAAAATCA	CGAATCATGT	CTTCCATCTT	TCCAGCATCA	ACTGGCCAAC	5640
CAGGACCAGG	AGAAAAGACC	AGACCATCTG	CTTTTTCAGC	TTCTTCATAC	AGCTTGGAAT	5700
CATCATTTCT	CAGAACCTGA	ACTTCTGCAA	AATTCCCAAT	GTATTGGGCC	AAGTTATAGG	5760
TAAAAGAATC	ATAGTTGTCA	ATCAATAAAA	TCATGGTCTT	AGTTCTCCAA	TTCTAGTCAT	5820
AGATTTTGCT	TTGTTAATGG	TTTCTTG GTA	TTCGTTTTGG	GCGATAGAGT	CGTAGACAAT	5880
CCCTGCCCCA	GCCTGCACAT	AGGCTCTTTG	ATTTTTGAGA	ATCATGGTTC	GGATGGCGAT	5940
GGCCAAATCC	ATATCACCCG	TCGCAGACAA	GTAGCCGATT	GCCCCAGCGT	ATACTCCCCG	6000
TTTTTCCGTT	TCCAGTTCAT	AGATACGTCT	CATCGCTCGA	ATCTTTGGTG	CTCCAGAAAC	6060
GGTTCCAGCA	GGAAGCGTTG	CTTTCAAGGC	ATCCATGGCA	GTGAGTTCTG	GAAGCAAACG	6120
CCCCTTGACT	ACGCTGGTCA	AATGCATGAC	GTAGCGGAAG	AGCTCCACTT	CCATATACTT	6180
AGTGACTTGG	ACACTGGTCG	TTTCAGAGAT	GCGGCCAATA	TCGTTACGCC	CCAAGTCTAC	6240
CAACATTCGA	TGTTCTGCTG	TTTCCTTCTC	ATCAGAGAGG	AGGTCAGTCG	CCAAGGCCCTT	6300
GTCTTCTTCA	TCCGTAGCCC	CTCTTGGTCG	CGTCCCTGCA	ATCGGATTGG	TTGTCACGAT	6360
GCCATTTTTG	ACAGAAACCA	AACTTTCTGG	ACTAGCTCCG	ATGATTTGAT	AATCCCCAAA	6420
ATCATAGAAA	TAAAGGTAAT	TAGAAGGATT	AGTCACGCGG	AGATTTCTGT	AGAAGTCAAA	6480
TGGATTTCCA	GTAACCTCTG	CTGAAAAACG	CTGGCTGAGT	ACACATTGGA	ACATATCTCC	6540
GTTACGAATC	AAGTCACGAG	CTGTTTCTAC	CATTCCCTCA	AACTTATGTG	GAGCGATATG	6600

1155

CGGTTTGAAG	TCTAACGGAG	ATAGATCCAA	ATCTTCAAAT	TCATTTGGAG	CAGGAATGCG	6660
TAATTCCTCA	AGCACTTGGT	TCAAGGATTT	TTCCAAGGCC	TCTTGACTGC	GCTCACTATA	6720
AAGTGCATCC	TCTATGACAT	GTATCTTCTC	CTTCTTGTGG	TCAAAGACCA	TATAGCTCTC	6780
ATAGACAAAG	AAATGCATGT	CTGGCGTCCC	AATTGTATCC	TCAGGGATTT	GACCAATTTT	6840
TTCATAAAGC	GAAATCATAT	CGTAACCCAC	AAAACCAATG	GCTCCACCAC	CAAAAGGTAG	6900
CTCTGAGTGG	TGCTGACTCT	TATGAATCAC	TTCATAAAGG	AAATCCAAGG	GATCCCGATC	6960
AATCACTTGA	CCATTTTGAT	AGAGAACCCC	ATTTTCAAAC	TTAATCTCAA	AAACTGGATT	7020
ATAGGCTAGG	ATAGAAAAAC	GAGCTGTTTC	CTTGTCTCTC	GGAATACTCT	CTAAAATAAC	7080
CTTATGTTGC	CCCTTTAAGC	GCATATAAGC	CAAGATTGGT	GATAAGACAT	CTCCATGAAT	7140
GATTCGTTCC	ATTGTAATTT	CCCTTTCAGT	TCTACTTCTA	GTCCGTGGTG	ACTGTATGAA	7200
AAATCCCCAC	GCAAAATAAC	TTGCGTGAGG	ACGAAATTCG	CGGTGCCACC	TCAATTATAG	7260
GATTTCTCCT	ATCTCTCATT	CCTGTCTCAG	ATATCTCCTG	TAACAGGCTG	TGCGATAAAG	7320
GGCACTCCCT	TGAGAATGAT	GTTTTCTTCT	CTCGTTTCAG	ATGAACCCAA	CTTTACAGCT	7380
TTCTCTGCTT	GTTTTTCAGCA	ACCACAAGCT	CTCTGTGAGA	GAAAGAACTG	TAATTTTTCC	7440
ATCTATTATT	TTTTAGCTTC	TAGTAGTCTG	CAATCGCAGC	TAGGTCCTTG	CCTCCACGAC	7500
CAGAGACATT	GATGAAGAGA	TGTTTCATCTC	GGTACACCTT	TATACTCTTC	GAAAATCTCT	7560
TCAAACCGCG	TCAACGTCCG	CTTGCCGTAG	GTATGGTTAC	TGACTTCGTC	AGTTCTATCT	7620
GCAACCTCAA	AACAGTGTTT	TGAGCTGACT	TCGTCAAGTC	TATCCACAAC	CTCAAAACAG	7680
TGTTTTGAGC	TGACTTCGTC	AGTTCTATCC	ACAACCTCAA	AACAGTGTTT	TGAGCTGACT	7740
TCGTCAAGTC	TATCCACAAC	CTCAAAACAG	TGTTTTGAGC	AGCCTGCGGC	TAGTTTCCTA	7800
GTTTGCTCTT	TGATTTTCAT	TGAGTATTAC	TAGCTTTTTT	CGTATTAGTC	CAGCCTTTTT	7860
GTTTGCTTTT	AGTAGTAGGC	ATGGAGCTGT	AGATAGAACT	CAAGTTCATC	AAAGCGACTT	7920
AAGGCCCTAA	TAAAAGATAA	ACCAAACGAC	GGATAGAAAA	AAGCCCACAC	ACAGAATATA	7980
CTTCCGTGTG	AGGGCGTTGG	TAACGCGGTG	CCACCTCAAT	TATAAAGGGA	CTATCCCTTT	8040
ACATCTCTGC	CTTGTTTAAC	AACAAGCTGC	ACTGTAAGGT	GTGCGCACCG	AATTTTCATT	8100
GTTTCAAATT	CATTTTCAAA	ATCAGCCCAC	TTTCACTACT	TCCAACCACC	TATTCACAAT	8160
CACCACAGGC	TCCCTGAAGA	TCAAAAATAG	TTACTTTTCT	GATTTGTTGA	ACTTATTTTA	8220
ATACTTTGTT	TTTTCTTTGT	CAAGACTTTT	TTACGATTTT	TTTGAAAATA	TCATTCGAAT	8280
ATGACCATGT	CTTCCTTAGA	TCGAACATGA	ACATGTCCCA	CTTCTTAGAA	ATTGGATCCA	8340

1156						
ACTCAATAGA	AACTGAATGG	AGGCTAAACA	GAACCTATTT	TAGAACACTC	CATCTTTTCC	8400
ACTAGGATTT	TCAAGAATTA	AACAATACTA	GAAACTCTGT	CTCCTAACAA	ATTTAGGAGA	8460
AACTTCAACA	GATGTGACAC	TTTCCCCCTT	AATAATTGCT	AAAACACCTT	CTATCATTTT	8520
TTTAGCCAAT	TTAACATAAT	TGGGAGCAAT	TGTAGACAAA	GCTGGAGTAT	AATACTGAGA	8580
AATAGGAATA	TTATCAAATC	CAATGATAGA	AATATCATCT	GGAATAAGAA	TTCCTTTCTC	8640
ATAGCACGCA	CGAATCAAGC	CCTGAACCTT	TTCATCTCCT	GAAACAAAAA	TAATGTCCGG	8700
ATAATTTTGG	GTAGTCAAGT	GCTGCATTGC	ATAAGAATAA	ACTGAATCAA	TTGTAGATAA	8760
GCCATAAATG	ACTTTTAAAT	CCATAAAGTA	ATTTTTTATCA	TTCAGAAAAG	AACGCACACC	8820
TCTTTTCACGA	TCCTTATTAA	CATGGGATTC	TCCTCCCATA	AGCAACCACA	TATTTTTTAAA	8880
TTTTTCTTCA	GTTACAGCTT	TCATCATATC	ATAAGTAGCT	TGAAAATTAT	TATTAGATAC	8940
ATAGACTACT	CCAGACGTTT	GAGATTCACC	GAAAACAAGA	AAAGGCATAT	GGTTCTTCTT	9000
TAAATACTGA	ATTCTGATAT	CATCTACACT	TTCATAAAAA	ACAATAACAC	CATCTACTAG	9060
GCTACCTGTG	CTTGATATAA	TTGAATTACT	AATTGTATCC	TCCTCTCCAA	AGTACTCAAC	9120
TATAGCATTA	ACACCAAATF	CTTTACACGT	CCGTAACACT	TTATCTAACA	GCGTATGAAA	9180
CCAAATTAAA	GGAAAAGAGT	CGATTTTTTT	TACAGAAATC	AATATATTTA	TAGCTTCTTT	9240
TTTAGTTAAA	TTTTTTGTCAT	ACGCATTTGG	AATATACGAC	AATTCCTCTA	TAACTTTTTG	9300
AATCGCTTGA	TAAGTTTCTT	CTTTAACATT	TACTCCACCA	TTAATAACTC	GTGAAACTGT	9360
TTTTGGAGAA	AAACCTGATA	AACGTGCAAT	ATCATAAATA	GTTACCTTTT	TCCCATTAT	9420
ATTTTTTCATT	TCAGTCCTCC	ATTACGAACA	TTCTAATATT	ACTATACAAT	ATTTAATTTT	9480
TTTTAACAAG	AGAATTTAGT	AAATTATTTA	AGATCCACAA	ATTCACAAAA	TTAATTTTAC	9540
AAATATTCTT	CCCCTTCAAA	AAAGTTTAAA	TTGCATTTCA	CACCTTTATT	TTTAAGAATG	9600
TTTCCAACCT	CACGACAAAT	AAATTCATAT	GAGAAAAAAC	TGCCATAAAA	TTGTAGATTA	9660
ACTTTTTTCAG	TAAAATGTGT	AGGATTTATA	AAAACATATA	ATAGCCTGTC	AATGTAACAT	9720
TTTAACATAG	AGTTAATTTT	TTCTTTAAAG	ATAACATTTG	TTATCAACTC	ATCAGGAGGT	9780
AAATGAAAGG	CAAACACCAT	TTACAAAATA	TCATAAAAAG	AAATAAATTT	GTATACTTGT	9840
ATCAAACAAT	TATTATCAAA	ATATTCTATT	TTACCTAAAT	CAAAATTGAT	TTTATAATCT	9900
TTCATAAAAA	CCTCTGAGCA	AAAATCTACT	CAAAAATTAG	ATGATTAAAA	CATCTAAAAA	9960
GCAAAAGGAC	AAAAACATCT	GTCCCTTTGT	TTACTAAATT	TCAGCTAATT	TCTTCGACAT	10020
AAATAACACC	TACAATATTA	GCAATTTCTT	CCATCAGTCG	AAGATGTTCA	AATCTACCTG	10080
ATAATTCCAG	AGTAATAAAT	GACGCTATTT	TTTTGTCCGG	AACATCAAAG	TATTCAATTC	10140

1157

TGTCAGAATT AACATCTCCA AACGCTGTTC TTGAATCGGT CATTCTGATA CCATTTTCTG	10200
CACAATAAAC CAATACACGA TTATAGGCTT CTGTAGATTT AACCACTATA TACAATTCAA	10260
TCATTTTAGA ACGATTTTGC AGATATTTTT TTAGTGGTTG GAACATGGAT ATCACACCCC	10320
AAACAGAAAT GGCTACTAAA AGAGCTCCCT CATAAGG	10357

(2) INFORMATION FOR SEQ ID NO: 192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6867 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

CGGGACATTC TCAATCTTCT GTCTTTTGTT TTTCTCTTCT TTCTATGATA CAATGGAAAA	60
AATAAATTCA AAAGGAGTTT TTTTATGACT TATCCAAATC TCTTGGACCG CTTCTTAACC	120
TATGTTAAGG TCAACACGCG CTCTGATGAA CACTCTACTA CTACTCCAAG TACACAGAGT	180
CAGGTTGACT TCGCAACAAA TGTCTAATT CCTGAAATGA AACGTGTTGG ACTGCAAAAT	240
GTTTACTATC TACCGAATGG TTTTGCTATT GGAACCTTGC CAGCCAACGA TCCGTCTTTA	300
ACACGTAAGA TTGGTTTTAT ATCGCACATG GATACTGCTG ATTTTAATGC TGAAGGAGTC	360
AATCCACAGG TAATTGAAAA CTACGATGGT GGTGTGATTG AACTAGGGAA TTCTGGTTTC	420
AAACTCGATC CAGCTGACTT CAAGAGTCTT GAAAAATATC CAGGACAAAC GCTCATCACA	480
ACAGATGGAA CAACCTTGCT AGGTGCTGAT GACAAGTCAG GAATTGCTGA AATTATGACA	540
GCCATTGAAT ATCTAACTGC TCATCCTGAA ATTAAGCACT GTGAGATTCG TGTGTTT	600
GGTCCAGATG AAGAAATCGG TGTGTTGCC AATAAATTG ATGCAGAAGA TTTTGATGTG	660
GATTTTGCCT ACACTGTTGA TGGTGGTCCA CTAGGTGAAC TTCAGTACGA GACTTTCTCA	720
GCCGCTGGTG CTGAATTGCA TTTCCAAGGT CGTAATGTCC ACCCTGGTAC TGCCAAAGGG	780
CAGATGGTCA ATGCCCTTCA GCTAGCAATT GATTTTCATA ATCAACTTCC AGAAAATGAC	840
CGACCTGAGT TAACTGAAGG TTACCAAGGT TTTTACCATC TAATGGATGT GACAGGTAGT	900
GTTGAGGAGG CGCGTGCAAG CTACATCATT CGTGATTTTG AAAAAGATGC CTTTGAAGCG	960
CGTAAAGCAT CCATGCAATC TATCGCTGAT AAGATGAATG AAGAACTTGG GAGCGACCGT	1020
GTCACCTCTCA ACTTGACAGA CCAGTACTAC AATATGAAAG AAGTCATTGA AAAAGATATG	1080
ACTCCAATTA CCATTGCTAA AGCCGTTATG GAAGATCTAG GTATCACGCC TATTATCGAA	1140

1158						
CCAATCCGGG	GTGGAACAGA	CGGCTCTAAG	ATTCCTTTA	TGGGAATCCC	AACTCCGAAT	1200
ATCTTTGCAG	GTGGCGAAAA	TATGCACGGA	CGTTTTGAAT	ACGTTAGCCT	TCAGACTATG	1260
GAACGTGCAG	TTGATACCAT	CATTGGCATC	GTAGCTTATA	AAGGCTAAAA	AGACGAGGTA	1320
GCTCAGCTAC	TTCGCCTTTC	TTTTTATTCT	ACTGGTTTTT	CTTGATTTC	AGTAGTTGTA	1380
GAAGATTCTG	TTGTTTCATT	TTCTGAAGTT	GATTCAGCAG	GTTTAGAATC	TCTTGTATTG	1440
CTTGGTTTGT	TTTCGTCGCT	AGCAGTTTCA	ATGTTAGATT	CTGCAGTTGC	GTTTGGTTGG	1500
TTCTCAGCAC	TGGTGTTATC	ACCATTTGCT	TCAGCATTTT	TTGCTGGACT	TGTTTCTTCA	1560
CTTGCGCTAG	CTTTTGA	GATTTGATGA	TTCAAACTA	GAATAGCTTT	TGTCGATTCA	1620
AGTAAAGCTG	TTTTGTCTTT	ACTCTTAGCA	GAAAGTTGAT	CTAATAATGC	ATCCACCTTA	1680
TCAAAGTCCG	CATCAGATCC	ATTATTACTT	TCTAAATAAG	AGTGAAGCGA	CATGAGAATA	1740
TCGTAGAGTT	TTTGATAGAG	TACAAGTGTC	TGAGGATCTT	GCTCAGCATT	TTCTTTTCT	1800
TGTTGAAGGG	CGCTAGCGAT	ACGAGTCAAG	ACATCTTTTA	CCTGACTGTT	TACTTCATCC	1860
AAGTCTGCAT	CAGCCTTGTT	TGTGGCAGCT	TTTAGATTTT	CTACTTCTTC	TGCCAAGGAT	1920
TGTCTGATTC	CTTCTTCATG	GATTTGTTCC	AAGAGTTGAT	TTGCCTTGCT	CAAAAGACTT	1980
TCTACTTCTT	CCTTGCTATC	TGTCGCAGAT	TATTGGTTGC	TATCTACCAT	GTACTCCTAA	2040
AACAGGAGAG	TTATAATCCA	AGATTACAAG	GCCTTACAGA	AATAAGAAAT	CCAGATAAGA	2100
CAATGTTTCGT	CCAAGACGCT	ATTTCGCTTCG	CACAGCAGCA	CGGATTCAAT	ATGCTTTAAT	2160
TTTAAAGTTT	AGGTGTCAAG	ACCTCTTTTT	AGTGTGCCCA	AAATTTAGAG	AAGTAATCAA	2220
TCAACTAACT	TTTATTTTTT	TCAAACTTTC	AGTAACTGA	CCTAAAGCTA	ACTCAATCTG	2280
TCTTTGTAGA	TGCTTCTGCT	ATCAGCTAGA	AGTTGATCTA	CTTTTGCCAA	GACTGCCTTC	2340
TCATCAAAAG	TTCCAGGTTG	ATAGTTGGAT	TGCAGGGATG	GAATCTTGTT	TTTCAAAGCC	2400
GCTTCATATC	CCTTAGTTTG	AACCTTGATG	TAGTGATTGT	GGTCGCCATG	AGGAATCACA	2460
AAACCTTCTG	AATCTTCACT	TATAATTCGA	TTGGCATCAA	AACCATGACC	ATCTTCTTCC	2520
TCATGATGGA	CATGTAGTGA	CGGATTACTT	AATACAGAAC	TAGAAGAACT	TCCTACCTCT	2580
TCCGTGTTAG	AGTGTGATGG	GGGATTGTTA	AGAGATGACT	TAGGAATATA	GTGATAGTGA	2640
TCCCCATGTC	TTACTATATA	AGCATCACCT	GTATCTCTGA	CAATATCATT	AGGGTTAAAG	2700
ACATATGTGG	CTGCTAATTC	ACCTGCCGAC	AAGTCACTCT	CAGGAATGAA	ATGATAGTGA	2760
CCACCATGTG	GTACTATAGT	AGATTGAAAT	AGAATATGAG	CAAATTGATA	AGGGGATTTT	2820
AAAGTAATTT	CTAACAATGA	TTTAGAACT	ATGATGTGCT	ATTCTAAATT	CAACTCACTA	2880
TATATAACCA	TCATCGGTAG	TATAACGTCC	CTGTAATTTT	GCTACAGATA	CTTCTGCACT	2940

1159

AGCTCCTTTA	TCGTCTTTAC	CATGTTCTTG	TTTTTGGCGA	TTGATTTCAT	CTTTTGTTCG	3000
TACATTTTCT	GCATGAGCTT	GATCTTTAAG	GTAAACATAA	TACTTTCCAT	CTACCTTAAT	3060
AATATATCCT	CCCTTAACCT	AACTGACGAT	ATCTTGATCT	TTCGGCTGAT	AGTTGGGGGC	3120
TTTCATTAAT	AGCTCTTCAC	TAAAGAGCGC	ATCAAAAGGA	ACTTTACCAT	TATAGTAGTG	3180
ATAATGATCG	CCATGAGAAG	TTACATAACC	TTGATCTGTA	ATCTTAATAA	CAATTTGTTT	3240
TGCTTGAATT	CCTTCTTTTT	GACTAACCTA	GTCTGGAGTC	AAATTTTCAG	TCTTCTTAGT	3300
GTCTTTATTA	CTGTTTACAT	ATGAAACACG	ATTTTATCT	GTATTGGCCT	GTTAGCTATG	3360
TTGGTTCAGA	GCATAAACAC	ACAGACTTAA	GGAAAGGATA	ACAACAGATC	CAGCTGCTAT	3420
ATATTTCTTT	TTAAATTTCA	TAATTACCTC	ATTTCTATAA	TTATTTATAT	GATGTCTTCA	3480
TTATTAAATG	ATTAAATAAA	TTAATTAACC	AATTAATTAA	CTAGTAAATA	TTCCACCTCT	3540
TTTTAAGTTG	TATGTCAAGA	AATTTTATAT	ATTAATAATA	AAATGAAATT	CTCCCAAAGT	3600
CAGAGTTTFA	TTTCTAACTT	TTGAGAGAAC	TTCATTTTTG	ATTCAGACTT	TTTCTACTGC	3660
TATTCCTTAC	GCTATGAGAT	CAGATAAATT	CTTTTTTATC	ACTTCTCCAC	TTGGCAATCT	3720
TAATTCAATC	GTTCCATCCA	TATTGAATAT	AACACTATCT	AAGCCTAATC	CGTAACTAGC	3780
TGTAAATTTT	TCTAATTTTT	CTTGTACAGG	ATCTACTGCT	GGAGCTTCCT	CTAATGCTGG	3840
ATCTAACATA	GGGTCACTCC	CCACATTCCC	TTCTGGATTC	AACATTCCAT	TATCCGTTGA	3900
GTTTTCTGGT	TTTACAGGTT	TTTCGTTTGG	TGCCTCTGGT	AAAGAATCTG	CTGGTTTATT	3960
TTCTGTTGGT	TGGTTCTCAA	CTGTTCCAGT	AGATACTTTT	CCATTTTCAG	ATGGTTTATT	4020
TTCACCATTT	CCTTGAGGTG	CTTCTCCTGT	AAAATCTGCC	ATATTCTTTT	TAATGACTTC	4080
TCCCGATGGT	AAATATAATT	CAATTGTTCC	GTCCATATTA	AACAAGACAT	TTTCTAGCTT	4140
CATCCCATAA	CTTTCAGCAA	ATTTTGCTAC	TTTTTCTTGT	ACAGGATCCA	CTGTAGGAAC	4200
TTCTTCTAAC	GTTGAATTAC	TAGTACTATT	CCCAGTTTCA	GAAAGTTTTT	CTTTTTCTAC	4260
CTTCTCACTA	GTCTTTGGTT	CTTCTACCTT	TTCATCAAGT	TTTAAGTTTT	CTTGTGCTTT	4320
ATTCCTTTTA	AATTGTGGTA	GAATACTTGG	TTTATCAGTT	TGATTTTCTT	TTTCCAAGAT	4380
AGGTACTTCC	ACAATATAAG	TCGATTGATT	GTCCAAATAA	GCATTTGCCA	TGAAGGTTAC	4440
AGGAATTTTA	TTTCCGGCCG	TTCTGGTTGT	TCCTTGGTTT	AATTTCCGAA	TCGGTAATTT	4500
GATTTCACCA	ACTTTATAGT	TATTTTCTAA	ATAAGCATTT	CCATGAAATT	CATCAAACAC	4560
TCTGACTAAA	GCATCAGTTC	CTTTAGGCAC	TGCAAATTGA	GGGTTCACTC	TTAAATAAGT	4620
ATCCCCTGCA	TGGAAAGGAT	AGAAAATCGT	TTGACTGGCC	ATTTTGTAAG	CTAAAGAGGT	4680

1160

TGGAAGCTGTA	AATGTACCAT	CATAACTTAC	TTCTGGATAA	TCTTTTGAAG	CGATAGTATA	4740
CTTAAATGTT	TGTCCTGGTA	AATAAGGTTG	ATCTAATTCA	AAGTTTGCAA	TATTCCTTAC	4800
TCCTTCTCCA	AATACTTTAC	CAGATACTTT	CTCCAATACT	TTTCCATCTG	GTGTTATTAA	4860
TTTTACTAGC	ATATTGATAC	CTAATTTTTT	CTCCAATTCA	GGCGGAAAAC	TAAAAGAAAC	4920
GCGTTTTTGA	CCATTGGCTA	GAGTAAAGTT	TTGATTATTA	AACGTACTAT	TTTTTAACAA	4980
ATTAACAACA	TTCGTTAATT	CTTCTCCAGT	ATAAACTTTA	TTCCCTTCTT	TTTTAGCAAC	5040
TCCTTCTTCG	GGTTTAAACA	GTTCATAGTT	ACTGTGAGAA	TGACCAATTC	CAACCGGTTT	5100
ATGTTTCATCA	ATCGGATCTG	CATGATGGTG	ATCTCCATGC	GGATAAATAA	TCGCATTTTT	5160
TTCTTTATTC	ACGACAATAC	TTTCACGTTT	GACACCATAT	TGTTTCATAA	TGCCAGCAAT	5220
TTTTTCTTCG	ATTTTTTTAT	CTAAATCTTT	CATTTCTTTG	GCATTACTTG	GATAATCCTG	5280
TTCATGAGAT	GACAAAGAAT	CTAATCCATT	ATGACTAGTT	TTAACTTCCT	CTAAATGTTT	5340
TTGCGCAsCT	TAATTTGCTC	TTCTGTCAAG	TCCTTCTTGA	AGAAATAATG	ATTGTGGTCT	5400
CCGTGACTCA	TGACAAAACC	TGATTCATCT	TCAGCGATAA	TACGATTAGC	ATCAAATCCG	5460
TATCCATCTT	CTTCATGTTT	CTCATGTGAA	GTTCTGGGAT	TGATTGGAAG	AGATGGAGAA	5520
GGTGTGCTA	GACTATTGTT	TGGAAGAGTC	GGTTGCCCAA	TTTGATTTGA	TTTTGGAATG	5580
TAATGGAAAT	GATCACCATG	TCTTACAATA	TAAGCTGTAG	CCGTTTCTTC	AACGATATCT	5640
TTTGGAATTA	AAATATAACC	ATCAGATGCT	GAAGAGAGCT	CCTTACTTGT	CGTTAAAGAA	5700
GAAGGATTGC	TTGAAAGACT	GCCTAGACTA	GACACTACTT	CATTAGGTTT	TGCATTTGTA	5760
GAAACTGTAG	AACCAGTTCC	ACTGATAGGC	ACCATTCCTG	CAATCTTTTC	TTCTAAGGCA	5820
GAAAGCTTGC	TGTAAGGAAT	AAAGTGGTAA	TGGTCGCCAT	GCGGAATCGC	AACTCCATTT	5880
GGTGTACGAC	TGATAATCTT	AGCAGGGTCA	AAGACCAGGC	CATCTGATTC	ACTGTAACGT	5940
TGGGCGCTAG	GTGAATCATA	GAGTTCCTTC	AAAAGACTCT	GGAGATTTTC	AGATTTATTT	6000
GCTGGCTTGC	TAGTTGATCC	TTTTGCTACA	GATTGCGTGT	TATTGTCACT	AGCTGTTGAA	6060
GAATAGCTTA	ACTGACTCGG	TTGCATATTT	TTTCCAGCCA	GATGTGCTTT	AGCTGCTGCT	6120
AATTCAC TAG	CAGATAAATC	GCTTTTGGGA	ATGTAGTGAT	AGTGACCTCC	ATGAGGAACG	6180
ATATAAGCAT	TACCCGTATC	TTCGATAATA	TCAGCTGGAT	TAAAGACATA	ACCATCATTT	6240
GTCGTATATC	GTCCCTGAGA	CCTTGCTACA	GCAACATTAG	AGTTAACCTT	CTCATTATCT	6300
TTGACATGTT	CTTGTTTTTG	ACGATTGATT	TCATCTTTAG	TTCGAACATT	ATCAGCATGA	6360
GCTGCATCTT	TCAGGTAGAC	ATAATATTTT	CCATCGACCT	TGATGATATA	ACCACCCTTG	6420
ACTTCATTGA	CAATATCAGC	GTCTTTAAGT	TGATAGTTTG	GATCCTTCAT	CAAGAGTTCT	6480

1161

TCACTAAAGA GGGCATCATA AGGAACTTTC CCATTATAGT AATGATAGTG GTCACCGTGT	6540
GACGTTACAT AGCCCTGATC TGTAATTTTG ATTACAATTT GCTCAGCCTG AATTCCTTCT	6600
TTCTGGCTAA CCTGGTCTGG TGTCAAGTTT TCACTTTTCT GACTTGACTG GCTGCCATCC	6660
ACATAAGAGA CACGATTATT GTCCTTATTT TCCTGCGAAC GATGCTGGTT TAGTGCATAG	6720
GCACATAGAC TCAAGGATAC GATAACAGCT GATCCAGCTG CTATATATTT TTTACTAAAT	6780
TTCATAAATC CCTCATTTCA ATAAATGATG AAGTTTTTTC TCAACTTCTT TTACTTTATT	6840
AAATAGTTTT CTAAACCCGG GGGTACC	6867

(2) INFORMATION FOR SEQ ID NO: 193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 999 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

CGTTCTAAAA ATGCAGTACG TTTGATTGAG AAATCAGTTA AAGGTATGCT TCCACACAAT	60
ACACTTGGAC GCGCTCAAGG TATGAAGTTG AAAGTATTTG TTGGAGCTGA GCACACTCAC	120
GCTGCACAAC AACCAGAAGT TCTTGACATT TCAGGACTTA TCTAAGGAAA GGAACAATAA	180
AGTATGTCAC AAGCACAATA TGCAGGTACT GGACGTCGTA AAAACGCTGT TGCACGCGTT	240
CGCCTTGTTT CAGGAACTGG TAAAATCACT GTTAACAAAA AAGATGTTGA AGAGTACATC	300
CCACACGCTG ACCTTCGTCT TGTCATCAAC CAACCATTCG CAGTTACTTC AACTGTAGGT	360
TCATACGACG TTTTCGTTAA CGTTATAGGT GGTGGATACG CTGGTCAATC AGGAGCTATC	420
CGTCACGGTA TCGCTCGTGC CCTTCTTCAA GTAGACCCAG ACTTCCGCGA TTCATTGAAA	480
CGCGCAGGAC TTCTTACACG TGAATCACGT AAAGTTGAAC GTAAGAAACC AGGTCTTAAG	540
AAAGCTCGTA AAGCATCACA ATTTAGTAAA CGTTAATTCG AAAGAATTAC TATACTTATA	600
CAGAGCACCT TTCGGGGTGT TCTTTTTTTA TACTTTCTTA CTAAATTGGT GCAATTGACA	660
CAGTTGTTGC GACTTTAGTC GCTTACAAAT GTGGCTGCAA CCTGACATGG TCAGTTGCCT	720
CAAAACGTTA ATCAATACGA TTATATCAAC GTTTCAAAGC ACTCAAGGGT TTACCCTATG	780
GGTGCTTTTT TCTATACTTT CTAAAAAAGT TTACCCTAAA ATTTGCCCTA AAATTACCCT	840
ACTTATTTTT AAGATGTTGG TAGGCAACTT GTCCAGCAGA TAATGGAACT ATGTTTGAAG	900
TATTAACATA AGTCTTAGTT GTAACGGTAT CGCTATGAGT TAATGCTTCA GAAATGGCTT	960

CTAAGCTCAT TCCTGCTTTT TTAGCAAGTG TCGCTCCTG

1162

999

(2) INFORMATION FOR SEQ ID NO: 194:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

AATATTATCA CTGTTCTTGA AGGCAGAACA CAAGCTGTCA TCCGAAATCA CTTTCTTCGC	60
TACGATAGAG CCGTTCGTTG TCAAGTGAAA ATCATTACGA TGGATATGTT TAGTCCTTAC	120
TATGACTTGG CTAAACAGCT TTTTCCGTGT GCTAAAATCG TTCTAGATCG TTTCCATATT	180
ATCCAACATC TCAGCCGTGC CATGAGTCGT TTTCGTGTTC AAATTATGAA TCAGTTTGAA	240
CGAAAATCTC ATGAATACAA GGCTATCAAG CGTTACTGGA AACTCATCCA ACAGGATAGT	300
CGTAAACTCA GCGATAAACG TTTTATCGC CCTACTTTTC GCATGCACTT AACAAATAAA	360
GAAATTCTTG ACAAGATTTT AAGCTATTCA GAAGACTTGA AACACCACTA TCAGATCTAT	420
CAACTCTTAC TTTTTCACCT TCAGAACAAA GACCCTGAGA AATTTTTCGG ACTCATTGAG	480
GACAATCTGA AGCAGGTTCA TCCTCTTTTT CAGACTGTCT TTAAAACCTT TCTAAAGAAC	540
AAAGAGAAAA TCGTCAACGC CCTTCAACTA CCCTATTCAA ACGCCAAATT GGAAGCGACC	600
AATAATCTCA TCAAACCTAT CAAACGCAAT GCCTTTGGTT TTCGAAACTT TGAAAACCTC	660
AAAAAACGGA TTTTATCGC TCTGAACATC AAAAAAGAAA GGACGAAATT TGTCCTTTCT	720
CAAGCTTAGC TTTTCTTCAA CCCACTACAG TTGACAAAGA GCCTATTTTC GCTGATTCTC	780
CACTACATTT GACTGGATTC TAATTTTTTA GAGAAATACA AAAGAGCTAG CTTTAGCTAG	840
CTCTTTTCCT ATGCGGAGAG AGGGACTTGA ACCCTCACGA CCTAAAGCGG TCACAGGATC	900
CTTAGTCCTG CGCGTCTGCC AATTCGCGCA TCCCCGCGTC GATTACTTTA CTAGTATATC	960
AACTTTGGG ATGCTTGTC AACTTTTTT TCAAATTTTT TCATTTTCAC CAACCAGGTT	1020
ACTCAAAAAG TTCATTTAGA TTTTCATCTA CTAACCTAGC TCCGAGTGTA TTTTGGAAAT	1080
GACCTAGGGC AAATTGATGA TTTTCAGGCC AGATGGAAGC AACAGCTGGT TTAACAATCT	1140
CGATGTCATA TCCTAGATTA TAGGCATCTA TAGCTGTATG TAGGACACAG ATATCCGTCA	1200
AGACACCTGT TAAGATAACG GTAGACACTC TACGCTCTCT CAAACGAATA TCTAGGTCAG	1260
TCCCTGAAAA AGCTGAGTAA TGGCGTTTAT CCATCCAAAA GACACGACTG TCTGAACCAT	1320
GCTCTTGATA AAAGATCCCC AAATCTCCAT ATAAATTCCG TCCACTCGTC CCAATCAGAT	1380

1163

TATGAGGAGG AAATAACTTA CTTTCCGGAT GGAAACAATC GTTTTCTTCA TGAGCATCAA	1440
TAGTAAAGAA GATATAATCT CCTCGTTCAA AAGCTAATCG AGTTACCTTG CTGATGGCAT	1500
CCGAAATCGC CTGAGCTGGA GCACCTGCTG TTAGTTTCCC ACTATCAGCA AAAAAATCTT	1560
CTGTATAATC AATCGAAATT AAAGCCTTTG TCATTAGTAA TCTCTTTTCT TCACTTCTTC	1620
AAAAATATCT GAAATCAAGA CCTTAAGATA GGTTCCTTC ATTCCAAGTG AGCGACTTTC	1680
AATAATCCCC GCAGACTCAA GTTTACGAAG AGCATTGACA ATCACAGAGC GAGTGATTCC	1740
GATACGATCT GCAATCACTG ACGCAGTCAA CTTCCCTTCA TTTCCATTTA ATTCCCCTAA	1800
AATTGCTGAA ACAGCACGGA GTTCGGAGTA AGAAAGGGTA TTGACCGCCA TGGTGACAGC	1860
AGTACGACGA CGAATATTTT TCTCATCTTC TTCACGTTGG AAGTTAAGAA GCTGAATCCC	1920
AACAACGGTA CTGGCAATCT CAACAAGAAC CAAGTCCTCA TCTTCGAATT TTTTATCATT	1980
ACGCCAAATA ATCAAAGAAC CAAGGCGAAT CCCCAGTACA TGAATCGGTG CAATAGTCGT	2040
CAAGCCATCT GGAAAATCAT CTCTACTCTC AATAGGGAAA ATACTCATAT CATGCTCAAC	2100
AGGCAAGTTT GCTTCTGTTT CGTAAATCAT ATTAGCCCCCT TGAACGTAGT CATCTGGGAA	2160
AATCTTAGTT TGGAAGAATT GCTtACGCGA TCTGTATTTG TTTTATAACG CATAAAATAG	2220
CCAAGCAGAC GTCCCTTACT ATTGATAATG CAGGCATTGC AATGAATAAT ATCCGCTAAC	2280
TGACGCGTAA TAGCGTTGTA AGGGAGCTCA TCTCG	2315

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6693 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

CGATTTCTTC CATTTCTTCA AATAAGAATA CTTCATCTGA CATATGTGTT ACCTTCTTCA	60
TCAAAAATTA TTTTGTAATC GATTACATTG CAGATCGTAA CATAAAGAAA AACAGATGTC	120
AAATATTAAA CGTAAAAACA TGGTCACTAA AGAACTATAA GAGAAAAGGT AAACCTAGCG	180
ACGCGATGAA CGCTGGGTCG TTTGGTTTCG ATTGCTCTCT TCCTCTTGTT TTTTCTGTTC	240
TTCTTCTTGT TTTTCTCAG CTTCCCTGGC CTCTTGTTTG GCTTTTTCCT CAGCTTCCAT	300
AATTAATTTA TCCGCCACAG TGTAGCTGTA GATTCCAGCT TCCATGTCGA CCACACTCGG	360
TTCTGACAAT TGAGGCTTAA TCTTACTGTA ATATGGCAGT TTCTTACTCA TTTCAGATAG	420

1164						
AGGAACCAAG	ACTTCGTCCG	AATCATTTCAT	GGTCAATCGA	ATTAAATCGG	ATGTCACCTT	480
GCTTGGGGCT	AATTCCACCT	TTTGGATAGC	CGCCTTGAGT	TCTGGGCTAA	TTTGAGCAAG	540
TTCTGAGACA	AAAACTTTGA	TTTGTTCAC	ATCATTAAAG	AGAACTGATA	AATAAGTTTC	600
TGGTAAACTG	TTCAGACTCA	CAGAACTAGT	CTCAAGCTGA	CCACTGGAAA	GAATAGGATA	660
ATGATTTTCA	CCAGAAATAT	AGTAGGCCAC	AATATCATAT	TCCTTGACCT	TAATAGTGAA	720
CTTAGTTGGA	AATTGATAGA	CAAGTTGAGC	TGATTCAACC	CAATAGTTAG	ACTTAATCTG	780
CTTTTCATAT	TTTGCCTTGT	CTAGCAGAAG	GTTAATCGTA	TAATCCGAAT	CCTGAATGCC	840
TGAAGCCTGT	CGAATATCAT	CAGCTGTAGT	TTGCACCGTT	CCCTCAACAC	GAATATCTTT	900
CATGGTCGCA	TAAGGACTGA	GCAAGTAGGC	AGAGACAAAC	AATAGAAGCA	GACTTGAAAA	960
TAAAATCGTG	AAGGCTCGCA	AGATATGGAT	ACCAGGAATC	TTTGCTTTGG	CTGGTTTTTC	1020
CTTTGTAGCC	TTTTTAGCAA	GCTTTTTATC	CTGTTCTCC	TTCTCTTTAG	ACTCTGGTTC	1080
TTCTTTCTCT	TCTTTCTCTT	TGTCAGCCTC	TGAGGATGCT	ACTTTTTCTT	CAGACTCTTC	1140
CTTAGCTGAT	TCTGAATCTT	CCTGGTCTGT	TTCACTCTCC	TGGTCCTGTT	TATCCTCTGA	1200
CTTCTCAGAT	TCTTCTCCCA	TTGAGCTTG	TCTTTCCTTT	TCCTTCTCCT	CAGCTAGAGC	1260
CGCCTCTTCT	TCAGCCTTCT	TTTTTAGATA	TTCTTGGTTT	CGTTTCTGCC	ATTCTGATAA	1320
CTCTTTCAAT	TCTTCGAGGG	TTCTTTTGTC	CTCATTTTTT	TTATCTTTTG	ACATTTACTT	1380
TCCTTATGAT	AAATCTTTTT	TCAACAATTG	ATAAAAATCT	GCTAGAGATT	TCAATTCCTT	1440
AGAAGCTTTC	ATCTTAGCTT	GGTAATCTTC	CTTGTGACTT	AGTAAGTGAG	AAAGCTTCTC	1500
TTCCAAACTA	TCCAAGGTCA	AATCGCTTTC	TTGAAGGTCT	TCTGCATAGC	CTTCTTAAC	1560
AAAGTAAGCT	GCATTTTCAA	TCTGGTCACC	ACGACTAGCT	TCACGACCAA	GCGGCACAAT	1620
GACATGCAAT	TTTGCTATCG	CCAAGAGCTC	AAAAATCGTA	TTGGCACCAC	CTCGTGTCAC	1680
AACAATATCA	GCCAATTCCA	TCAAGGGTTG	ATAGAGATCG	GTCACATAGT	CAACACGAAA	1740
AAGATTTTGC	CTCAACTCAT	TCAGACTAGA	ATCTCCAGTT	AGATTGATAA	TATTGTAGCG	1800
CTCTGTTAGT	TCTTTCTTAT	GGTCTGTCAC	CAATTGGTTA	AAGACACGAG	CGCCTGCAGA	1860
ACCGCCAACA	AACAATACAG	TTGGCAATTT	GGGATTAAAG	TGGGTTTGAA	TATCCACCAA	1920
TTCATCTGGT	TCTGGAGTGT	TTTTGTCCGA	AACCTTGGTC	ACCGCTCCCA	CATGCTCAAC	1980
CTTAGCCAAA	CTCGAAGCTT	GTTCAAAGGT	TGAATACATC	TTAGTCGCAA	ATTTATAGGC	2040
GATTTTATTG	GCCAAGCCCA	TAGACAGGTC	AGATTTCGTGA	ATAAAGACAG	GCACTCCTGA	2100
CACACGCGCA	GCGATAACAG	GCGGTACTGA	GACAAAGCCC	CCCTTTGAAA	AAAGGGTCTG	2160
TGGACGCAGT	CGCAACATGA	TAAAGAGCGA	TTGGACAATT	CCCCAACCAA	CTTTGAAGAC	2220

1165

GTCCAGCATA	TTTTGCCAAG	AGAAATAGCG	ACGCAATTTT	CCAGTCGCAA	TAGAATGGAA	2280
GGTGACATCC	AAACCTGACT	TAAGGATTTT	TTGGTGTTTC	ATACCACACT	TGTCCCCGAT	2340
ATAGTGGACT	TCCCAACCAT	CTTCGATGAA	CTTGGGCATT	AACAAAAGAT	TGAGGGTAAC	2400
GTGTCCAACC	GTCCCCCCAC	CTGTAAAGAC	AATTTTTTTT	ATATTATTCT	TTTAACTCCG	2460
CTACTGTGTC	GATAAAGAGG	TCGCCACGTA	CTTCAAAGTT	AGCATACATA	TCCCAGCTAG	2520
CATTGGCAGG	ACTAAGAAGA	ACCACATCTC	CTTGAGTCGC	AAGCTCATAG	GCCTTGCGGG	2580
TCGCATCTGC	AATATCTGTC	GCCTCCACAT	AAGCGACACC	AGCCTTGTCT	GCTGCCCATT	2640
TGACACGTTT	TGCAGATTGA	CCCAGGATGA	CCATCTTCTT	GAGTCCAGTA	ATGTCTGGCA	2700
CCAATTTCGTC	AAACTCATTG	CCACGGTCCA	AACCACCTGC	AATCAAGACG	ACCTTGCTGT	2760
TGTCAAATCC	TGACAAGGCT	TTTTGAGTAG	CCAAGATATT	AGTTGATTTA	CTGTCGTTAT	2820
AGAATTTAAC	ACCCTTGATG	TCATCCACAA	ACTGGAGACG	GTGTTTGACA	CCACCGAAGG	2880
CTGAAAGAGT	TTCTTGATG	GTTTGATTGT	CCACATCACG	AAGCTTGGCT	ACAGCAATAG	2940
TCGCAAGGGC	ATTTTCCACA	TTGTGGCTAC	CTGGAACACC	GATTTTCATTC	GCTGCCATGA	3000
CTACTTCACC	ACGGAAGTAG	AGTTGACCAT	CTTCCAGATA	AGCTCCATCA	ACCTTTTCAA	3060
GTGTTGAAAA	TGGTACAACA	GTGGCTTCTG	TCTTGGAAGT	CAAGTCTTTT	GCCAAGTCTT	3120
GATTAAAGTT	CAAGACAAGG	AAATCAGCTG	CTGTCATCTT	GTTCTGGATA	TTCCACTTGG	3180
CTGCTACATA	TTCCGAAAAT	GACCCATGGT	AGTCGATATG	AGTTGGCATG	AGGTGGGTAA	3240
TAACCGCAAT	CTCTGGATGG	AATTCTTGAA	CACCCATGAG	TTGGAAAGAA	GAAAGTTCCA	3300
TAACAAGCGT	GTCCTTATCT	GATGCTATTT	GAGCAACCTG	ACTAGCTGGA	TAGCCGATAT	3360
TCCCTGATAA	AAGACCATGT	TGGCCAGCAG	CAGTCAAAAC	TTCCCCAATC	ATAGTCGTTG	3420
TGGTTGTCTT	ACCGTTCGAT	CCTGTGATAC	CAATAATCGG	TGCTTCTGAA	ATCAAATAAG	3480
CCAATTCCAC	CTCAGTCAAG	ACTGGAATTC	CCTTGGCCAA	AGCCTTTTCA	ATCATGGGAT	3540
TGTTGTAGGG	GATACCTGGA	TTTTTCACCA	TAAGGGCAAA	CTCTTCATCC	AAGAGTTCCA	3600
AAGGATGGCC	ACCTGTAATG	ACCTTGATCC	CTTCTTCCAG	CAAACCTTGG	GCAGCTGGAT	3660
TGTCCTCGAA	AGGTFTCCCA	TCATTTACTG	TCACAATGGC	ACCTAGCTTG	TCCAACAAAC	3720
GAGCTGCAGA	TTCAACAGAC	TTGGCCAAAC	CTAAAACAAG	GACTTTCTTA	TTTTTAAATT	3780
GATCTATTAC	TTTCATGTCT	CGAACTCCAT	TTCTACTCCT	ACTATTTTAC	CATTTTTATG	3840
GAAATAAAAA	AGCCACAAAG	TGTGTTTGTG	ACTCTTCTCT	CTAACTGAAT	CTTACCATAT	3900
CATCTATGTG	ATAAATCGGT	AACTCGAATG	ACCTGATCCA	CTTGCTCCCA	AATCAGAGGA	3960

1166

TTATGGGTCG	CAATAATAAT	GGTCCGATTC	GGATTTTTTA	AAGATTCTAG	GATGGAAAGT	4020
AATTCCTCAG	AGTTTTTGGG	GTCTAAGGAA	GCGGTTGGTT	CATCTGCGAG	GATCAAAGGT	4080
GGATCCTTTA	AAATTATCTT	CGCTAGTGCA	ACACGTTGTG	CTTCTCCTCC	TGATAACTCA	4140
AATATAGGTT	GCTTCAAATC	CAAATAAGAG	AGGTTTACAC	GGTTTAGAGC	TTGTTTCATC	4200
AAAGAGATTT	TCTCTTTTTC	CTTCAACTTT	TTACCAACTA	AACCCAGATT	GAGATTCTCT	4260
TTGACGGTTT	GGCTTTCAAT	TAAGCCAAAA	TCTTGAAATA	AGTATCCTAA	GTAATCTCTA	4320
AAGAAAACAG	AAGGCTTGAT	GTCCTTAAGA	GAAGTGCCAT	CATAGATGAT	TTGCCCTTTG	4380
TCATATGGCT	CCAATCGTCC	AATCATATTC	AAGAGTGTTG	TCTTACCACA	GCCACTTGTA	4440
CCGATTAAGG	CATAAATTTT	CCCACCTTCA	AAATGAAGAT	TCATATCTGA	AAATAGCTGA	4500
CGGCTTCCAA	ATTTTTTAGA	TATATTCTTT	AGTTCAATCA	TCCTATTTTC	CTTTCATAAT	4560
TGTCATAGAA	ACACGAGATT	CTTCTGCGC	TTGACGGTAA	AGCGTCAAAA	CTGCACTAGC	4620
TAGAAAGACC	AATAAAGTGA	GCAAGCCAAT	CACCAAGTCT	CGACTGCTTA	AAATAAAGAG	4680
ACTAGCACCA	AATACAAAAC	TAGCAAATTG	GCTAACCATA	TACTGAGCAT	GTGTTTCAAA	4740
AAATCGTAAA	CCTGAAATTC	GTTTAATCAA	GATATCTCGG	CGGAATTGCT	CGAAATATAG	4800
AAGATTGACA	GAATAAAAGA	GTAACAAGGA	ACTGGCTATT	CCAACAATAG	CTCCTAAGAT	4860
TAAAGTTGCT	GTTTCAGTTT	GAACTTCATT	ATAACGAGTT	AGATAAACAC	TTCTTCCTTC	4920
TTTAAGATAG	GATACTTGCT	CATAAATTCC	AGCTTTCCTC	AAGAGTTCTA	GCCCCTCTC	4980
ATATCCTTTG	ATAAAGAGTT	GTTTTCCAGC	ATTGATAGAC	CAACTAGATA	AGGATATAAA	5040
ACTATCACCT	GTAGAAGTCG	GCGTGAATAC	CACTAAAATC	GGATCAGTCA	AATACTGAGT	5100
AGATACGGGA	TTCTCACCGT	TATTATAAAC	AAACCGCTTT	TCTCCCATTG	AAAGATAACT	5160
AACGTGCGCT	TTCATCTCAT	AATCCAAAGG	AGCACTTGCC	TCCTCACCAG	ATTTTCCATA	5220
ATAACTCAAT	CTTTCTTCAA	AAACTTTCTT	AAGTTCTGCT	TCTCGAGAGC	GCAAATGTTC	5280
TGGGAGCAAG	AGGATAAACT	CACCTTTTTG	GAGATGGGCT	AACTTCTGTT	TGGTCTCAGC	5340
ATCTACCACG	ACCTTTTCCT	TGTCCAAATA	ACTGGGACTA	ACATAGAGCG	TATTAGCATC	5400
TGAACTATAG	GTATCCAGTG	TCTCTCCCTG	TTCATTTTTT	CCTTGTGGAT	TGGCAAATG	5460
GAGCAGATTA	TCCTTTACAT	AAAGAGCTTG	TTCTTCTTCG	ATTGCTTCCT	TGGCAAAGGC	5520
ATACCACTTG	CTCTGATTTT	CTGTATCTTT	TCCTCTATCA	CCTAAGCCAA	AGGAAATCTG	5580
GTAATAGTCT	GCTCTGTCCT	GCCATGCTTG	TTTTGAAATT	TCAAGTTCTT	TCAATCGTTG	5640
GTAAGACGTC	AAACCTGTCT	TAACAGCGTA	GCCTACTGTA	AAAACAGCTA	CTAACTGACA	5700
CAATAGGGTT	AAAGCCATCA	AGCGTTTAAG	GGGTAATCTT	CCCTTAATAA	CGGGAACATA	5760

1167

TGCTTTGTAA CTCAAACCTCA TTAGGTAAAG GAGCATTAGT AAAATTGAAA TCGCCAATAA	5820
AAACAACAGA TAGAAACTAA TCCCAAAACC ATAGGTGGCT AACAAAGATAG GATAAAACAA	5880
ACCTTGACTA AAAAGAACGA CTCCCCCACC TAGGAAGGAA AGGAGGGCTG ATAGAAGGAG	5940
CCATTTGATA TCAGTAGATA AAGAATGCCC CATGATGGAT AAGAGAGTCT GACCAGAAAA	6000
GAGTTTTATA CCTGCTGCTC TCATTTTCCTT AATCCGAGTG ATAATCACTA AAGCAAAGAA	6060
AGATAAGCCA AATATTGCTA AACTAATTAA AATAAGGGGA TTTAGTAATA TTCGAAAAGC	6120
AAGAAAATAG GCGGTATCT TTCGGTCAGC ACTTGCTTTA TAACCCAAAT CTCCTAATTT	6180
ATCGGCAAGC TTTTCTTTTCG TCAAGGAGCC TGACAAAAGG AGATAACTAT TTAGCGGAnT	6240
AtACGTTTAC GACTTTCTTG GCTAGCTTCT TGGAATTCTT TTGGTAAAGT TCCCTGACCA	6300
TAAGTTGCAT AAGTAAAGTG AGTCGTCCCA TCCTTACTCG GCTCTACAAT TCTTCTAGCT	6360
ATTAAACTCT GTTCTGAGTT TGCAAAATTC TCCAATTCCCT GTTCAAATAC CTCACGCGTC	6420
GGTTCCTGAG TATCTTTTTT GACACGAAGT AAAGAAACGG AATCATAGCT TGCATATAAA	6480
TATTGTGGCG CACGTAAGAC AATAATCCAA GCAAGGAAGA AGCTGAGAAA AAAAGTTGAT	6540
AATAATATGA ATAGTTTCTT CATAGTAGAC TCCTTGTAAG CAAAATTCCC CCTGTAATTT	6600
CTTACAAGGG GAACGATTTA AATCAATGAA CGATTAGTCA TAATCACAGT AAAATGCTAC	6660
TTGTTCTCCC CATTTAGTCC AAATCCATGC AGG	6693

(2) INFORMATION FOR SEQ ID NO: 196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1847 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

CCGGTCTATG TACCCACTAC TTTGGGACAA TATGGGGATC AGCTACCCAA AACTAATCGA	60
GCGTTTGTTT GACCTTGCCA AGGAAAGTTT TGACAAGCGC GACGATTTGA TATAAAATGA	120
AAGAGAGGGT AGAAGCCAGA ACCATCACTG CACGGTGAAG AGAGTTCTCG GACTTCAGCC	180
CTTTTTTAAAG GAGTAGAAAT GAAATTAACA ATCCATGAAA TTGCCCAAGT TGTTGGAGCC	240
AAAAATGATA TCAGTATCTT TGAGGACACC CAGTTAGAAA AAGCTGAGTT TGATAGTCGT	300
TTGATTGGAA CTGGAGATTT ATTTGTGCCA CTAAAGGTG CGCGTGATGG CCATGACTTT	360
ATTGAAACAG CCTTTGAAAA TGGTGCAGCA GTAACCTTGT CTGAGAAAGA GGTCTCAAAT	420

1168

CATCCTTACA TTCTAGTAGA TGATGTTTTG ACAGCCTTTC AATCCTTAGC ATCCTACTAT	480
CTTGAAAAAA CGACTGTTGA TGTCTTTGCT GTTACAGGTT CAAATGGCAA GACAACGACT	540
AAGGATATGT TGGCGCATTT ACTGTCAACA AGATACAAGA CCTACAAAAC ACAAGGCAAT	600
TACAATAATG AGATTGGCCT TCCTTACACA GTTCTTCATA TGCCTGAAGG AACAGAAAAG	660
TTGGTTTTGG AGATGGGACA GGATCACTTG GGCGATATTC ATCTCTTGTC TGAATTGGCT	720
CGTCCAAAAA CAGCCATCGT GACCTTGGTT GGAGAAGCCC ATTTGGCCTT TTTCAAAGAC	780
CGTTCAGAGA TTGCTAAGGG AAAAATGCAA ATTGCAGACG GAATGGCTTC AGGTTCCCTG	840
CTTTTAGCGC CGGCTGACCC TATCGTAGAG GACTATTTGC CAACTGATAA AAAGGTGGTT	900
CGTTTTGGGC AAGGGGCAGA GCTGGAAATT ACTGACTTGG TTGAGCGCAA AGATAGTCTG	960
ACCTTCAAGG CCAATTTCTT AGAGCAAGCC CTTGATTTGC CAGTAACTGG CAAGTACAAT	1020
GCGACAAATG CTATGATTGC ATCCTATGTT GCCTTGCAAG AAGGAGTTTC AGAGGAGCAA	1080
ATTCGTTTGG CCTTCCAAGA TCTTGAATTG ACGCGTAACC GTACCGAGTG GAAGAAAGCA	1140
GCCAATGGAG CAGATATCCT GTCAGATGTT TACAATGCCA ATCCAAGTGC TATGAAACTG	1200
ATTTTAGAGA CTTTCTCTGC CATTCCAGCC AATGAAGGTG GCAAGAAAAT TGCAGTGTG	1260
GCGGATATGA AGGAGCTTGG TGACCAGTCT GTTCAACTTC ATAATCAGAT GATTTTGAGC	1320
CTTTCTCCAG ATGTGCTTGA TACCGTGATT TTCTATGGAG AAAATATTGC TGAATTAGCC	1380
CAATTGGCCA GTCAAATGTT CCAATCGGC CACGTTTACT ACTTCAAGAA AACAGAAGAC	1440
CAGGATCAAT TTGAAGACCT AGTCAAGCAG GTCAAGGAAA GCCTTGGAGC CCATGACCAA	1500
ATCCTGCTCA AAGGCTCTAA CTCTATGAAT CTAGCCAAGT TGGTAGAAAG TTTAGAAAAT	1560
GAAGACAAGT GATTTTGTCA AGTATTTGCA AAGAATGATT GCCATTACAG ATACTGGCTT	1620
AACCTTTACA AAAGATCCGT TTGACCGTGA GCGCTACGAA GACTTGCGAA GTCTGTTATC	1680
TGAAATGTTG AATCAAGCAT CAGACCTTGA TTCCGAAGAA GTGGCAGAAG TCTTGAAGCC	1740
AACTTCTGCT TATGCGACTC CGTTAATGGA CGTCCGTGCT TGGATTGTTG AGGATGAGAA	1800
GATTTGTCTG GTTAGGGGAC AAGGAGAGGA TAGTTGGGCT TTGCCGG	1847

(2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1062 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

1169

CAAGCGAAAA CATTTTTTAT TCCAAATAAA CAGAGCATTT TAGGAGAACA AGAGATTTTG	60
AATGCCAAGT CGATCTTGGC CTTGCTAGAC GGTTTGGAGT CACATAGCTA TGATGTAGTC	120
TATCTCCGTC AGCCTCTTAA TCGTCTCGAA TATATCGAGT GTGCGATAGT GGGGCAATCA	180
CAATTTCTCT TTAAGGTCAG TTATGCTGAT GGTCAAAAGG CTTACCGTGT CGATCTTCCT	240
GACCTACTAA CAAAGACAGA CTGGCAGATT ATCAAGTCAT TTTTAGATGC TTTGCTTGCT	300
TATACAGGGA CTGATATTGA AGGGCTAGAT GGTTTTGATT TTGAAGCTTA TTTCCAAGCA	360
AGTATTCAAG CCTATCTAGC AGACCCTGTA GCTCGTTTTA CGATTTGCCA AGGAATTTTT	420
AATCCTATTT TCTTTAGTCG TGAGAACTTG AAAAGCTTTT TAGAGGCAGA TGGCTTGGCT	480
CAGTTTGAAG CGCGTGTGCG TCGGGTTCAA GAGACAGATG CCTACTTTGC GAGAGTTTCC	540
TTCTATCAGG ATGGAGAAGG AAAAGTGCAT GGCGTTTACC ATCTAGCTCA AGGAGTCAAG	600
ACAGTTTTAC CGAGAGAACC GTTTGTTCCCT GCAGCCTATA TTGAGCAATT GGTGGATAAG	660
GAAGTCCAGT GGGAGATTGA CTTGGTTCAA ATCACAGGAG ATGGCTCTAA ACCAGAAGAC	720
TATGAAGCCA TTGCTCGCTT GGACTATGCA AAATTCTTAG AGGTATTACC CCCATCTTTT	780
TACCACCAAC TAGACGCCAA TCAAATAGAA GTGCAACCCA TATTAGACAA AGATTTTAAA	840
ACATTAGCAC AAGAAAAGTA AAGCAGAAGC AGGTCAATCG ACTTGCTTTT TTGACATAGA	900
AAAAATCCTG CCAAGaTGAC AGGATTGCTA CTCAATGAAA ATCAAAGAGC AAACTAGGAA	960
GCTAGCCGCA GCTGTACTTG AGTACGGTAA GGCGAAGCTG ACGTGGTTTG AATTTGATTT	1020
TTGAAGAGTA TGAAGTTTAA AGAAAAGCCA AGATACGAAG AT	1062

(2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6846 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

TATCTACAAC CTCAAAAACA TGTTTTGawG gCTCGTCAGT cTATCTACAA CCTCAAAAAC	60
ATGTTTTgAa kGctcGTCAG tTCTATCTAC AACCTCAAAA ACATGTTTTG AcaGCcTcGT	120
CAGTTCTATC TACAACCTCA AAAACATGTT TTGAGCTGAC TTCGTTAGTT TCATCTACAA	180
CCTCAAAAAC ATGTTTTGAG CTGACTTCGT TAGTTTCATC TACAACCTCA AAAACATGTT	240
TTGangnCnT CGTCAGTTCT ATCTGCAACC TCAAAGCAGT GCTTTgagcG CTTCTGTCAGT	300

1170

TCTATCTACA	ACCTCAAAAC	AGTGTGTTGC	GCAGCCTTTA	ATCAGCCGCC	TAGTCCGCTC	360
TATGGTATTC	ATTAAGTCAA	CATCTCTTGT	TTAAGAGCAC	CAAATCAGGA	AATCTTCTCG	420
ATTCCCTGAT	TTTTTCTATT	TACGTTTTCG	TGTTGAGCTA	CGTTCTGTCA	AACCATGAGG	480
TAAGAGAACT	TCACGTTCTT	CCAACCTCTC	CTTATGCATA	ATCTTGGTCA	ACATACGCAT	540
ACTAATGGCA	CCAAGGTCAT	AAAGAGGTTG	GGCAATCGTT	GTCAAGTTTG	GACGGGTAAA	600
GCGTGAGATT	TGTGAATCAT	CACTAGTAAT	AATTTCAAAA	TCTTCTGGCA	CAGAAACACC	660
CTTATCAGCC	AAACCGTTCA	AGACTCCTGC	TGCCAACTCA	TCACCTGTCA	CAACTGCTGC	720
AGTTGCATTT	GATGAAATCA	AACGCTCTGC	TAAGGCGTAA	CCATCATCAT	AGCTATATTT	780
AGATTCAAAT	ACCAAACCCCT	CACTATAAGT	GATTCCTGCT	TTTTTCAAGG	TTTCCTTGTA	840
GCCAACTAAA	CGAACCTTAC	CATTGATGTC	ATCCACTAGC	GGACCGCTAA	CGAAAGCAAT	900
ACGCTCATTT	TCTTTAGCAA	GGTAACTCAC	TGCATCAATT	GTTGCTTGCT	TATAGTCAAT	960
ATTGACACTT	GGCAACTGGT	GCTCAACATC	GACAGTTCCT	GCGAGAACAA	TCGGAGTACG	1020
TGAACGCGAA	AATTCTGAGC	GAATTTTATC	TGTCAAGTGA	TACCCCATAT	AGATAATGCC	1080
ATCTACCTGC	TTTGAAAAGA	GGGTATTGAC	AACAGAAACT	TCTTTCTCGT	TATCTTCATC	1140
GCTATTAGCT	AGGACAATAT	TGTACTTGTA	CATTTCTGCA	ATATCATCAA	TCCCCTTAGC	1200
CAAACCTGAA	AAATAACCAT	TGGTAATATT	TGGAATCACG	ACACCGACAG	TGGTTGTCTT	1260
TTTACTTGCA	AGACCACGCG	CAACTGCATT	TGGACGATAA	TCCAAACGAT	CAATTACCTC	1320
TAGCACTTTT	TTACGGGTAT	TCTCTTTTAC	ATTTTATTG	CCATTGACCA	CACGGCTGAC	1380
CGTCGCCATG	GAAACACCTG	CTTCACGAGC	GACATCATAA	ATGGTTACTG	TATCATCTGC	1440
ATTCATTCCCT	TTTCCTGTCC	TTTCTATCTC	ACACATTCTT	TTACAAGTAG	AGGTACTGAT	1500
TGAAGCTCTA	TATCTACTTA	CAAAAGTGAA	GATGTGAAAA	TTTCGTTTTT	ATATTTCTAC	1560
TTATTCCATT	CTATCACTAA	TTGTAAACAC	TTTCAAGTGT	TTTTTGAAGA	TTGATTGAAA	1620
AAATTTCATA	GAAAACCTAG	GTTTAGCTCC	TTGCTACCAC	CTTAGACTAA	ACAAAAAGGA	1680
GGAAACTAAG	CCCTCCTAAA	GTTATAGTAA	AATGAAATAA	GAACAGGATA	AATCGATCAG	1740
GACAGTCAAA	TCGATTTCTA	ACAATGTTTT	AGAAGTAGAG	GTGTACTATT	CTAGTTTCAA	1800
TCTACTATAG	GTATTGTTCC	ATTCACTACC	GTCAATTTTA	GCACATAGTC	TTCATGAAAA	1860
TATTATATCA	TCATAACCAA	CCAGATTCTT	TCGCGATATT	AGCTGCCTCT	GTTTCGATTAC	1920
CTGCATCTAG	TTTCGAAAGA	ATATTGGTGA	CATAGTTTCG	GACTGTTCCG	TTGGATAGAT	1980
AAAGTTTGTC	TGCAATTTCT	TGGTTAGAGA	AGCCCTGAGC	AATTCCTTTT	AAAAC TGCGA	2040
TTTCTTGCTC	CGTTAATGGA	TTGGGATGCA	TCATCACCAC	TTCCATCAAT	TCAGGCGAAT	2100

1171

ACTCCTTGCG	TCCTTCGAGG	ACGGTGTGCA	AGGTTTGCAT	GAGGTCTGCA	ATGTTTCTTT	2160
CTTTTAATAC	ATAAGCATCT	ACTCCAGCCT	TGACCGCACG	TTCAAAATAC	CCAGGACGCT	2220
TGAAGGTCGT	CACCACAACC	ACCTTTGTTT	CAAGCTTTTC	TGCTCGTATC	CACTCCAAGA	2280
CTTCAAGACC	TGTCTTAACA	GGCATTTCTA	CGTCAAGGAT	GGCGATATCT	ACAGACTCCT	2340
TTTCTAATAG	TTGGATTGCT	TCTTGCCCAT	TCTTGGCTTG	AAAGACAGAC	TCTACATCCG	2400
GTTGAAGCAT	GAGCAACTGG	CACATGGCAT	CTCGCAACAT	ACTTTGATCT	TCTGCGACTA	2460
ATACTTTCAT	CTACTTTCTC	TCCTTATAAA	GTAGTCGAAC	CTGCACTTCA	GTTGGATGTT	2520
TCTGACTGAT	TACACTTACT	TCTCCTGAAA	ATGGAAAAAC	ACGATTTCCG	ACTGTATGGA	2580
GCTCATCCCC	GCTTATAGAG	GCAAAGCCAC	AGCCATCATC	TCTCACTGTT	AGAATGAGTT	2640
CTTTCTCTGT	CCGTTCTAAT	TTCAAGTAGA	CTTTAGACGC	TTTAGCATGT	TTGATGATAT	2700
TGGTCACTAA	TTCAAGCAAA	ATCATGGAAG	CCGTTGACTC	CAATTCCTGA	GTTAAGCTAG	2760
ACTTGTCCAA	GTGATTCTCA	ACTTGAACCT	CAATTCAGC	AATTTCTAAC	ATCTTTTCA	2820
CAGTCTCTAG	TTCGGATGTC	AAAGTTCTAG	ACTTAAGATT	TTCCACAATG	GTTCGCACTT	2880
CATTCATGGA	TCCTTGCTGA	TCTGGTGAAT	TTCTTTTAAT	TCCTTTTCCA	CCTGTGGATA	2940
AGCCTCCATC	TGAAATAACT	GCAAGGCTAA	ATCTGTCTTG	AACTCAGCA	TAGCAAAGGT	3000
ATGTCCCAGA	CTATCATGCA	AATCCTGACC	GATACGACTA	CGTTCATTTT	CAGCAAGCAA	3060
TAGATTTATC	TGAGCATTTT	GCTTGACCTG	AGCTTCTTTC	AAATCCTCGA	CAATACGAAT	3120
CCGAACCAAT	CCAAAAGTCA	TTAAATCGAC	AAAAGTAAGA	ATTACAAGTA	GATAGAATAG	3180
AAACTCAACT	TCGATTCTCT	GAAAAATCAA	CAGTTGCCCC	ACAACAAGGA	CTTGAGCAAG	3240
AAGAAAAGTC	CAGACATGTA	AAGACTTTAA	ACTACGTACG	CTGAAATGAT	AACTTAAGAG	3300
ATTGGATAGG	AAAAAGAAAA	ACCAGATATA	ATTAACAGCA	ACAAAGGCAG	TATTTCCCAAC	3360
TACATAAGTC	AGCATGAGGC	CCCAATATAG	CCAAGATAGG	CGCTGGCTCT	TAGTTGTTAA	3420
AACACCCAAA	TATGCCACTA	CAAATAGAAT	ATCAATCAAT	AAATGCCAGG	CAGAAAGCCA	3480
CCCAGTCACT	ACAGACAGGA	TGGGGAAAAT	CATAAAAATT	AACTGATCC	AAAACATATA	3540
ATGTATTCTT	TTCACTCTTT	CAAGCATTAA	GCATTCTCCT	TATGACCTTG	AAGGTAAATG	3600
GTCAAACCAA	ACAAAACACT	TGAAAAAACA	AGTAAATAAA	CTGTGGCTGA	TAGATTGATG	3660
CCACCCTCAT	TTAAGAAGGT	CTTGAGCAAC	TCCATCAACT	GATAGGTCGG	GAGACACTTA	3720
CCTACTACTT	GCATCCAGTC	TGGAAATAAA	GAGATAGGCA	TCCAGAGTCC	ACCTAAAACA	3780
GCCAACCCTA	GATAAAGAAG	ATTGCCCACG	ACAGACATCA	ACTGACTAGT	TGGTAAGAGA	3840

1172						
GTCAAGGTCA	AACCAAGCGC	TACGAAGGCA	ATACTTCCTA	CTATCAGCAA	AAGTGCAGCC	3900
CCAATCCAAT	TTCCAAGAGA	CATGTCCACA	CCTCTTACAA	AATGCCCAAC	TGAGAAAACC	3960
ACCAAGATTG	AAACCAAATA	ATCAACCAGC	ATACTTGTTA	TCTTTGATAG	ATAATATTCT	4020
ACCATATTTA	CAGGGCTATG	ACGCAATGTT	TTCTGCCAGT	TGTTGATCTT	GTCGGTATGT	4080
AAAACAAC TG	GGAATGAGAA	GATAGCTGTT	GACATCATGG	AAAATGCAGT	CATGGAGATA	4140
AGATAATCAC	GCATAAAATT	CGCGAGTTCA	CCTGGTGTGT	CCTGATAGAT	ACCAGAAAAA	4200
AATAAATAGA	AAGCCGTCGG	CATCCCTACT	GACAATAGAT	AATAGATCAA	TTGTCGTTTG	4260
GTCAATAAAA	ATTCTATCTT	ACTAAGTGCT	AGCCATCGTT	TCATCTTAGT	TATCTCCCTT	4320
CTGCGTTTCT	TCAAAGATTG	TATCCAACAA	ACTACGATTA	TTAACTTCAA	TTTCTTGTAT	4380
GCCACATCCT	GCTTGAAC TA	ACAGTTCCCA	AAAAGCATCT	GCTTCGCGTG	TGACTACTTG	4440
TAGAGCATCC	TGTTTTTGTG	ACCAGTTTTTC	AACCAAGTTA	GACTGCTCAA	TGACTTCCTT	4500
GTATGCCAGA	GGAAGGATAA	AATGCTTTTC	AATTCCTCA	CTACGCATAG	CTAGAGGCGT	4560
CGTATCACGA	ATCAACTCTC	CCTTATTTAA	AACCAAAATC	CGGTCAGCCG	TATGCTCTAC	4620
CTCTTCAATA	TAATGAGACG	AATAGAGAAT	CGTGACTCCT	TGCGCTTTTA	GGTCCC GAAC	4680
GATTTCCCAA	AAGCGTTGAC	GAGTTGAAGT	ATCCATGGCA	GCAGTTGGTT	CATCTAAAAA	4740
GACAAGCTTT	GGTCGCCCAA	TCAAGGTCAA	GACAAAAGAG	AAGAGACGCT	TTTGCCCGCC	4800
TGACAAATTT	TCTGCGAATT	GCTCTTTTTG	TTGCTGGTCA	AACTGCAATA	GTTGATCGAT	4860
TTCCTGATCG	CTCAAGGAAT	TTGGATAGAT	ACGTTGAAAG	AAAGCAATCA	ACTCTTTGAC	4920
CTTTAATTTT	TGAACGATGA	CATTTTCTTG	AGGCAGATAA	CCTCTAATAT	AGTCTAACTG	4980
AGAACTCGTC	ACTGACAAGC	CTTGGATGGA	TACTTGACCG	CTTGTGACCA	GTTTATCTCC	5040
AAGCAGACAG	TCCAAGAGTG	TGGTCTTCCC	AGCACCATTG	GGCCCAATCA	AGGCGACGCA	5100
TTCACCTTCA	GCTACCTCAA	AGGAAATACC	CTTCAAAATA	GCCTTGCCCT	TGATGTTTTT	5160
ATTTAGGCTT	TCTACCTTAA	TCATATTCAT	GATATTCTCC	TTTCAACCAC	TCCATTCTCA	5220
TAAGGAAAAC	GACGAAAATC	ATAAATCCAA	ACCCCAAAGC	ACCACGAATG	AATTGGCGAA	5280
gCAAGGTTTG	GTCAAACCAA	CCTGTAAACA	TTTCCACTAA	CCATACCAAG	AGTGACAGGC	5340
CGATAAAGAA	ATAGATGATC	CCTCTCTTCA	TTCCTCAAGC	TCCTTTTTC A	CATCTCCGAC	5400
TAATTTCAAA	CCTTCTCTAA	CAAGCCAAGA	CATCATTTCA	AAGCCAGCAA	AGAGCTCCCA	5460
AGGAAAATGA	TAGAAACTCT	CATCCAATCC	CGAAAACATG	AGTTAGGTCA	TAACTCCTGC	5520
TACTACTAAA	CTCACTGCGA	TAATCATTTT	ATTTCTCATC	TCTTCTTCCT	CCATTT CATA	5580
CTACAATTAT	AGTCTTTTGA	AATCAGAGGA	GACAGAAGCT	TCTGTCACTA	GAAAATATGA	5640

1173

CAAATGTCAT	AAAAAATTCT	GTTCAAAACA	AGCAAGATAC	ACTATACAAT	AAAACACAAT	5700
TAGAAAAATC	TAAGGCAACT	TCCTCAAAAG	AGATATCAAA	CCCAATTAC	ACCATAATGT	5760
AAACTAATAC	TTATTTAAAA	TCAAAAAGAG	TAGAAATTTT	TATCAGACAA	ACACATATAT	5820
AGTGTATTGA	ATCTATAACA	GTAGGCCTTA	AATACTAAAA	TATTTCTATA	AATTAATTTA	5880
ACTTTCCTGA	TAGAGCTGTT	CATATCTTAT	TTCAATTCTC	TAAATTATAC	GTTGAACAAA	5940
ACCCTTCTAT	TTCTTTCTTA	AAGATTTATA	AGAGTTATAA	AATCTGTTAA	ATTTCAATGT	6000
GTATACCTAA	ACTACGGTAT	TTATTGAAAA	GACTGGAGAC	AAAAAGTATA	CGCTGCCAAA	6060
ATGAATTACT	GAAAATCAAA	AAAGAGAGAA	CCAAACTGAT	TCCCTCTTAA	TGTATATAAT	6120
ATCTAGTTTT	AAAAATACAC	ACTCACATAT	CTCTGTAATG	AATCGGGAAG	ACAGGATTCG	6180
AACCTGCGAC	ACCTTGGTCC	CAAACCAAGC	ACTCTACCAA	GCTGAGCTAC	TTCCCGAGTT	6240
AAATAGAAAA	ATGCACCCTA	GAGGAGTCGA	ACCTCTAACC	GCCTGATTCG	TAGTCAGGTA	6300
CTCTATCCAG	TTGAGCTAAG	GGTGCTCCAT	ATTATGCCGA	GGACCGGAAT	CGAACCGGTA	6360
CGATCGTTAC	CAATCGCAGG	ATTTTAAGTC	CTGTGCGTCT	GCCAGTTCCG	CCACCCCGGC	6420
CTCTCTAAGC	GAACGACGGG	ATTCGAACCC	GCGACCCCCA	CCTTGGCAAG	GTGGTGTTCT	6480
ACCACTGAAC	TACGTTGCA	CTGTTTTCTT	CTATCTAAAA	ATGCCGGCTA	CATGACTTGA	6540
ACACGCGACC	CTCTGATTAC	AAATCAGATG	CTCTACCAAC	TGAGCTAAGC	CGGCTCATTT	6600
GTTATATCTT	AATGCGGGTT	AAGGGACTTG	AACCCCCACG	CCGTTAAGCG	CCAGATCCTA	6660
AATCTGGTGC	GTCTGCCAAT	TCCGCCAAAC	CCGCATATAT	GACCCGTACT	GGGCTCGAAC	6720
CAGTGACCCA	TTGATTAAAA	GTCAATTGCT	CTACCAACTG	AGCTAACGAG	TCTAAAATAA	6780
cTTGCGTTAC	CTTAAACGGT	CCCGACGGGA	ATCGAACCCG	CGATCTcGCC	GTGACAAGGC	6840
GACGTG						6846

(2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2911 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GAATTCATTT	TAAATAAAGA	TACGGGAGAG	GTAAGTGAAT	TAAAACCTCA	TAGGGTAACT	60
GTGACCATTC	AAAATGGAAA	AGAAATGAGT	TCAACGATAG	TGTCGGAAGA	AGATTTTATT	120

1174

TTACCTGTTT	ATAAGGGTGA	ATTAGAAAAA	GGATACCAAT	TTGATGGTTG	GGAAATTTCT	180
GGTTTCGAAG	GTAAAAAAGA	CGCTGGCTAT	GTTATTAATC	TATCAAAAGA	TACCTTTATA	240
AAACCTGTAT	TCAAGAAAAT	AGAGGAGAAA	AAGGAGGAAG	AAAATAAACC	TACTTTTGAT	300
GTATCGAAAA	AGAAAGATAA	CCCACAAGTA	AACCATAGTC	AATTAAATGA	AAGTCACAGA	360
AAAGAGGATT	TACAAAGAGA	AGAGCATTCA	CAAAAATCTG	ATTCAACTAA	GGATGTTACA	420
GCTACAGTTC	TTGATAAAAA	CAATATCAGT	AGTAAATCAA	CTACTAACAA	TCCTAATAAG	480
TTGCCAAAAA	CTGGAACAGC	AAGCGGAGCC	CAGACACTAT	TAGCTGCCGG	AATAATGTTT	540
ATAGTAGGAA	TTTTTCTTGG	ATTGAAGAAA	AAAAATCAAG	ATTAAGATAA	AAGCTATAGA	600
AAAAAATGGT	TTATGTACTG	AGATTAGATA	GTGAGGTGAT	GACATAGTTT	TGTGAAAATA	660
GCCATTTATA	ACTCAATTAT	TTAGTTTACT	TTACTTTACT	AGTGATACTA	TTTGGAGTTA	720
TTAATGGACT	TAGTTTATAT	AACTAATGAA	TTGATTGAAA	GGGTTAGTAT	TGACAATATT	780
GGTCATATTG	ACTAGAAAAT	AGAGTCTATC	AAAATTTAAA	GGCTAATAGA	GGTGATGAGA	840
CAATTTTCGGC	TCTTTGTCAA	CTGTAGTGGG	TTGAAGTCAG	CTAAGCTCGA	GAAAGGACAA	900
ATTTTGTCTT	TTCTTTTTTG	ATATTCAGAG	CGATAAAAAT	CCGTTTTTTG	AAGTTTTCAA	960
AGTTTCGAAA	ACCAAAGGCA	TTGCGCTTGA	TAAGTTTGAT	GAGATTATTG	GTCGCTTCCA	1020
GTTTGGCATT	AGAATAGTGT	AGTTGAAGGG	CATTGACAAT	CTTCTCTTTA	TCTTTGAGGA	1080
AGGTTTTAGA	GGATGAACTT	GATTCAGATT	GTCCTCAATG	AGTCCGAAAA	ATTTGTCAGG	1140
CTCCTTATTC	TGAAAGTGAA	AAAGCAAGAG	TTGATAGAGA	TTATAGTGGT	GTTTCAAGTC	1200
TTCTGAATAG	CTCAAAAGTT	TATCTATAGT	AGATTGAAAC	TAGAATAGTA	CACCTCTGCT	1260
TCTAAAACAT	TGTTAGAAAT	CGATTTGACT	GTCCTGAATG	ATTTGTCCTG	TTATTATTTT	1320
ATTTTACTAT	AAATCCACGT	TTACGAATCT	CTTTCCACAC	TTGTTCAATG	GGGTTTCTCT	1380
CTGGTGTGTA	TGGAGGAATA	AATGCAAAAC	CAATATTAGT	CGGAATCTTT	AAGGTACTTG	1440
ATTTATGCCA	TATAGCATTG	TCCATAACGA	GTAAAAGATA	ATCATCTGGA	TAAGCTTGTC	1500
AAAGCTCCTA	TTCTTAAAGC	CCCTTTTATA	CCTCTTGCGA	GAGAGACTAT	TGACTCAGCC	1560
CTTACTTCAT	GCGGATGAAA	CTTCTTATCG	GGTTCTAGAG	AGTCATAGCC	ATCTGACCTA	1620
CTATTGGACC	TTTTTGTCTG	GGAAAGTTGA	GAATCAAGCA	ATCACGCTGT	ACCATCATGA	1680
TCAGAGTCGG	AGTGGTTCGG	TAGTACAAGA	ATTCCTAGGA	GATTATTCTG	GCTATGTTCA	1740
TTGTGATATG	TTGCGGCAGT	AACTTAGGAC	TTTAGTCCTC	TAGTTCTGCC	TATGCGATAG	1800
CAGTCCAAGG	TTTAGGAGCA	AGGCGACGCT	AAGCTTGGTA	AACTGCGAAC	CGCTAGAAGC	1860
TTATCGTCAA	CTGGAAGAAG	CTGAACCTGT	TGGATGTTGG	GCGCATGTGA	GAAGGAAATT	1920

1175

TTTTGAAGCG ACCCCCAAGC AAGCAGATAA ATCATCCTTA GGAGCTAAAG GTTTAGCTTA	1980
TTGTGATCAG TTATTTTCCT TGGAAAKAGA CTGGGAGGCT TTGCCAGCTG ATGAACGACT	2040
ACAGAAACGT CAAGAACATC TCCAGCCCCCT AATGGAAGAC TTCTTTGCTT GGTGCCGCCG	2100
TCAGTCAGTT TTAGCAGGTT CAAAAC TAGG AAGGGCAATT GAATACAGCC TCAAGTATGA	2160
AGAAACCTTT AAGACTATTT TGAAAGACGG ACATCTGGTC CTTTCCAATA ATCTAGCTGA	2220
ACGCGCCATT AAATCATTTG TTATGGGACG GAGTAAAAGA GTCCAGTGGA CTCTTTTAGC	2280
CTGAGCTCAG TTTAAAAAAG CGAGGGTGGT TATTTTCTCA AAGTTTTGAA GGAGCTAAAG	2340
CAAGAGCTAT TGTTATGAGC TTGTTGGAAA CAGCTAAACG TCATCAATTA TAGTGCGTTG	2400
AATCTATAAC AGTACGCATC GACTGCTAAA ACATTTCTAT AAATCAATTT TCCTTTCCTA	2460
ATCGATTTGT TCATATCTTA TTTCAATCCA TTATAAATAG CGAGAAATAT CTATCCTATC	2520
TTCTAGAATG TCTTCCAAAC GAGGAACTC TCGTAAACAA AGAGGTTTTA GAGGTTTATT	2580
TACCATGGAC TAAAGTTGTA CAAGAAAAGT GCAAATAAGA AATCTCCAGA TTAGGAACTA	2640
TCCGTGAGTT CACTAATCTG GAGATTTTTC AATAGATTCG TTATTGGGCG GTTACGATAT	2700
GATcACTACT TCGTCAGTCT TATCTACAAC CTCAAAACAG TGTTTTGAGC AACCTGCGAC	2760
TAGCTTCCTA GTTTACTCTT TGATTTTCAT TGAATATTAG AACAGAAAAA ATGCTTGGAG	2820
TATTTGTTTG TGTGTTTATT TTTATATAAC AACTATAAA CAAAATAAAA ATATAAAAAA	2880
AGAGACAAAA AAGAACAGAA AGTAATTGAC A	2911

(2) INFORMATION FOR SEQ ID NO: 200:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6854 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

GAAAATAAGT CTTGACAGAA AGCGCTATCA ATGATAGAAT GAATTCAGAT AAAAAGATTT	60
ATTTTAAAA CAAAATGAA ACGTTTCAAA AAAAGAAATA AAGAGACAGC GCCAAGCGCT	120
ATCTTTTCTA GAAAAAATG AAACGTTTCA AAAAAGGAGG TTGCTATGAA TAGCAAAGCG	180
AAGCAAGTTT CTCTTTGGGA AAGAATCAAG AAACAAAAAC TCTTGTTATT GATGACTGTC	240
CCCGGTTTAG TTTAACCTT TATCTTTAAA TACATCCCTA TGTATGGGGT TTTAATCGCA	300
TTTAAAGATT ACAATCCTTT AAAAGGAATT TTAGGGAGTG ATTGGATTGG TTTTCTGAG	360

1176

TTTACAAAAT	TCATATCCTC	TCCCAACTTT	GGTATCTTGT	TAGCCAACAC	ATTAAAATTA	420
AGTATCTATG	GTTTATTGCT	TGGCTTTTTA	CCACCAATCA	TTCTCGCGAT	TATGCTCAAT	480
CAACTCTTGA	GTGAAAAAGT	CAAAAAACGA	ATTCAGCTCA	TTTTATACGC	ACCAAACTTT	540
ATCTCAGTCG	TTGTTATTGT	CGGTATGATT	TTCCCTCTCT	TTTCAGTGGG	AGGACCAATC	600
AACAATTTTC	TTTCTATGTT	TGGAATGAAG	GCTGACTTCT	TGACAAATCC	AGACTTCTTT	660
AGACCTTTAT	ACATCTTTAG	TGGTATCTGG	CAAGGAATGG	GCTGGGCTTC	AACGCTCTAC	720
ACGGCAACAT	TGGTAAATGT	AGATCCAGCC	TTAGTAGAAG	CAGCCCGACT	GGATGGAGCC	780
AATATCTTCC	AACGAATCTG	GCACATTGAT	ATTCCAGCTC	TTAAGCCTAT	TATGGTTATC	840
CAATTTGTTT	TAGCTGCAGG	TGGAATTATG	AATGTCGGAT	ATGAAAAAGC	ATTCTTGATG	900
CAGACATCGT	TAAATTTGCC	AACTTCTGAA	ATTATCTCGA	CATATGTCTA	TAAAGTTGGT	960
CTTGTATCAG	GAGACTATTC	TTACTCAACA	GCGGTTGGTT	TGTTTAATGC	AGTGATTAAC	1020
GTAGTATTGC	TTGTTGCAGT	TAACCAAATC	GTTAAACGCA	TGAATAATGG	TGAAGGAATT	1080
TAAGGAGGAA	AGTATGAAAA	ATTCGATTAT	GGATACAAAA	TTTGATAGAC	GTATCTTACT	1140
CTTAAATAAA	ATCATTATTG	TCTTTATCGT	TTTGATGACT	TTGCTTCCTT	TACTTTFATAT	1200
CGTCGTAGCA	TCCTTTATGG	ATCCTAAGGT	TCTGGTTAGT	AGAGGGATTA	GCTTTAATCC	1260
AGCCGATTGG	ACTGTAGAAG	GTTACCAGCG	TGTATTCACT	GACCAATCTA	TTCTAAGAGG	1320
TTTTATCAAT	TCTCTACTAT	ACTCTTTTGG	ATTTGCAGCT	TTAACAGTCT	TGCTATCTGT	1380
GTTTACAGCT	TATCCTCTTT	CTAAGAAAGA	CTTGGTTGGA	CGTCGTTGGA	TTAACTACTT	1440
CTTGATTGTA	ACTATGTTCT	TTGGTGGTGG	TTTAGTCCCA	ACTTACTTGC	TCGTAAAAGA	1500
ATTGGGAATG	CTCAATACTC	CATGGGCTAT	CATTGTTCCA	GGTGCTGTTA	ACGTTTGGAA	1560
TATTATTCTT	GCTAGGGCCT	ATTTCCAAGG	ATTGCCTGAA	GAATTAGTTG	AAGCTGCTGT	1620
CATTGATGGT	GCAAATGATT	TACAGATTTT	CTTCAAAATC	ATGCTTCCTC	TTGCAAAACC	1680
AATTATGTTT	GTTCTCTTCC	TTTATGCTTT	TGTAGGACAG	TGGAACATCAT	ACTTTGATGC	1740
AATGATTTAT	ATCAAGGATC	CAAACCTGGA	ACCATTGCAA	CTTGTAATTC	GTAAAATTCT	1800
CATTCAGAGC	CAACCAGGTC	AAGACATGAT	TGGAGCACAA	GCGGCTATGA	ATGAAATGAA	1860
ACGTTTAGCT	GAATTGATTA	AATACGCAAC	TATTGTCATT	TCCAGCTTGC	CATTGATTGT	1920
TATGTATCCA	TTCTTCCAAA	AATACTTTGA	TAAAGGAATT	ATGGCTGGTT	CACTTAAAGG	1980
ATAAAAAAAG	AAAAAATAAA	AGGAGTTTTT	TCATGAAATT	CAAAACATTC	TCAAAATCAG	2040
CAGTTTTGTT	GACAGCTAGT	TTAGCAGTAC	TTGCAGCCTG	TGGCTCAAAA	AATACAGCTT	2100
CAAGTCCAGA	TTATAAGTTG	GAAGGTGTAA	CATTCCCGCT	TCAAGAAAAG	AAAACATTGA	2160

1177

AGTTTATGAC	AGCCAGTTCA	CCGTTATCTC	CTAAAGACCC	AAATGAAAAG	TTAATTTTGC	2220
AACGTTTGGA	GAAGGAAACT	GGCGTTCATA	TTGACTGGAC	CAACTACCAA	TCCGACTTTG	2280
CAGAAAAACG	TAACTTGGAT	ATTTCTAGTG	GTGATTTACC	AGATGCTATC	CACAACGACG	2340
GAGCTTCAGA	TGTGGACTTG	ATGAACTGGG	CTAAAAAAGG	TGTTATTATT	CCAGTTGAAG	2400
ATTTGATTGA	TAAATACATG	CCAAATCTTA	AGAAAATTTT	GGATGAGAAA	CCAGAGTACA	2460
AGGCCTTGAT	GACAGCACCT	GATGGGCACA	TTTACTCATT	TCCATGGATT	GAAGAGCTTG	2520
GAGATGGTAA	AGAGTCTATT	CACAGTGTCA	ACGATATGGC	TTGGATTAAC	AAAGATTGGC	2580
TTAAGAAACT	TGGTCTTGAA	ATGCCAAAAA	CTACTGATGA	TTTGATTAAA	GTCCTAGAAG	2640
CTTTCAAAAA	CGGGGATCCA	AATGGAAATG	GAGAGGCTGA	TGAAATTCCA	TTTTCATTTA	2700
TTAGTGGTAA	CGGAAACGAA	GATTTTAAAT	TCCTATTTGC	TGCATTTGGT	ATAGGGGATA	2760
ACGATGATCA	TTTAGTAGTA	GGAAATGATG	GCAAAGTTGA	CTTCACAGCA	GATAACGATA	2820
ACTATAAAGA	AGGTGTCAAA	TTTATCCGTC	AATTGCAAGA	AAAAGGCCTG	ATTGATAAAG	2880
AAGCTTTTCGA	ACATGATTGG	AATAGTTACA	TTGCTAAAGG	TCATGATCAG	AAATTTGGTG	2940
TTTACTTTAC	ATGGGATAAG	AATAATGTTA	CTGGAAGTAA	CGAAAGTTAT	GATGTTTTAC	3000
CAGTACTTGC	TGGACCAAGT	GGTCAAAAAC	ACGTAGCTCG	TACAAACGGT	ATGGGATTTG	3060
CACGTGACAA	GATGGTTATT	ACCAGTGTA	ACAAAAACCT	AGAATTGACA	GCTAAATGGA	3120
TTGATGCACA	ATACGCTCCA	CTCCAATCTG	TGCAAAATAA	CTGGGGA	TACGGAGATG	3180
ACAAACAACA	AAACATCTTT	GAATTGGATC	AAGCGTCAAA	TAGTCTAAAA	CACTTACCAC	3240
TAAACGGAAC	TGCACCAGCA	GAAGTTCGTC	AAAAGACTGA	AGTAGGAGGA	CCACTAGCTA	3300
TCCTAGATTC	ATACTATGGT	AAAGTAACAA	CCATGCCTGA	TGATGCCAAA	TGGCGTTTGG	3360
ATCTTATCAA	AGAATATTAT	GTTCCCTTACA	TGAGCAATGT	CAATAACTAT	CCAAGAGTCT	3420
TTATGACACA	GGAAGATTTG	GACAAGATTG	CCCATATCGA	AGCAGATATG	AATGACTATA	3480
TCTACCGTAA	ACGTGCTGAA	TGGATTGTAA	ATGGCAATAT	TGATACTGAG	TGGGATGATT	3540
ACAAGAAAGA	ACTTGAAAAA	TACGGACTTT	CTGATTACCT	CGCTATTAAA	CAAAAATACT	3600
ACGACCAATA	CCAAGCAAAC	AAAAACTAGA	GGTTGATTAT	GGGAGATAAG	AAATACACAG	3660
TAGAAAAAGC	CAATCGTTTT	ATAGCAGAAA	ATAAACATCT	CGTTAATACT	CAATATAAGC	3720
CTGAAGAACA	TTTTTCAGCT	GAGATTGGTT	GGATCAATGA	TCCAAATGGA	TTTGTCTATT	3780
TTCGTGGAGA	ATACCATCTC	TTTTATCAAT	TCTATCCATA	TGATAGTGTT	TGGGGGCCTA	3840
TGCACTGGGG	ACATGCTAAA	AGTAAGGACT	TGGTGACTTG	GGAGCACTTG	CCAGTGGCAC	3900

1178

TTGCTCCTGA	CCAAGATTAT	GACCGAAATG	GTTGTTTCTC	AGGCTCTGCC	ATTGTCAAGG	3960
ATGATCGCCT	CTGGCTCATG	TACACTGGAC	ATATCGAAGA	AGAAACCGGT	GTCCGCCAAG	4020
TGCAAAATAT	GGTATTTTCA	GATGACGGGA	TTCACTTTGA	AAAGATTTCC	CAAAATCCAG	4080
TTGCAACTGG	ATCAGACTTA	CCAGATGAGT	TGATTGCTGC	TGATTTCCGT	GATCCAAAAC	4140
TCTTTGAAAA	AGATGGACGC	TATTACTCCG	TAGTAGCTGC	CAAACACAAG	GATAATGTGG	4200
GCTGTATCGT	TCTACTAGGG	TCCGATAACC	TAGTAGAATG	GCAGTTCGAA	TCCATCTTTT	4260
TAAAAGGGGG	AGAACACCAA	GGTTTTATGT	GGGAATGCCC	AGATTACTTC	GAGTTAGATG	4320
GGAAAGATTG	CCTTATTATG	TCACCCATGC	GTTATCAGCG	TGAGGGAGAC	TCATATCATA	4380
ACATCAACTC	ATCGCTTTTG	TTCACGGGTA	AGGTAGATTG	GAGAGAAAAA	CGTTTTATCC	4440
CAGAATCAGT	TCAAGAAATT	GATCATGGCC	AAGACTTCTA	TGCGCCTCAA	ACATTGTTGG	4500
ACGATCAAAA	TCGTCGTATC	CTGATTGCTT	GGATGCAGAC	ATGGGGGCGT	ACCCTTCCAA	4560
CCCATGACCA	AGAACACAAG	TGGGCATGTG	CCATGACTCT	ACCTAGAATT	CTAAGATTGG	4620
AAGATGGCAA	ACTAAGACAA	TTCCCTGTTA	AAAAAGGCCA	ATATCAAATC	CAAATAGATA	4680
AAGATTGTCA	TTACCACTTA	GGAAATGATA	TAGATTATCT	TGAATTTGGT	TATGACAGTA	4740
ATGCGCAGCA	AGTTTACATT	GATCGTAGCC	ATCTTATTCA	AAAAATTCTA	GGTGAAGAAG	4800
AACAGGACAC	TAGTCGACGG	TATGTAGATA	TTGAAGCTAA	AGAATTGGAA	GTTGTTCTAG	4860
ATAAAAATTC	CATCGAGATT	TTTGTCAATC	AAGGTGAAGC	AAGCTTGACT	GCAACTTATT	4920
ACTTAACGGT	GCCAGCTGAG	CTATCACGAA	TTGATTAAAA	ATTAAGTTAT	TTCTCCTAAA	4980
GAAAAAGTTC	TCTTTCTAAA	ATAGTGAAAA	GAGGACTTTT	TGTGTTTTGG	GTATATAAGC	5040
TTAGTTTATG	GTATTTGTAA	AATTGGTGTT	GGATTATGAT	TTAAGCTAGT	TTTCTAAAGA	5100
ATTTGAAAAA	AATTTTATTT	AAGCAAAAAA	ACCTTGGTTC	CAAGGCTTTT	CCTGTTGTAT	5160
TTAGATGCCC	CCTACAGGGA	TTGTAGGAGA	TATGTTGCTT	AGATGTTCTT	GATTTTCTGG	5220
TGTTTTGTAA	CGTTTAAATG	AGTTTTTTGA	GTTTGTGGT	GGGGCGTTGC	CCGGCAATTG	5280
CCCGACTTAT	TGCTTGAAAA	AGAATTTAAA	ATATAGTATA	GTAAATTATA	GATTAACACT	5340
TGCTTGGAGG	AAGTGATGAA	GAACAATGAA	AGATTAGGTA	TTAAATTAAG	TAGAGATAGC	5400
GTTTTAGGAT	TGAGGGAAGT	TAGAAGGCTT	TATTTAGGCA	GTTTCAGATAT	CCCAGTTTCT	5460
GATGGCTATG	TGATTGAAGT	TGCTTATAAC	CAGATATCAC	ATGAGATTGA	TATTATTGAT	5520
TGGGTAGAGT	TGAACAAGTC	AAAAATTAAG	ATAAGTGAAA	TTAGTGAAAG	CGTGGATATA	5580
GATGCCACTA	GCTTGAGAAC	AACTTTGACT	TTAGACACAT	TAGTATATGA	AGGTATGAGA	5640
GATATACAGT	TAAAGTTGAG	AGAGCTTACA	AAGGGGAGAG	TATTCCTTTC	ATTTGTAGTG	5700

1179

AAGTTAGTTT TGTTTGCTTC TATTTTAAAG AAAAAAGATT TACTAGAAAA ATTTCAAGAA	5760
AAGTGTTAAT CAAGTATTGA CACTTTATCT GGATTTCCGT ATAATATGCT TAGAAAGGAA	5820
TCTTTCTAAA TTTTTTTCGT CCTTATGTGT TAATCAAAGA CGAATACAAA AACATATTTT	5880
TTTACTCTAA AAAGTGTTAA TCAATGATGT ATTTGTTAGA GAGGTAGATA AATGGAATTG	5940
AGAGCACCAC CAGTTATAAT AGTATAAAAC GTATAATAAA AATATTTTAA CTTGAATTAT	6000
AGAAAAGGAG AAACAAATCA TGAAACAAAA ACAACCGATT GTTTCTAGAA CGAAACAACA	6060
TACATTTGAA GAGCTTATTC AAGACCAAAA GTTAGAAAGA TTGGCTAAGT TGTCGCCCCG	6120
TTTGGTTGGA AGGTATGGTT TTTACTGCTAG CTGTGCGTCT TCATTTGCGA ACTTGATTAA	6180
AGAAGCGTAT GGGGGTAAAA ATCTAAACGT AGTTTATGCG AGTCGGATGT TGGCTCTCTG	6240
GAATATTGCT TGCAGTTGTT ATCATAAGGC TGATGGGTAT TCTTTAGCAG ATGCGCTTTT	6300
TAGTGATAAA AAAATTTGTC TAGATTCTTA CTATTACCAC AAGAATACCT CTAATACCAT	6360
AACTAGTGAT GTGATAAAAG ATGTTTACGA TAATTATAAT AATTATATGG TTTTAACTCG	6420
AGAAGCGACA CCTGAATACA TTTATGTTGT ACAAAC TGAA ATGCCAAAAG ATTCAGATTT	6480
ATATTTTAT ATTAGAGAAG TTCTGGGATT ATCGTTTAGT ACCATGCATT ATGCATTTT	6540
AGTCAAGGTT CTTGCAGGAG CGCTTGCTAG AAAATATAAG CCATATCGAA ATTGAATTAT	6600
TTAAATTTAT ACTCTTCGAA AATCAAATTC AAACCAAGTC AGCTTCGCCT TGCTGTACTC	6660
AAGTGCTGTC TGTGGCTAGC TTCTTAGTTT GCTTTTGTAT TTTCATTGAG TATTACTCTT	6720
ATGGTAGTTA TTTATGGCAT AATAATATTG ATTTGGGAGT TATAGCGAAA ATTTTAGGTT	6780
CTATAATATT TGTAGTGGGT AAACCACTAT AGATATTATG GAGCCTATTT ATTGTAGAAA	6840
AAAGTCCCAT ATGA	6854

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3895 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

TCCTTGCTAA GTTTATACTC AATGAAAATC AAAGAACAAA CTAGGAAGCT AGCCACAGGT	60
TGCTCAAAGC ACCGCTTTGA GGTGTCAGAT AAAACTGACA CGGTTTGAAG AGATTTTCGA	120
AGAGTATTAA TTTACATAAA TAGCCAGTGT TTGATAGGGT TTGAGTAGAA TTTTCTCAGA	180

1180						
CACTTCTGCA	TCTTCATAGT	TTGATATCAA	AATCTGTCCA	TTTTGGTAGA	CTGCTGGCAA	240
GTCGATTTCa	CTTCTTTAGC	ATAAAAGTTA	TTGAGCACTA	GTAACCTTTG	ATCCTCAAAC	300
TGGCGTTCAA	AAGCGTAGAC	TTGTTTGCTA	TCTTCAAAGG	CTGGTTTGTA	ACTTCCTTCT	360
GAAATGATTG	GCATTTCCCT	ACGCATCGAA	TCAAGTCTTG	ATAGAAGGTA	AAAATCGGAC	420
CCTGGATTTC	ATTTTCTACA	TTGATGTATT	TATAGGATTT	ACCAGCTTTC	AACCAAGGAG	480
TGCCTGTTGA	AAATCCTGCA	TTTTCCGAAG	CATCCCCTG	CATGGGAATG	CGTGAATTAT	540
CACGCGACTT	AGCTTGAATA	ATCTGGAAGG	CTTCTTGCTG	ACTCTTTCCT	TCTTCTAAGA	600
GCATCTGATA	GGCATTAAAG	GATTCGACAT	CCACATAATC	AGCCATAGAA	TCATAGTCTG	660
GGTCAATCAT	CCCGATTTCC	TCACCCATGT	AGATATAAGG	TGTCCCACGT	GACAGGTGAA	720
TGCTGGCTGC	TAGCATGGTG	GCTCCTTCCT	TGCGGAAGTT	TTGAATATCG	ACAAAACGGT	780
TCAAGGCACG	TGGTTGATCG	TGATTATTCC	AAAAGAGGGC	ACTCCAACCG	TCTTTATCAC	840
TCATTTCCCT	ACCCCAACTA	TGGTAAAGAC	TCTTCAACTC	TTCAAAATCA	AAGGGAGCCA	900
AGGTCCACTT	TTGTCCATCC	TTATAGTCCA	CCTTGAGGTG	ATGAAAATTA	AAGGTCATGG	960
ATAATTCCTG	ACGATCAGGC	GACGAATAGA	GGACACAGTT	TTCCATGGTG	GTAGAAGACA	1020
TTTCCCCAAC	TGTCATAAAG	CTATCGTCGG	ATCCAAAAGT	GGCTTGGTTC	ATCATACGCA	1080
AATAGTTATG	AACGATGGGT	TTGTCTGTAT	AAGCTGGCTT	CCCTTCATTT	TCAGGACAGT	1140
CCACTGAAAC	CTCGTCCTTA	CCGATCAAAT	TGATCACATC	AAATCGGAAA	CCTTTGACAC	1200
CCTTGTCGCG	CCAGAAATTA	ACAACCTTGA	AAAGCTCCTT	ACGGACATTG	GAATTGCGCC	1260
AGTTAAGGTC	AGCCTGGGTC	TCATCAAATA	GGTGAAGATA	GTATTTCCCA	GTATCCCCGA	1320
AAGGCGTCCA	TGCAGAACCA	CCAACTTAG	ACTGCCAATC	TGTTGGTTGG	TCTTGGATGA	1380
AGAAAAAGTC	TTGATAATAC	TTATCACCAG	CTAGGGCTTT	CTGAAACCAT	TCATGCTCTG	1440
TCGAACAATG	ATTAAGTACC	ATGTCCAGCA	TAAAGTCAAT	CTTGTGCTCT	TTACCGACAC	1500
ACACCATTTT	CTCAAAATCA	GCCATATCAC	CAAAAAGAGG	ATCCACTGCC	ATATAATCTG	1560
AAATATCGTA	ACCATTATCC	CGTTGAGGGC	TTGGATAGAA	TGGATTGAGC	CAGACCATAT	1620
CCACACCTAG	TTTGGCTAAA	TAGGGAATTT	TTTCGATAAT	CCCACGGAAA	TCCCCAATAC	1680
CGTTTTCAGT	GGTGTCTTTG	TAAGATTTTG	GATAGATTTG	ATAGACTACT	TTTCCTTTAT	1740
CAAGTGTCAT	CTGTTTCTCC	TTTCTGATA	AAAGGGAGGA	AGCAGTCTTC	CGTCCCTATT	1800
TGTGCTATTT	CAATTATACT	CAATGAAAAT	CAAAGAACAA	ACTAGGAAGC	TAGCCACAGG	1860
TTGCTCAAAA	CACTATTTTG	AGGTTGCAGA	TAGAGCTGAC	GTGGTTTGAA	GAGATTTTCG	1920
AAGAGTATTA	GATTCGTGTA	GCGACCATGA	GAGATGCTCC	AGCTTGGATC	GTTGTCCGAT	1980

1181

AAGTTCCGGG	AATAGTCGCT	GTATAAGCAT	CTTGGTTGGT	GATGATAACA	GGAGTTTCTG	2040
TCACCAGACC	TGCAGCCTTA	ATGACATCCA	TATCAAAACG	AATCAGTTGC	TGACCAACTG	2100
TAACGTGATC	TCCTTGGACT	ACAAGACTTT	CAAAACCTTT	GCCATCAAGA	CCTACTGTAT	2160
CCATACCGAT	GTGGATGAGC	AATTCAACTC	CCTCGTCAGA	GACAATGCCG	ATGGCATGCT	2220
TGGTAGGGAA	AAGAACCGTC	ACTGTCCCAT	TAACTGGAGA	GGTCAACTCA	CCTTGGCTTG	2280
GTTCAATGAC	TAGACCTTGC	CCCATGACAC	CTGATGCAAA	AATAGGATCC	GTCGCTTGAC	2340
TCAATTCTTT	CACTTGGCCA	GTTAGTGGGC	TGATAATTTT	TACCGAAGTA	AGTTCTACTG	2400
GTTTCATGGT	CACAAATTCT	GCTTCTTCTT	GAGCAACGAA	TTCTGCCTGC	AAGTTCGTAT	2460
CGCCCTCTGT	TTTTGTAAAG	AGACCAGCCT	TGCGGAAGAA	GAAAGTCAAG	AGCATTGGAA	2520
CAACAATCGC	AACTAGCATA	GTTCCCTGCAA	ATGGCAGCAT	GTATTGAGGT	TGAATAGAGA	2580
GAATACCTGG	CAAACCACCG	ATACCAATAG	AAGCCGCAGT	TACATTAAAA	GTAACGGATA	2640
ACATGCCTGC	AAGGGCTGAA	CCAGTCATCC	CAGCAACAAA	TGGATAAATA	TATTTTACGT	2700
TAACCCCAAA	AAGAGCTGGT	TCTGTAACAC	CGAGATAGGC	TGAAATGGTT	GCAGGAAGTG	2760
AAACCTGAGC	CTCACGCTCA	TCATGGCGAT	GCATGAAATA	ATAGGCAAAC	ACGGCTGAGC	2820
CTTGAGCAAT	ATTAGAAAGA	GCAATCATTG	GCCATAGGGC	AGTGCCACCA	GCATCCGCAA	2880
TCAATTGTGT	ATCAATGGCA	TTGGTCATAT	GGTGCAGACC	TGTGATGACA	AATGGAGCGT	2940
AGAGGGCGCC	AAAAATTGCA	CCGAAGAGCC	ATTTAACTGG	ACCAGTTAAA	CCTGCCAAGA	3000
CAACTGATGA	AAGTCCTTGT	CCAATTGTCC	AACCGATTGG	TCCCCAAAACA	GTATGAGCCA	3060
AAATCAAGGC	TGGAATCAAT	GACAAGAAAG	GTACAAAAAT	CATAGAAATG	ACTTCTGGGA	3120
TATGCTTGTG	CCAGAAGATT	TCAAGATAAG	ACAGACTCAA	ACCTGCAAGC	AAGGCTGGGA	3180
TAACTTGGGC	TTGGTAACCG	ATACGATTAA	CAGTAAAATA	GCCAAAATTC	CAAACCCAGT	3240
TTGCCGCGAT	ATCAGCTGCT	GGCGTTGAAG	CAACCGCATA	GGCATTGAGC	AACTGAGGCG	3300
ATACCAAACA	GATTCCGAGA	ACAATTCCCA	AAATTTGGCT	GGTTCCCATC	TTACGAGAAA	3360
CAGACCAAGT	AATCCCTACT	GGTAAGAACT	GGAAGATAGC	TTCACCAGGC	AACCAGAGGA	3420
AGTGATTGAC	ACCTGCCCAA	AACTGAGAGG	ATTCTGTGAT	GGTCTTGCCA	TCCAACATCG	3480
ACCAATGGAC	ACCTTCCAAG	ACATTACGGA	AACCGAGGAT	CAATCCTCCG	ACTATCAAGG	3540
CTGGAATAAT	CGGAGTAAAA	ATCTCCGCCA	GAGTGGTCAT	AACACCTTGG	ACCACGTTTT	3600
GATTACTCTT	AGCTGCAGAC	TTGGCTGCTT	CTTTGGAAAC	ACCTTCAATA	CCTGAAACGG	3660
CTGTAAAAATC	ATTATAAAAG	ATGGGCACGT	CATTTCCAAT	GATTACCTGA	AATTGACCTG	3720

1182

CATTTGTAAA	GGTTCCTTTA	ACAGCTGGAA	TTGACTCGAT	AGCTTTAACA	TTAGCCTTCT	3780
TATCATCTCC	TAAAACAAAC	CGCATCCGTG	TCGCACAGTG	AGTTACGGCA	GTCACATTTT	3840
CTTTGCCTCC	GATTGCCTGA	AGCAGATCTT	TGGCTTCTTG	TTCAAATTTT	CCCGG	3895

(2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3936 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

AGGATCGCCG	CTCCAGCTAC	TAAGTCTCGT	GCAGTGCCGA	TTTATCAAAC	AACATTTTTTT	60
GTTTTTGATG	ACACGTAGGA	AGGTGCCGAT	CTGTTTGCCT	TGAGGAAACC	AGGGAACATT	120
TATACTCGTA	TCACCAATCC	TACAACAGCT	GCCCTTGAAG	GTGGTGTTGA	AGCGCTAgcA	180
ACAGCATCAG	GTATGACTGC	AGTGACTTAT	ACGATTTTGG	CGATTGCCCA	TGCTGGTGAC	240
CATGTAGTGG	CTGCTTCGAC	TATTTACGGT	GGAACCTTCA	ATCTTTTGAA	AGAACCCCTT	300
CCTCGTTATG	GTATCACAAC	AACCTTTTTTC	GATATTGATA	ATTTGGAGGA	AGTAGAAGCA	360
GCTATCAAAG	ACAATACCAA	GCTTGTCTTG	ATTGAAACCT	TGGGTAACCC	CTTGATTAAT	420
ATTCCAGACC	TGGAAAAACT	GGCAGAGATT	GCTCATAAAC	ATCAAATCCC	ACTTGTGTCA	480
GACAATACTT	TTGCAACACC	TTATTTGATT	AACGTCTTCT	CTCATGGCGT	TGACATTGCC	540
ATTCACTCTG	TGACTAAGTT	TATCGGTGGG	CATGGTACAA	CTATTGGAGG	AATAATTGTC	600
GATAGTGGTC	GTTTTGACTG	GACGGCTTCA	GGGAAATTCC	CTCAATTTGT	TGACGAGGGT	660
CCAAGCTGCC	ACAATTTGAG	CTATACTCGT	GATGTGGGTG	CAGCAGCCTT	TATTATAGCT	720
G TTCGAGTTC	AATTGCTTCG	TGATACAGGT	GCAGCCTTGT	CACCATTCAA	TGCTTTCCTC	780
TTGCTACAAA	GACTTGAAAC	CTCTTCACTT	CGTGTGGAAC	GCCATGTACA	AAATGCTGAG	840
ACAATTGTTG	ATTTTCTTGT	CAACCATCCT	AAGGTAGAAA	AGGTAAATTA	TCCAAAACCTT	900
GCAGATAGTC	CTTATCATGC	CTTGGCTGAG	AAATACTTGC	CAAAAGGTGT	CGGTTCAATC	960
TTTACCTTCC	ACGTCAAAGG	TGGCGAGGAA	GAAGCACGCA	AGGTCATTGA	TAATTTAGAA	1020
ATCTTTTCTG	ACCTTGCAAA	CGCGGCAGAT	GCTAAATCGC	TTGTTGTCCA	TCCAGCAACA	1080
ACCACTCACG	GTCAATTGTC	AGAAAAAGAC	CTAGAAGCAG	CAGGTGTCAC	ACCAAACATA	1140
ATTCGTTTGT	CAATCGGTCT	TGAAAATGTA	GAAGATTTGA	TTGAAGACTT	GCGCTTGGCC	1200
TTGGAAAAAA	TTTAAAGTAA	AAGAAGATAA	ACAGTGGGCT	TCGACTCACT	GTTTTTGATT	1260

1183

TTCCCTCAGG	CATGATATAA	TGGTTACAGA	AGTCTAGAAA	GAGGAACGAT	ATGAACGAAA	1320
TCAAATGTCC	CAACTGTGGG	GAAGTCTTTA	CAGTAAATGA	GAGTCAGTAT	GCCGAACCTCT	1380
TGTCCCAAGT	GAGAACGGCA	GAGTTTGATA	AGGAACTACA	CGATAGGATG	AAGCAGGAAC	1440
TGGCCTTGGC	TGAGCAAAAAG	GCCATGAATG	AGCAACAGAC	TAAACTGGCT	CAGAAGGATC	1500
AAGAAATTGC	GCAATTACAG	AGTCAGATCC	AAAACCTTTGA	TACAGAAAAA	GAATTGGCCA	1560
AGAAAGAGGT	TGAACAGACA	AGCCATGAGG	CTCTCTTGGC	TAAGGACAAG	GAAGTACAGC	1620
TCTTAGAAAA	TCAGTTGGCT	ACCTTGCGTT	TGGAGCATGA	AAATCAACTA	CAAAAGACCC	1680
TTTCTGACCT	AGAAAAAGAA	CGGGATCAGG	TTAAAAACCA	ACTACTTTTG	CAGGAAAAGG	1740
AAAATGAATT	ATCTTTGGCT	TCTGTTAAGC	AAAACCTACGA	AGCCCAGCTC	AAGGCAGCTA	1800
GTGAACAAGT	CGAGTTTAT	AAGAATTTTA	AGGCTCAACA	ATCTACAAAA	GCGATTGGGG	1860
AAAGCCTAGA	ACAGTATGCA	GAGAGTGAGT	TTAACAAGGT	TCGTAGTTTC	GCCTTTCCAA	1920
ATGCTTACTT	TGAGAAGGAT	AACAAGGTCT	CTTCGCGTGG	GTCTAAAGGG	GACTTTATCT	1980
TCCGTGAGTG	TGATGAAAAT	GGAGTTGAAA	TCATTTCTAT	CATGTTTGAG	ATGAAAAACG	2040
AAGCGGACGG	AACAGAGAAG	AAGCACAAGA	ATGCAGATTT	TTACAAGGAA	TTGGACAAGG	2100
ACCGTCGGGA	GAAGAACTGT	GAGTATGCCG	TTTTGGTGAC	CATGCTTGAG	GCTGATAATG	2160
ACTACTTTAA	CACAGGGATT	GTTGACGTCA	GTCACGAGTA	TGAAAAAATG	TATGTTGTTC	2220
GTCCTCAATT	CTTTATCCAA	TTGATTGGTC	TCTTACGTAA	TGCGGCGCTA	AATTCCTTAA	2280
AATACAAGCA	GGAGTTGGCC	TTGGTTCGCG	AGCAAAATAT	TGACATTACG	CATTTTGAGG	2340
AAGATTTGGA	TGCCTTTAAG	CTAGCTTTTG	CTAAGAACTA	TAATTCAGCT	TCGACTAACT	2400
TTGGAAAAGC	TATTGATGAA	ATCGACAAGG	CCATCAAACG	CATGGAAGAG	GTTAAGAAAT	2460
TCCTGACCAC	ATCTGAAAAC	CAACTCCGTT	TAGCTAACAA	CAAATTGGAA	GATGTCTCTG	2520
TTAAAAAATT	GACCCGGAAA	AATCCAACAA	TGAAAGCGAA	GTTCAAGCA	CTGAAGGGGG	2580
AGTAGAAAGC	AAAAATGAAC	GGTATTATTA	ACTTAAAAAA	GGAAGCAGGA	ATGACCTCGC	2640
ATGATGCGGT	TTTTAAACTG	CGTAAGATTT	TGGGAACCAA	GAAAATTGGT	CATGGTGGAA	2700
CCTTGGATCC	GGATGTGGTG	GGTGTTTTGC	CGATTGCGGT	TGGCAAGGCG	ACACGCATGG	2760
TCGAGTTTAT	GCAGGACGAG	GGTAAGATCT	ATGAGGGGGA	AATCACTCTG	GGCTATTCCA	2820
CGAAGACTGA	GGATGCTAGT	GGGGAAGTGG	TCGCAGAAAC	CCCTGTTTTG	TCTCTCTTGG	2880
ATGAAAAGCT	TGTTGATGAA	GCGATTGCTA	GCTTGACTGG	GCCTATTACT	CAGATTCCCC	2940
CTATGTATTC	GGCAGTTAAG	GTTAATGGTC	GCAAGCTCTA	TGAGTATGCG	CGTGCTGGTC	3000

1184

AGGAAGTGGG	GCGTCCAGAA	CGTCAGGTGA	CCATTTATCA	ATTTGAGCGA	ACAAGTCCGA	3060
TTTCTTATGA	TGGCCAACTT	GCCCGATTCA	CTTTTCGTGT	AAAATGCAGT	AAAGGGACGT	3120
ACATCCGTAC	TTTGTCAGTT	GATTTGGGTG	AAAAGCTTGG	TTATGCGGCT	CATATGTCCC	3180
ATTTGACTCG	TACTAGTGCT	GCTGGCTTAC	AATTAGAAGA	CGCTCTTGCC	TTGGAGGAAA	3240
TTGCTGAAAA	AGTAGAGGCT	GGGCAATTAG	ATTTTCTCCA	TCCTTTAGAG	ATTGGGACAG	3300
GTGACCTTGT	CAAAGTTTTC	CTAAGTCCAG	AAGAGGCTAC	AGAAGTTCGC	TTTGGTCGTT	3360
TTATTGAGCT	AGACCAAACG	GACAAAGAAC	TGGCTGCCTT	TGAAGATGAT	AAATTGTTAG	3420
CCATTCTAGA	AAAACGGGGC	AATCTCTATA	AGCCAAGGAA	GGTTTTTAGC	TAGATCGTTT	3480
AGGAATAAAA	ATCGGGTGAT	AGATAACAAT	TGCTTGATAA	AACCCCATAC	TAATAGTAGA	3540
ATGGTTTTGG	GAATTATAAT	ATTCCAATTG	TTGCGAGTTG	TAGGTACTCA	AATAATCTAT	3600
ATAGAAATTT	AGAGGTGTGA	AATGAAGCAA	TTTAAAATTC	TTTCAGATAA	ATATTTAGAG	3660
TCCATTACAG	GTTCTGATGG	GAACCTAGGC	CCAGGATTTG	GTGTGATAAT	TCCATGATGC	3720
GAAATGAGTT	TCGAGAAAGG	GTGGAGCAAC	TTCTTCAACA	AAAAGAAATA	AATGAAAATA	3780
GTGAGTTGAG	TCACCTGTTT	CGTCTTGCTA	TACAAAATTT	AGACAGAAAT	GAAAAATACC	3840
AATCGGTCAT	GGCCAATTTG	AGTCAAGGGT	TGTCACTTTA	CCTCATGACG	CATCATTACC	3900
AGGCACCTAA	GTCTGTCATT	GATTTTGTTT	TATGGA			3936

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

CATCCAGCAA	CTGCTCCTCT	GAGCGTTTCA	AAATTGATGT	AATTTTTCTA	GTTTTTTCTA	60
ATAAATGTGC	CATTTTTTCA	CTCGAATTTA	ATCGCTATCA	TTATAACATA	AAAACGTCTC	120
TTTTTCAATA	ATTATCTGAA	AATTCCTTAT	TGACTTGCAT	TGACTTACAA	TTTAATTAAA	180
AACCAGAATA	TTTTTAATTA	AATTGTTTCT	TTTCTATTGA	CAAGTTGCCT	ATTTTTGTGT	240
ATCATAATAT	TATAAAAGAT	AATATAATAA	TTTTATTGTG	CTTTTCACAT	TCGGTCTCCT	300
TATATAAAAA	AGCGATTTCAT	TTTGAACCGC	TTTTTCTTAT	TTATCGCCTT	TGTTACGAAT	360
AACAAAGCCT	GTTTGCTTTT	CGCTTAAAGT	ATTGCGTGGT	TTTTTATTAT	CCTTACGGTA	420
ACGTTTTTCC	TTATCAAAAC	GATCGTTGCC	ACGACTTCCT	TTTTTGAAC	CATCACGGCG	480

1185

ACCATTGCCA	CGGCGATCAC	GCTCTCGACG	GTCGTCCCCA	CGACGGCCTC	CACGACCTCC	540
CTTAGCTTTA	CCACCGAAAC	CATTACCTGA	TGGTTTAAAC	GGTAGTGGtT	TTTCACGTGC	600
AATCTCCACT	TCTGGAAGGC	TATCTGGGTC	TTGGACTGTC	AGACTCAAGA	TATACATTGC	660
CAATTCTTCT	GGAGTAAACT	CAGCAGCCAA	TTTGCGAGCA	TCCTTACCAA	ATTTCTCAAA	720
GTTGGCACGA	ATGGTTTCAT	CTGCAAAATC	ACGTTTCGATT	TTCTTGAGAG	CTACCTGTTT	780
TTTTGATTGG	AAGGATTCTT	CTACACTTGC	AGGTTTGAGA	CCTTTCATGC	GTTTCTTAGT	840
CAAGTTTTCA	ATGATTTGAA	GGTAACCCAT	TTCGTTTGGA	GCAACAAAAG	TAATAGATTG	900
ACCTGACTTA	CCAGCACGAC	CTGTACGACC	GATACGGTGA	ACATAACTCT	CAGGATCTTG	960
TGGAATATCG	TAGTTGTAGA	CATGGGTCAC	ACCTGAAATA	TCCAAACCAC	GCGCTGCAAC	1020
GTCTGTCGCA	ACCAAAACAT	CAAGATTGCC	ATTTTTAAAG	TCACGAAGGA	CACGAAGACG	1080
TTTGTTTTGG	TCTAGGTCGC	CATGAATTCC	TTCTGCACGG	AAGCCACGAA	TTTTCAAACC	1140
ACGAGTCAAT	TCATCCACAC	GGCGTTTGGT	ACGACCAAAT	ACAATAGCGA	GTTCTGGTTG	1200
TGCCACATCC	ATGAGACGAG	TCATGGTGTC	AAATTTTTCT	TGTTCCCTTA	CACGGATATA	1260
GTACTGGTCA	ACCAATTCTG	TTGTCAATTC	CTTAGCCGCA	ATCTTGACAT	GTTCAAGGGC	1320
TTTCATAAAC	TGAACACCGA	TACGTTTGAT	GGCATCTGGC	ATAGTTGCTG	AGAAAAGCAA	1380
AGTTTGACGG	TTCTCAGGTA	CACGGGAAAT	AATGGCTTCG	ATGTCTTCAA	GGAAGCCCAT	1440
GTTAAGCATT	TCATCCGCTT	CGTCAAGGAT	AAGGGTTTCA	ATGTCTTGTA	ATTTCAAGGC	1500
CTTGCGTTTA	ATCAAGTCCA	AGAGGCGACC	TGGAGTTCCC	ACCACAATAT	GGGCACCAGA	1560
TTTAAGAGCC	TTAATTTGTT	TTTCAATGCT	TGATCCGCCA	TATACTGAAC	GGACTTTGAC	1620
TCCCTTACTA	CGACCAAAGC	GGAAGAGTTC	TTCTTGACTT	TGGACAGCTA	GTTCAAGAGT	1680
TGGAGCGATG	ACCAAGGCTT	GGATAGTCGC	TTCTTCTGTA	CGGATTTTTT	CAAGGGTAGG	1740
CAAGCCAAAG	GCTGCAGTTT	TTCCTGTACC	AGTCTGAGCT	TGACCGATAA	CATCCTTGCC	1800
TTCAAGGGCC	AAAGGAATAG	TTTGTTCCTG	GATAGGACTA	GCTTCTACAA	AACCAGCTTT	1860
TTCAATTTCT	GCTAGCAAAT	CAGCAGACAA	GTTTAATTCA	TTAAATTTCA	CGTTATTCTT	1920
CTTCTCTAAAG	GTGGTGCGAA	GCCACCCTAT	AGGGCTTAGT	TTATACTTTT	CTTTTTATGA	1980
CGTATTTTCA	TATAACTAGA	TATAAAATCG	TGTTGCTTCT	TTTCCACAAA	AGAAAAGTAC	2040
TGTTTTCTTT	GCAACCTATC	TAGTATAACA	CAAGACCAGA	GCAAAAGATA	GCCCCATTTT	2100
TACAGAAAAT	CATGTAAGCG	CTTTTTGACT	TTCTTTTTTG	ATTGAACGAC	CTAGATAATA	2160
AGACAAAGCC	AAGGCGATAC	TGTATAAAAT	GAGAAAAACG	AACAAGGTTT	GTGTGTACGA	2220

1186

ATGAGCCATT TTATAAGTCT CTGCTAATAA AATAGGTCCC GCTAAACCAG CCATTGCCCA	2280
AGCTGTTAAA ATATAACCAT GCAGAGCGGC CAATTCCTTG GTTCCAAAAA TATCACTGAG	2340
ATAAGCTGGA ATCAAAGAAA AACCAGCTCC ATAGCAAGTC ATCAAAATAG ACATAGCAAC	2400
TACAAATAAA ACGGAATCTG TAAAGAGCCA AAGTGAGAGA GAAAAGAAAA GATTGACAAG	2460
CAGTAATATA CTAAAGGTTA GAGGGCGACC GATATAGTCA GACAAACTCG CCCAGAGCAA	2520
GCGACCAAAT CCATTGAAAA TCCCCAAAAC ACCCACCATT ACTGCTGCAT GACTTGTAGA	2580
CAAGCCAGCC ATCTCCTGTG CCATTGGCGA TGCCGCTGAA ATTAAGCCTA AACCACAAGC	2640
TATGTTGATA AAGAAAATAA TCCAAAGCAT ATAAAACCGA TTGCTTTTTA GAGCCTGATT	2700
TGCAGCCATT CCTTGCGTCA AAGAGGCTGT TTTTCTTTC CCTGAAGAAG ATAAAATTGC	2760
AAGCTCTTGC TCATTTGGAC GCTTAATGAA TTGTGAAGCT AGGAGCATGA TAATAAAGTA	2820
ACTTGCTCCT AAAATATAAA AAGTTTCTAC AAGCCCTACC CCTGCGATGA GGTGTTGCGC	2880
TATGGGACTA GTCAATAAAG AAGCAAAACC AAACCCATA ATCGCTAAAC CTGTTGCGAG	2940
ACCACGTTTA TCAGGAAACC ATTTTATAAT CGTCGACACA GGGGTAATAT AGCCTGCTCC	3000
CAAACCAAGC CCACCTAAAA TGCCATAAGC GAGATACAAC AACCACAGCT CTGACGGTCT	3060
ATTGCAAATC CTGTTAAGAT ATTTCCACCT GCGTATAGAA AAGCAGATAG ACTTCCCATG	3120
ACTTTCGGAC CAAATTTTTC TACCAAACGC CCCATAAATG CAGCCGATAA GCCCAAACAA	3180
AAGATTGCTA GACTAAAGGC GAAGGCAACA GAAGCCTGAT CCCATCCCGT	3230

(2) INFORMATION FOR SEQ ID NO: 204:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5096 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

CCTATGAAGA CTGTCCAAC TGGGTGTCCT TCTAGGCTAT CTGGTCCTGC CACTCCAGTC	60
AAACTAATTC CAAAATCAGA CTGGGTCTTG CTTCGTGCCT GCTCAGCCAT CTTCTGAGCT	120
GTAAATTCAG ACACCACACC ATGTTCTTCC AAATTCTTGG CAGGAATATC CAACATCCTT	180
GATTTTTCCT CCAAGCTATA GGTCACAAAA CCACCCTTAA ATATACTTGA AACTCCAGAA	240
AAATTCGCCA CGGTAGCTTG GAAAAGACCT GCCGTCAAAC TCTCTGCAGC CGCGATGGTT	300
TTCCCTTGCC TTTTCAGTTC TTCTACCACA ATGCTGGCTA AACTAGTTTC TTCCCCATAA	360
CCATAGCAAA AGTCTCGTAA AGAAATTCCT TCGAAAGTCT GGCAGTCCAA GATTTGATTT	420

1187

TCCAAGATAT	CCAGCGCTTG	ATTCGCCTCT	TCTTGACTGC	TAGCCTTTGT	TGACAGACGT	480
AGAGTGACTT	CTCCTGTCTT	GGCATAAGGG	GCCAAGGTAG	GATCGATCTG	ATTATCAATT	540
AAATCAGCCA	AAATCGTAAC	CAACTGGCTC	TCGCCAATCC	CAAAGAAACG	AAGAACTCGG	600
GAATACAGCT	TGCTCCCTGT	CATCAACTTG	GGTAGAAGTT	GGTTTAAGAC	CATGGGTTTC	660
AATTCACTTG	GCGGACCTGG	AAGGACGACA	TAGGTCACTC	CGTCTACTTC	TAATTTTCCT	720
CCAACAGCCA	GTCCTGTTTC	GTTTGGCAGT	GGAATCGCTC	CTTCTACAAT	TTGAGCTTGT	780
CTTTCGTTAT	TCGGTGTTTCG	GGCATAGTCT	GGTCGCAGGG	TAAAAAAGAT	ATCCAACCTC	840
TCCTGAGCCT	GAGGATCAAA	GACTAATGCT	TTCCCTAAAA	ATTTAGCTAG	GGTTTGTTTG	900
GTTAGGTCGT	CCTCAGTTGG	CCCCAAACCG	CCTGTCAAAA	TCACCAGACT	GCTACGTTGA	960
CTGGCAATCT	CAAGCAAAGA	CAAGAGACGA	ACTTCATTGT	CTCCTACAGC	CGTCTGAAAA	1020
TATACATCTA	CCCCAATCTC	AGCTAGTTTT	TCCGACAAAA	ACTGGGCATT	GGTGTTGACA	1080
ATCTGCCCTG	TCAAAATCTC	TGTTCCAACA	GCAATGATTT	CTGCTTTCAT	GTTTCCTCCT	1140
ACCTATCTAT	TCGTATTTTT	TTGAAAAAAT	CGCAGGAATT	TTCTTACGAT	TGATTTTTTT	1200
ATTTGTATCA	AAAGTTAATT	ATCTTCATCA	CCAACAGGTG	CTCTGCCAAA	TAAATCTTCA	1260
AATAAAACCG	CATTGGTTTC	AAGCTGAGTA	ACTTCTTCTT	GTCCCAAAGA	ACGTCGGAGT	1320
AGATTTTGCA	TTTCCAACAT	ATGTGCTCTC	GAAACAATCT	GGTAAGAAAC	ACCTTGAAGT	1380
ATCTCTCCTT	CACCCTGCAA	CTGCTGAGTT	TCAATGGTTT	TAAATGAATC	TTTATAGCCT	1440
AGCAAGTTAG	GGATACTTTT	TGCAGACAAA	TCAATATTGG	TCTGCATATT	GTCACTCAAA	1500
GCTTTTAGAA	TCTCTTGATA	ATGACCAATG	CTATTTAAAC	TGAGAGCTTT	TTCCATGACT	1560
TTTTGAATAA	CTTCACGTTG	ACGTTTTTTGA	CGACCATAAT	CCCCCTCAGG	ATCTTGGTAA	1620
CGCATTCGTG	CATAGACTAG	GGCTTCTTCT	CCCCCAATAT	GTTGCTCCCC	AACACCGATA	1680
GAAATAGTAT	TAAATTCTTC	TTGGTCACTG	ATAGAAATTG	GGAAACCTAG	GATATTATTG	1740
ACTGTAATAC	CTCCTACTGC	ATCCACTAGT	TTTTGCAATC	CTCTCATATT	GACCATCACA	1800
TAGCGATCAA	TATGGATATT	CATCATTTTT	TGAATGGTTT	CTATAGCAAG	CTCTGCTCCA	1860
CCATCTGCAT	ATGCTGAGTT	CAGTTTCGCT	TCATGAGCCT	GACCATTCCC	TGATTCAATG	1920
CGCGTCAGAA	TATCCCGCTC	TAAACTCATC	ATTGTTGTTT	TTTTCGTTTT	AGGATTCACT	1980
GTCATCAAGA	TCATGCTATC	ACTTCTACCG	ACCCAAGTTT	CAGTTCGTTC	AACATTTCCG	2040
GTGTCCACTC	CCATTAACAG	AATGGTTAGA	GGTTCAGTCG	CTTCAATAAC	CTTGGTTTCT	2100
TCACCGATTT	TTTTATAGGT	TTTAGCTAAG	GTTTCTGTCC	CTTGTTGATA	AATAGTATAA	2160

1188

GCAAAAACAC	CTACTCCTAC	TACAGTTACA	GAAAGTAAAG	CTAGCACCAT	TCCAATAATT	2220
TTTTTAACCA	TATTTCTACT	AACCTATCAG	TTTACCCATC	AAGTAAACAT	CGATAAATTT	2280
CCCTTCTTCT	ATATATGCCC	CACGCTCTTG	GCTACCTTCA	ATGACAAAGC	CATGCTTTTG	2340
ATAAAGATGG	ACTGCTGCTT	GATTACGAGT	TTGGACAGTC	AGTTGGAGAC	GACGCAGAAT	2400
GCCACTTGCT	TGTGCCCACT	CTATCGCTTC	TTCTAGCAAC	AACTTCCCA	AGCCATTATT	2460
CCAATATCTT	TTTCCAATCA	CAATGAAGAG	ATCTCCAATA	TGACGGACTC	TCTTACGCTG	2520
ATCAGCTGTA	ATATTTACAA	TACCAGCAAT	TTTGCCATTT	AAGAATGCAA	GTAAGGTTAT	2580
CTGATTGTCC	GAAC TAGCTT	GCTTGTTGAG	GAATATTTCC	ATCTCCTCAC	TAGTCAAGAG	2640
AATACCATCT	CCGTCTAGGC	TGGTAAAGTC	TGTCTCCAAA	CTCACACGAT	TTAAAAAGGC	2700
CACTAATTCA	GCTGCATCTT	TGGGCTCTGC	TTCCCTAATG	AGCAATTCAT	ACTCCATATT	2760
GAAGCTCCTC	TAACAATTTT	TCAGCAGCA	AACCCTTTGC	CTGAAAATTT	AAACGGCGTC	2820
CATCTGCTTC	TTTTAGAATT	TCCAATTCTA	AATAAGCATC	TGGCAAGGCA	TCTCCTAAGA	2880
GATTTCCCCA	CTCAATAACA	GTCACGCCGC	CACCAAAGAT	AACTCATCC	AAGTCGATAG	2940
AATCAGCATC	TCCTTCAATA	CGATAAACAT	CTAGGTGATA	AAGTGGAAGT	CGACCTTCAT	3000
ACTCTCTCAC	GATAGTATAG	GTGGGACTTT	TAATCATTTG	AGAAATCTGT	AATCCTTTTG	3060
CAAGTCCTTT	AGTAAAGGTC	GTTTTACCTG	CACCCAGTTC	TCCAGTTAAG	ATTAAAACAT	3120
CATTCTTTGC	TAATAGATGG	CCCAAACGCT	CCCCTAAGGC	TTGCAACTCT	TCTTCATTTT	3180
TTGTGTACAT	ACTCTTATTA	TACCAAAAAC	TTTTCTTTTG	TGTCTATTTT	CCTACTAAAC	3240
TTATCATCAT	AACATCCATA	AAAAACAGGC	TTTCTCTAAA	AGAAAATGAG	CGTAACAATG	3300
ACCAATACAA	GATCTCGGAA	AATATGACCA	TAAAAGGAAA	CTTCCTTCTT	AACCGAATTT	3360
GGGACAAGAT	AGGCTGCAAA	AAACAAGCCC	AGTCCAATAT	AAATCAGAAG	TGAGACAATG	3420
GTCATTGGAT	TTCTTAAGAA	AAGAAGTGTT	GCTAAAATAG	TCACCAACAC	TGTCTTTTTT	3480
CTGTCCAGCA	TAGCAAGAAA	ATCGCGCACG	TATTTTTTCA	AGGGTAAAAA	AATCAGCAAA	3540
TCTAGCCCAA	ATAGGAAAAA	GAAGGATGGC	AATAAAAAGT	CAACTAATTC	TTGCTGCAGC	3600
GTATTTTTGA	TGAACAAGTT	ATCTGACAAA	ACAAGAACAG	CTCCTAACAA	ATTAATTAAG	3660
AGTAACATAC	TGTAAAAAAG	CTTCACCGAC	TTCTTACTGG	CTAGGACACT	ATGGACTTCT	3720
TGCTTACGGG	TATAAAGATA	ATTTACTCCA	GCACAGATTC	CTGAAACGAA	AACCATGCTT	3780
CCGATGAAAA	AAGCTGTACT	TTGTTTAAAG	GACAAGATGC	ATTCCTTCCA	TAGGAAACAG	3840
CTACTCAAAC	TGATTTGAAT	TAAAGCTAAC	AAAAATAAGA	TTCTCATTGA	TTTCATCTTC	3900
TCTCTCCCTT	CCTACCAATC	ATTATACTAG	GAGAAAAGAG	AGAACTGTTT	CTAATCTTCT	3960

1189

CAAATGTCTC TTTAAGACGC TAAACAAACA CTAGAGACTA ATACTCAATG AAAATCAAAG	4020
ATCAAAC TAG GTAGCTAGCC ACAGGTTGCT CAAAACAGTG TTTTGAGATT GCAGATAGAG	4080
CTGACGTGAT TTGAAGAGAT TTTCGAAGAA TATAAATTTG AAATCATGAA AATCCGTCAA	4140
ACGGGTGGTT GTTTTGTCTC GCACCTCACG GAGCGAGACG GACTCAGAGT CACATAATTA	4200
TAAGGCTGAT AGTATTAATC TAACTATCAG CtTmCAGGTT ATTTAACGTT TCAGAAAAAC	4260
TATAATGTCA AGATTAAC TAACAGTATCT AGTTCCTTCA AATAATTTTC TATCTTCATC	4320
AACATTAAAG GATTGTTATA AATCTTACAT AACTCTCTTG CTTCTATATA ATAATTTTGT	4380
ACTTGTCTC TGTCTAGAAA TTTGGCTCCA GCATTTCCCTA CAAGAATAAG TAGAGGAGCC	4440
AATTGGTAGC TTGTCTGTCT TTGTTTACAG AGTTCAATCG TTCAAGAGC TTCTTGGATG	4500
GCTTCATTAT ATTTTTCCTT TGATACTAGG TAGTGAGCGT AGTTGTAACG AACTCTGATG	4560
TAGCCAAATA AAAACTCTTG ATGGTCCAAA TTTTTTGTCT GATACAACCTC TATTAAATGA	4620
GAGTAGTTTG CCTCATATTC TTGTTACGA CCCACTAAGG AATAGAAATT AGATAGAGTA	4680
TTCAACGCCT TTAAATAAAT CAGAGTATTT GAAGAGACTT TTAATAATAT ATTTTCCAAT	4740
GACGAAATTG CCTCACACTT ACTGTCATAT TGATAGAAGT CAATTATAGA TTTAATCCAT	4800
TCAAGGTAAG TTCGGTCTTC TAATGTTAGA AAAGTGCTTC GTTCTACTTC TATTTTATAA	4860
AGATATTCTA AATCGTCATA ATTTCTGTCA TCTAATAGGC GAGCAGATAG ATGTTTGAAA	4920
TTAGAGAGGT TAGACTTAAC TTCGATTTGT TCATTGAAAA AGTAATCCAA AGGGACTTCA	4980
AGTCGTTGAG AGAGTTTGAA TAACAAGTCT GCGGAGGGAA TAAAATGACC TCTTCAATT	5040
TTACTAATCT GGCTTTGTTC ACAAATTCCT TCTGCAAGAG TTTGTTGGGA GAGTCT	5096

(2) INFORMATION FOR SEQ ID NO: 205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

ACAAGATAAA AATAAAGGAT TACAATGGGG AATATAAAGT AAACCGGTAA ACCTAAAAAG	60
AAAGGAGAAA AGATGAAAAT TGTACTTGTA GGGCATGGAC ATTTTGCTAC AGGGATTTAT	120
AGTTCTTTAC AATTGATTGC AGGTAATCAA GAAAATGTGG AGGCGATTGA CTTTGTGGAA	180
GGAATGTCAG CAGATGAACT CAAGCAAAAA ATCTTACTTG CAATTTCAA TGAAGAAGAA	240

1190

GTTTTAATCC TAAGTGATCT CTTGGGAGGA TCGCCATTCA AGGTTTCTTC TACCATAATG	300
GGAGAAAATC CAGCCAAGAC AATGAATGTT CTCTCGGGTT TGAAGTTAGC CATGTTAATG	360
GAAGCAGTCT TTGCTAGAAT GGCTCATAGC TTTGATGAGG TTGTTAATAA ATCAGTAGTG	420
GCGGCCCAGG GCGGAGTCGT AAATGGTAAA GAATTGTTTT CAACGGATGC AGAGGAAGAG	480
GAAGAAGATT TCGAATCGGG TATTTAAAGG GTAAAAGAAT GATAAAAAAG GTTACGATTG	540
AAAAAATAAA ATCGCCTGAG CGCTTCTTAG AAGTACCACT TCTGACGAAA GAAGAAGTCG	600
GCCAGGCAAT CGATAAGGTT ATTCGGCAGT TAGAACTCAA CCTTGACTAT TTCAAGGAAG	660
ATTTCCCGAC GCCAGCTACC TTTGATAATG TCTATCCAAT CATGGATAAC ACGGAATGGA	720
CCAATGGTTT CTGGACAGGA GAACTGTGGT TGGCTTATGA ATACAGTCAA CAGGATGCAT	780
TTAAAAACAT CGCTCATAAA AATGTTCTTT CTTCCTGGA TCGTGTCAAT AAGAGAGTAG	840
AATTGGATCA CCATGATCTC GGCTTCTTGT ACACACCGTC TTGTATGGCT GAATATAAGA	900
TAAATGGAGA TGGAGAGGCT AGAGAAGCAA CCTTGAAAGC TGCAGATAAG TTGATTGAAC	960
GCTATCAAGA AAAAGGTGGT TTTATTCAAG CTTGGGGAGA CTTGGGCAAG AAAGAGCATT	1020
ACCGTTTGAT TATCGACTGC TTGCTCAATA TCCAACCTCTT ATTCTTTGCT TATCAAGAAA	1080
CAGGCGATCA AAAATACTAC GATATTGCAG AAAGCCATTT CTATGCTTCA GCTAATAATG	1140
TAATCCGTGA TGACGCTTCG TCCTTCCACA CCTTCTATTT TGATCCTGAG ACAGGTCAAC	1200
CCTTTAAAGG TGTAACGAGA CAAGGGTATA GTGATGATTC ATGCTGGGCA CGTGGTCAAT	1260
CATGGGGAGT CTATGGTATT CCTTTGACTT ATCGTCACTT AAAAGACGAG tCCTGCTTTG	1320
ACTTGTTTAA GGGTGTGACC AATTATTTCT TGAATCGTCT GCCAAAAGAT CATGTGTCCT	1380
ATTGGGATTT GATTTTAAAT GATGGTAGTG ATCAATCACG AGATTCTTCA GCAACAGCTA	1440
TCGCCGTCTG TGGGATTCAT GAAATGCTAA AACATCTCCC AGAGGTGGAT GCTGACAAAG	1500
ATATTTATAA ACATGCTATG CATGCCATGC TTCGTTCCCTT GATCGAACAT TATGCAAATG	1560
ATCAATTTAC CCCTGGTGGG ACAAGTCTCC TCCACGGTGT GTACTCATGG CATTCAAGTA	1620
AAGGAGTGGA TGAAGGCAAT ATCTGGGGTG ACTACTATTA CCTAGAAGCC CTTATCCGTT	1680
TCTACAAAGA CTGGAACCTA TATTGGTAGG AGGAGAAATA TGACAATGCC AAATATTATT	1740
ATGACCCGTA TCGATGAACG GTTGATTTCAT GGACAAGGAC AACTTTGGGT AAAATACCTA	1800
GGTTGTAATA CGGTCATTGT TGCCAATGAC GAAGTAAGCA CGGACAAGAT GCAACAACT	1860
CTGATGAAAA CAGTTGTGCC AGACTCAGTT GCCATGCGTT TCTTCCCTTT GCAAAAAGGTG	1920
ATTGATATCA TTCACAAGGC TAATCCTGCT CAAACGATCT TTATCGTTGT AAAGGATGTG	1980
AAGGACGCTT TAACCTTGGT AGAAGGTGGT GTCACTATCA AAGAAATCAA TATTGGGAAC	2040

1191

ATTCACAATG CCCCTGGTAA AGAGCAAGTG ACACGCTCCA TCTTCCTGGG TGAAGAGGAC	2100
AAGGCGGCCC TCAAGGAATT GAGCCAAACT CATCAAGTAA CATTTAATAC GAAAACAACT	2160
CCAACAGGAA ATGATGGAGC TGTTCAAGTC AACATTATGG ACTATATTTA ACAGAGGAGA	2220
TCGTTATGTC GATTAATGTA TTTCAAGCGA TTTTAATTGG ATTATGGACA GCTTTCTGTT	2280
TTAGTGGAAT GCTGTTAGGA ATTTACACCA ATAGATGTAT TGTTCTGTCA TTTGGTGTCTG	2340
GAATTATTCT AGGTGATCTG TCATGCTCTT GCAATGGGAG CCAATGGTGA ATTGG	2395

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

CCTTCTTTAG AGGTTAATTT TGCAAAATCG TCGATTGTTA TATAAGGATT ATTATAGAGA	60
CTGTTTCGCAA AGAATCTCTG ATATGTTTTT GAATCTTTTG AATACAAAAC TATCTCTCTA	120
ATAGCATTGC CATCTGTTCC ATCAATTGGT AACATACCG TAACTAGAAA AAGAATTATA	180
TTCAAAATAA AAAATTCTGA TGCGTACGGC ACAAATCCCA AAAGTGCTAA TATTGCGACA	240
ATTAGGTTAG CTCCACCTCC CCCAAAGAAG TAGAACACCA AATTCCTATC ACTATTTTTT	300
TCATTAGTAA TGTTTCTATT ACTCATTTGA CAATAACCGA ATGCTAATAA CACTGGAAAT	360
TTGAAATATA TTTTTTTTCT GAAATAGAAG AAAAAGGGAG TAGCAAGCAT CTCTAGTTTA	420
TAAGATAAAC ATCTTCCCAC TAAAAAATGA CCTAGTTCAT GTAATGTAAT TGATATTAAC	480
GAAATTAAAA TCAATCGAAA ATAATAGATT AATGAATCAT TTGGAAAAAT TATCAATAAT	540
AGGAACAATA ACGGAATCAA ACATAAATAT ATGACAGAGT TATTTAATAT TTTCAACATA	600
ATACCATTC TCTAAACTAT TAGCTTCAAA AAGGCGTTTT TTCTCCCAAT ACATCTTCTC	660
AAAAATGTTTCG GAATCATAAT TTTCTAAAAT TAATTTTATG TCTGGTAAGC TCTTTCTTGA	720
TAATCCGTTG TTTTGTACTT AATTTTCCCT TCAAGTACAT CTTCAATTTT ATAAGTTGCC	780
TCCATCAACT GAGCCTCTGC AATATCTTTG AGTGAATTGG TAATTGAAAC TTGGTGTAAT	840
ATCTGTCCTs CCATATATGA AAATATATCT CTAAGATATT CTGACACATT ATCAGAGCCG	900
TTACTCTCAG CAACATCTAA TGTTACAACA AACTTTCCAG CTAATCGAAA AAGATGGCTC	960
CACCCCCCAA TCCTTTCAAT AAAGTTTTTT GTGTCCACAG ATACGTTTTG TAAATATACA	1020

1192						
GGAGAAGAGA	TAATTATAAT	ATCAGACTCT	AATAACTCTT	TTTTTATAAC	ACCTCCATCA	1080
TCAGCATTAC	TTTGCCTATC	AATTCCTTTC	TTAAACAAC	CTTCTGAATC	AGAATTAGAT	1140
ATTTCTAGCT	CTGAATTGAA	AGGTGTCCTG	AAAGATATAT	CAACATTATT	TCTACTAGAA	1200
ATGATACTTG	AAAGTCTCTT	AGTATACTCT	AAAGTCTTAG	AGTTATGATT	TCGCACTCCT	1260
GCATATATAA	ATATTTTATT	CATTTTAATT	CATCCTCTCA	ATTTGAATTT	AGTAGATTTT	1320
TCAAGATAGT	ATGGTACAAA	AACAGACTTT	TGTTGACTCA	CATTATTACA	TATGTTTTGT	1380
ATTAAACCAA	AATCAATACT	ATTTTGGAG	TAATTTTGAT	TTTAGTTTAA	AATCATTTCT	1440
ATAACAGTAG	CATATACCTC	AAGCCGTTTA	GCAATTAGAA	TAGAACTTTT	CTTTATTATA	1500
TTATTATCTC	AACGAAAAGC	TACACTATTA	AAAATATTTT	ATAGAATTAC	ATATTAAACT	1560
AGTCAATCTT	GGTATTTTTA	TATTGCTTAA	TGAGTGGACA	CCTCTATTTT	AGAAACAAAA	1620
CTATAAATTA	AGCTAGATTT	CAAGTAATGA	GGGGATAACT	ATCTTTTTGT	CATTCTGATT	1680
CAGTGCGATA	TACCTTAAAA	AAGTATAAGC	AATACCAGTC	ACACCTGTAT	ACAAAGAAAA	1740
ATCTGGGAAA	TTGCTTGTTT	GGACGATACG	ATACTCTCCT	TCTTTTGATT	TATTCATTAC	1800
AACACTACAC	AATAAAGACT	CCAATTCCAT	ACTAGTATCC	ATTTCTTTCA	TGTAGTCGAT	1860
GTAAAAATTT	ATTATGGCCA	TACTTCCATG	GCAAAATGTA	TCATTATCTA	AACTAGCTAC	1920
AATTCCTCT	GGAACACTTT	GGGGATGATT	AACTAATGTC	CCAAATTCTC	CACTACACCA	1980
CTTCAAAGAA	TGAATTTTGA	TTTTCTCCCT	AGGAAC TAGT	TGTAAAATTA	ATTCTTTATA	2040
TTTTTTAAGT	CTTGTCACCT	TATAAATATT	TTTAAATGTA	AAAATTACAC	CTGATAGTCC	2100
ATGGCCAAAA	CTATATCCAA	AATTACTATT	ATCTCTCTCG	CTTACATCAT	TATATAGCGT	2160
ATCACCTAAA	CTTAATACTA	GCCTTAGAAC	ACGTTCCCTC	TCTATTCCTC	TCCTATAATA	2220
TCTTACCAGT	GTATTAATTA	AAGGTAGAAG	ACCATTAATA	TAGTCAGACT	TGTTTGAAAC	2280
ACTTGCAAAA	TCAGTCTTTT	CAAGCTCAGT	TAAAACACTC	TTTATATAAT	TTAAGCATGC	2340
GAGAGTATTT	GTATCGTAAT	CCTCTATAAT	GGATAGAACA	ATGAAATATC	CTATATCCCC	2400
AGTTAAACCA	AATGTGGTCT	TAGATAAAGA	AACAGATGGC	GGAATTGCAG	ATAACATTTT	2460
ATTGTACAGT	TGAGTATATG	ATGATTTATC	TTTCAATAAT	TTTACATAGT	ACATAAACAG	2520
TAATATTCCA	GCTCTACCCC	TATACATATC	ATTmCCCGTT	TGTTCAAGAC	ACCATTTAGA	2580
ACCTTTAAAA	TTAACAGGTA	TACTCCAAAT	TGGATATTCG	TCATAAATAT	TATTAATAAC	2640
CAAAGAGTCT	GCAATATTTT	CTACTTCATT	ATGCAGAATA	GTAACATAAC	TTTCATTTGG	2700
GAGTTTTTTT	CTATTAGATA	AGTTTAATTT	ATATCCTTTT	TTTCGCTGAT	CAAAGCTTGG	2760
AAAATAAATT	TCAATGATAT	CAAGTTGCTT	TTCTAAATTT	TCCAAATTAT	TATTAGGTAA	2820

1193

ATATTTTCATA AAATAGTCAT ATCCAGAAAA TTGATGTAGG GAAATAAAAT GATTTCCAAA	2880
ATCATCGTAG ATTTTCATTGA TATTTGTATC TGTATAAAAA ATCGGAATAT CTAATAACCT	2940
CATTTGTTCA CATTCGCTTG CTACAATACC TTGATTAGAA AACTTATTGC TCCAGAGATT	3000
TTCCAATGCT TTTTCTCTAT CTAACATTTT TTCATAAAAA TCAGGATGAT ATAAAAAAGA	3060
TAGTACTGAA GCATAGCTAT TTGTGTCTCT AAAAAGTACC CTTGTCTTTA AACCATACAA	3120
GTTTGCTTTT AATAGCATTT TAAATTCTTC TGTTTTATTT AACTCTTCAA ATATCAGATA	3180
AAAATCCCTA AAACCTTTTT TGAAATCTTT TATATACTTA TCAAATTCTA TATCACCATC	3240
CCGAACAGGC AGGTTTTTCC CACCTTCAAA ATCAATTTTC CCAATATCAA ACTTTACCTT	3300
ATCAGTATTT AAATTAATTA AACTTGACC AGGGATCCTC TA	3342

(2) INFORMATION FOR SEQ ID NO: 207:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

GAGAAAAGAA TGTTAAAGAA AAATGATATT GTAGAAGTTG AAATTGTTGA TTTGACCCAT	60
GAAGGGGCAG GAGTTGCCAA GGTAGATGGT TTGGTCTTTT TTGTAGAGAA TGCTTTACCG	120
AGTGAAAAAA TTCTCATGCG TGTCTCAAG GTCAATAAAA AGATTGGCTT TGGAAAAGTT	180
GAAAAATACC TTGTCCAGTC ACCACACCGT AATCAAGATC TAGATTGGC TTACCTGCGT	240
TCAGGAATCG CGGATTTAGG ACACCTTTCT TATCCAGAAC AGCTCAAGTT TAAAACCAAG	300
CAAGTCAAGG ACAGTCTCTA CAAGATTGCT GGAATTGCAG ATGTAGAAGT TGCTGAAACG	360
CTTGGTATGG AACATCCAGT CAAGTATCGC AATAAGGCGC AGGTGCCCCG TCGTCGAGTG	420
AATGGTGTCT TGGAAACAGG ATTTTCCGT AAGAATTCGC ATAACCTCAT GCCCCTTGAA	480
GATTTCTTTA TCCAGGATCC TGTCATTGAC CAAGTCGTAG TAGCTCTTCG AGACCTGCTC	540
CGTCGTTTTG ATTTAAAACC TTATGACGAA AAGGAACAGT CTGGATTGAT TCGGAATCTT	600
GTGGTGCGTC GTGGTCACTA TTCAGGACAA ATCATGGTCG TTTTGGTGAC AACTCGTCCA	660
AAAGTTTTTC GTGTTGACCA ATTGATTGAA CAAGTTATCA AGCAGTTCCC AGAGATTGTG	720
TCTGTCATGC AAAATATCAA CGACCAGAAT ACCAATGCGA TTTTGGTAA GGAGTGGCGC	780
ACTCTTTATG GTCAAGACTA TATTACGGAC CAGATGTTGG GAAATGACTT CCAAATCGCT	840

1194						
GGCCCAGCCT	TTTACCAAGT	CAATACTGAA	ATGGCGGAGA	AACCTCTATCA	AACAGCCATT	900
GACTTTGCAG	AGTTAAAAAA	AGATGATGTG	ATTATTGATG	CCTATTCTGG	TATTGGAACC	960
ATTGGTTTAT	CAGTCGCCAA	GCATGTCAAA	GAAGTCTACG	GTGTTGAACT	GATTCCAGAA	1020
GCAGTAGAGA	ATAGCCAGAA	GAATGCTTCT	TTGAACAAGA	TTACTAATGC	CCACTATGTC	1080
TGTGACACGG	CTGAAAATGC	CATGAAGAAA	TGGCTCAAGG	AAGGTATTCA	ACCAACCGTT	1140
ATCTTGGTTG	ATCCTCCACG	CAAGGGCTTG	ACAGAAAGCT	TTATCAAAGC	AAGCGCCCAA	1200
ACAGGAGCCG	ATCGCATCGC	CTATATCTCC	TGCAATGTCT	CAACCATGGC	GCGTGATATT	1260
AAACTATACC	AAGAGTTGGG	ATATGAATTG	AAGAAAGTCC	AGCCGGTGGA	TCTATTTCTT	1320
CAAACGCATC	ACGTCGAGAC	GGTAGCACTT	TTGTCCAAAC	TCGATGTCGA	TAAGCACATA	1380
AGTGTGAAA	TTGAGCTGGA	TGAGATGGAT	TTGACAAGTG	CGGAGAGCAA	AGCAACATAT	1440
GCTCAAATCA	AAGAATATGT	TTGGAATAAA	TTTGAATTAA	AAGTTTCGAC	ATTATATATT	1500
GCACAGATAA	AAAAGAAATG	TGGAATAGAA	TTACGAGAAC	ATTACAACAA	GTCTAAAAAG	1560
GATAAACAAA	TTATTCCACA	GTGTACACCT	GAAAAAGAAG	AAGCCATCAT	GGATGCTTTG	1620
AGACACTTCA	AAATGATTTA	ATAGAAAAGA	ATGACAGTAT	ATGACTTTCT	GCATTTATTA	1680
CATTCCTACT	TGGTATAGGA	ACAGCTATTA	TTCTTTCTTT	GCAAGGTATC	AATTAGAAAA	1740
TAGGCTCAAT	ATAAAGATTG	ATAGGATCAT	TTTTATATTT	AAAGGAGCGT	TGAAATGATT	1800
GATAAAGGCA	ACAAAAAATT	TTAGGATAAA	TTTGCTAAGT	TGTATGCCTC	TTTTATGAAA	1860
AAAGATAAAG	AGGTTTATGA	TAAAGTTTGT	GAATATCTTA	GTCCCTCATTT	GAATAAAGAT	1920
ATGGAGGTGC	TTGAACTTGC	TTGTTGGTTT	CGTGTCATAA	CAGTTATAGA	GGCAAATAGT	1980
TATGTAAATA	TAAGGAGTTC	AAGACTTCTA	CCAAAGTTTA	AAACTCAAAA	AATAAATAGT	2040
TGGTGTGCTG	CTTACAATAT	CCATTTTAAT	AATGGATATT	GTAAGCAGCA	CCCCcAtGAA	2100
TTTAAAGATT	CTTTAAAGAG	TCTTATTTTG	TGATGAAAAT	TTAATATGTA	AATCTCAGAC	2160
GATAGAAATT	AAAAACTCTA	TCGTCTTTTT	TATACTCAAA	ATTAGGAGGT	AAAAATGGTA	2220
AGGATAAGAG	GTCCCACTTA	AAACAATTTA	TGGCAAAATA	AGGACGGAAT	AACACAACAA	2280
ATTCTCTAAA	ACAAATCACT	AAATCAATGT	AAGATTGAAT	GAAATCAATA	TTTATGCTAT	2340
AATTAAATAA	ATTTAATGAA	GAAAAAAAGA	GGGATATTAT	GGCACTTAAC	TATAAACCAT	2400
TATGGATACA	GTTAGCAAAA	AAAGGACTAA	AGAAAACAGA	TGTAATAGCT	ATGGCAGGAC	2460
TTACAACAAA	TGTTATGGCA	CAAATGGGAA	AGGATAAACC	AATTACATTT	AAGAATTTAG	2520
AAAGAATATG	TAAGGCTTTA	TCTTGCACTC	CTAATGATAT	TATTAGTTTT	GAAGATAATT	2580
TTAGTGACGA	GGAATAGAAA	ATGACTTTAA	GGACAGAAGA	TCAAGTTAGG	GATTATGCAA	2640

1195

GAGAAGTATA GGCTTTAATG AAGTTGAAGA AAACATCAAT CAAGGTACTG GTCAAATAAC	2700
TACTTTTAAT CAATTAGGCT TCAAGGGATA TTCAAATAAG CCAGATGGTT GGTATTTACC	2760
TAAAAATATG AATGATGTAG CAATAATCCT TGAAACAAAA TCAGAAGAAA GAGATATTAG	2820
CAAACAAATT TTTATTGATG AGTTAATGAA AAATATAGAC ATAATTTAAC TAAAAATAAA	2880
AACTAGATCC TTTTTTGAAA AAATTATATT ATTAAATTTG TAACTGTATC TATTGACAAT	2940
GATAATTATT ATCGATACAA TAGACTTGAA ATATGTTTAA GGAGTTTTTA TGAAAaCAA	3000
TTTTTTCTAA TmGCTATTTT AGCTATGTGT ATAGTTTTTA GCGCTTGTTT TTCTAATTCT	3060
GTTAAAAATG AAGAAAATAC TTCTAAAGAG CATGCGCCTG ATAAAATAGT TTTAGATCAT	3120
GCTTTCGGTC AAACATATATT AGATAAAAAA CCTGAAAGAG TTGCAACTAT TGCTTGGGGA	3180
AATCATGATG TAGCATTAGC TTTAGGAATA GTTCCTGTTG GATTTTCAAA AGCAAATTAC	3240
GGTGTAAGTG CTGATAAAGG AGTTTTACCA TGGACAGAAG AAAAAATCAA AGAACTAAAT	3300
GGTAAAGCTA ACCTATTTGA CGATTTGGAT GGACTTAACT TTGAAGCAAT ATCAAATTCT	3360
AAACCAGATG TTATCTTAGC AGGTTATTCT GGTATAACTA AAGAAGATTA TGACACTCTA	3420
TCAAAAATTG CTCCTGTAGC AGCATACAAA TCTG	3454

(2) INFORMATION FOR SEQ ID NO: 208:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3752 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

CGGGAGTATA CTTAATATAA TTATAGTCTA AAAATGACTA TCAGAAAAGA GGTAATTTA	60
GATGAATAAG AAAAAAATGA TTTTAACAAG TCTAGCCAGC GTCGCTATCT TAGGGGCTGG	120
TTTTGTTACG TCTCAGCCTA CTTTTGTAAG AGCAGAAGAA TCTCCACAAG TTGTCGAAAA	180
ATCTTCATTA GAGAAGAAAT ATGAGGAAGC AAAAGCAAAA GCTGATACTG CCAAGAAAGA	240
TTACGAAACG GCTAAAAAGA AAGCAGAAGA CGCTCAGAAA AAGTATGAAG ATGATCAGAA	300
GAGAACTGAG GAGAAAGCTC GAAAAGAAGC AGAAGCATCT CAAAAATTGA ATGATGTGGC	360
GCTTGTTGTT CAAAATGCAT ATAAAGAGTA CCGAGAAGTT CAAAATCAAC GTAGTAAATA	420
TAAATCTGAC GCTGAATATC AGAAAAAATT AACAGAGGTC GACTCTAAAA TAGAGAAGGC	480
TAGGAAAGAG CAACAGGACT TGCAAAATAA ATTTAATGAA GTAAGAGCAG TTGTAGTTCC	540

1196

TGAACCAAAT	GCGTTGGCTG	AGACTAAGAA	AAAAGCAGAA	GAAGCTAAAG	CAGAAGAAAA	600
AGTAGCTAAG	AGAAAATATG	ATTATGCAAC	TCTAAAGGTA	GCACTAGCGA	AGAAAGAAGT	660
AGAGGCTAAG	GAACCTGAAA	TTGAAAAACT	TCAATATGAA	ATTTCTACTT	TGGAACAAGA	720
AGTTGCTACT	GCTCAACATC	AAGTAGATAA	TTTGAAAAAA	CTTCTTGCTG	GTGCGGATCC	780
TGATGATGGC	ACAGAAGTTA	TAGAAGCTAA	ATTAAAAAAA	GGAGAAGCTG	AGCTAAACGC	840
TAAACAAGCT	GAGTTAGCAA	AAAAACAAAC	AGAACTTGAA	AAACTTCTTG	ACAGCCTTGA	900
TCCTGAAGGT	AAGACTCAGG	ATGAATTAGA	TAAAGAAGCA	GAAGAAGCTG	AGTTGGATAA	960
AAAAGCTGAT	GAACCTCAAA	ATAAAGTTGC	TGATTTAGAA	AAAGAAATTA	GTAACCTTGA	1020
AATATTACTT	GGAGGGGCTG	ATCCTGAAGA	TGATACTGCT	GCTCTTCAAA	ATAAATTAGC	1080
TGCTAAAAAA	GCTGAGTTAG	CAAAAAACA	AACAGAAGCT	GAAAACTTC	TTGACAGCCT	1140
TGATCCTGAA	GGTAAGACTC	AGGATGAATT	AGATAAAGAA	GCAGAAGAAG	CTGAGTTGGA	1200
TAAAAAAGCT	GATGAACTTC	AAAATAAAGT	TGCTGATTTA	GAAAAAGAAA	TTAGTAACCT	1260
TGAAATATTA	CTTGGAGGGG	CTGATTCTGA	AGATGATACT	GCTGCTCTTC	AAAATAAATT	1320
AGCTACTAAA	AAAGCTGAAT	TGGAAAAAAC	TCAAAAAGAA	TTAGATGCAG	CTCTTAATGA	1380
GTTAGGCCCT	GATGGAGATG	AAGAAGAAAC	TCCAGCGCCG	GCTCCTCAAC	CAGAGCAACC	1440
AGCTCCTGCA	CCAAAACCAG	AGCAACCAGC	TCCAGCTCCA	AAACCAGAGC	AACCAGCTCC	1500
TGCACCAAAA	CCAGAGCAAC	CAGCTCCAGC	TCCAAAACCA	GAGCAACCAG	CTCCAGCTCC	1560
AAAACCAGAG	CAACCAGCTA	AGCCGGAGAA	ACCAGCTGAA	GAGCCTACTC	AACCAGAAAA	1620
ACCAGCCACT	CCAAAACAG	GCTGGAAACA	AGAAAACGGT	ATGTGGTATT	TCTACAATAC	1680
TGATGGTTCA	ATGGCAATAG	GTTGGCTCCA	AAACAACGGT	TCATGGTACT	ACCTAAACGC	1740
TAACGGCGCT	ATGGCAACAG	GTTGGGTGAA	AGATGGAGAT	ACCTGGTACT	ATCTTGAAGC	1800
ATCAGGTGCT	ATGAAAGCAA	GCCAATGGTT	CAAAGTATCA	GATAAATGGT	ACTATGTCAA	1860
CAGCAATGGC	GCTATGGCGA	CAGGCTGGCT	CCAATACAAT	GGCTCATGGT	ACTACCTCAA	1920
CGCTAATGGT	GATATGGCGA	CAGGATGGCT	CCAATACAAC	GGTTCATGGT	ATTACCTCAA	1980
CGCTAATGGT	GATATGGCGA	CAGGATGGGC	TAAAGTCAAC	GGTTCATGGT	ACTACCTAAA	2040
CGCTAACGGT	GCTATGGCTA	CAGGTTGGGC	TAAAGTCAAC	GGTTCATGGT	ACTACCTAAA	2100
CGCTAACGGT	TCAATGGCAA	CAGGTTGGGT	GAAAGATGGA	GATACCTGGT	ACTATCTTGA	2160
AGCATCAGGT	GCTATGAAAG	CAAGCCAATG	GTTCAAAGTA	TCAGATAAAT	GGTACTATGT	2220
CAATGGCTTA	GGTGCCCTTG	CAGTCAACAC	AACTGTAGAT	GGCTATAAAG	TCAATGCCAA	2280
TGGTGAATGG	GTTTAAGCCG	ATTAAATTAA	ATCATGTTAA	GAACATTTGA	CATTTTAATT	2340

1197

TTGAAACAAA GATAAGGTTT GATTGAATAG ATTTATGTTT GTATTCTTTA GGTACCTATC	2400
TTATGATTTT AGGAAATGTC ATTAAAAAAA CGACTCATTT TCTCTAACCT GAAAAATAGA	2460
TTAGAGAAAA TGGGTTGTTT TATCTATTAT AGTTATTTGA ATGAAGmTAA GAAGAAGGTA	2520
TACTCACATC ATTCACATAA TCTGTATATT GACTATAAGT TTTAAAAAAC AATTTTAAAG	2580
CTCTTCCTTG TCTTCTCTAA CCAAGCGTGT TATAATGAAT ACTGCTCAAG CGACCTTCAA	2640
TCGTGAAGCA CACACGACCT TCAATCGTGA ATAAACGAAT AGATGGGAGA CTTACCATGA	2700
GTGATAACTC TAAAACACGT GTTGTCTGGG GGATGAGTGG TGGTGTGAT TCGTCGGTGA	2760
CGGCTCTTTT GCTCAAGGAG CAGGGCTACG ATGTGATCGG TATCTTCATG AAGAACTGGG	2820
ATGACACAGA TGAAAACGGC GTCTGTACGG CGACCGAAGA TTACAAGGAT GTGGTTGCGG	2880
TGGCAGACCA GATTGGCATT CCCTACTACT CTGTCAATTT TGAAAAAGAG TACTGGGACC	2940
GCGTTTTTGA GTATTTCCCTA GCGGAATACC GTGCAGGGCG CACGCCAAAT CCGGACGTTA	3000
TGTGCAACAA GGAAATCAAG TTCAAGGCCT TTTTGGACTA TGCCATAACC TTGGGGGCAG	3060
ACTATGTAGC GACTGGGCAT TATGCTCGAG TGGCGCGTGA TGAGGATGGT ACCGTTTACA	3120
TGCTTCGTGG CGTGGACAAT GGCAAGGATC AGACCTATTT CCTCAGCCAA CTTTCGCAAG	3180
AACAACTTCA AAAAACCATG TTCCCACTAG GACATTTGGA AAAGCCTGAA GTACGCAGAC	3240
TAGCAGAAGA AGCAGGCCTT TCGACTGCTA AGAAGAAAGA CTCGACAGGG ATTTGCTTTA	3300
TCGGAGAAAA GAACTTTAAA AACTTTCTCA GCAACTACCT GCCAGCTCAG CCTGGTCGCA	3360
TGATGACTGT GGATGGTCGC GATATGGGCG AGCATGCAGG TCTTATGTAC TATACAATCG	3420
GTCAGCGTGG CGGACTCGGT ATCGGTGGGC AACACGGCGG TGACAATGCC CCTTGGTTCG	3480
TTGTCGGAAA AGATCTAAGC AAGAATATTC TCTATGTAGG ACAAGGATTC TACCATGATT	3540
CGCTCATGTC AACTAGCCTA GAAGCCAGTC AAGTCCACTT TACTCGTGAA ATGCCAGAAG	3600
AGTTTACGCT AGAATGTACG GCTAAATTCC GTTACCGTCA GCCTGACTCT AAGGTGACCG	3660
TTCATGTCAA AGGAGAAAAG ACAGAGGTCA TCTTTGCGGA ACCACAACGC GCGATTACAC	3720
CAGGACAGGC AGTTGTCTTT TACGATGGCG GG	3752

(2) INFORMATION FOR SEQ ID NO: 209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3580 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

TATTTATATT	TTTTTATCTC	TGGCATACTT	TGATACCTTT	TTAGACTTAA	AGTCTTTAAT	60
AGTGCCTTTC	CACCTCTTTT	TATCTATAAA	GATTCTCCTA	CATCATAATT	CATTTTTTTA	120
TTTAAACCTT	TCTGTCTTAG	TTTGTCTTTA	TCTTCTTCAT	ACCATTTTAA	GATTGTCACA	180
TAGTGGTTTT	GATAGGTCTT	ACCACTGCTT	TCCATGTATC	TGGATAGTTT	ATTTATCATT	240
ATATCTGTGT	GTGAGTTTAA	TTTTTCTTTT	AGATTTTAT	ATTCTTCTTT	GCTTAACCTT	300
ACATTTTGA	ATTCTCCATA	AAAAATGGGG	GTGGACTTTT	TATCTATCTC	TCCCTCTCTC	360
TCTTTATCTA	TCTCTATATC	TTTCCATGTA	ATTCCAATCT	GGAGTACCTC	TACTGTCTAT	420
CGGTAATTTA	ATTTTGATAT	CTGGCAATAC	TGTGCTAGAT	ATTTGATCTT	TATATTCAGT	480
ATTTTAA	GCTTGCCTAA	TAATTGAAGT	TAAATAGAAT	GCTACTTCTT	TATTCAATTC	540
TTTATTTTTT	AATTTTAAAC	AATGAATTTT	CATATCTAGG	CTTGCTTTAT	ATTTATGATA	600
AAAGACTGCT	CCTAAAAATG	AAACAGATAT	AAAATTTTCA	AAAACCTCTAT	AATTTTATC	660
ATCTATATCT	TCGTAGTAAC	CTAAGATACC	ATTGTCAATA	TTTGTAGCAC	TAATTCTAGG	720
AGTTTTTCCA	TCGAGTAAAT	ATCTTTTTGG	AATAGATGAG	CCTGTTGGTA	CTTAACTCGA	780
TTTCCCCTTT	TTTTCGGTAA	TAAATATTTT	TTTTTATTTT	GTTGTCTGAT	ATTTTTCCTA	840
CCTGTCCTTT	GTAGGATGAG	TATTTTCTAG	ATTTTCyTGA	ATAACTTTTT	ACTTGAAGTT	900
TTAGCTTTTG	AACTAGTCGT	TGTACTTTCT	TTTTGTTTAT	TATCAGTCCT	GATCTTTTTA	960
ATATTGCTGT	TATTCTCTAT	ATCCTATTTT	TCATTCATGA	TATTCTTTTA	CTAATTTTAT	1020
CTTAAATTCT	GTGCTGTATT	TGCCATTAAA	AAACTGACCT	CCTTTAGTTA	GTTTTTTGGC	1080
CTAACTTTTG	AGGGTCAGTT	CAAATTTTGC	GACTTTTAAA	TGAATTCCAA	TATTCAATTA	1140
TTAAGAGTTA	ACATGGTGCT	TGCCAATAGG	AATCATTAGA	GGCGAATTGG	AAATAGGGTC	1200
ACGTATAATT	TTTGCTTCAA	GATTAAAGAT	ATCTTTAACT	AGTTTATCAT	TTAGTATATC	1260
TTCAGGCTTT	CCCTCTGCAA	CAAGTTTACC	TTCTTTAATT	GCAAATAGGT	AATCAGCGTA	1320
TCTTGCTGTT	AGATTTATAT	CGTGCAAAAT	CATGCAAAATG	GTTGTCTTAT	ATTTTTGGTT	1380
TAGATCAGTC	AAGAGGTCTA	ATAGTTCTAT	TTGATATGAG	ATATCCAAGT	AAGTAGTTGG	1440
CTCATCTAAA	AGTAGGATAC	TTGTATCTTG	GGCTAGGGCT	AGAGCTATCC	ATACTCTTTG	1500
CCTTTGACCC	CCAGAAAGTT	CTTCAACTAG	GTTATTTGCT	AGATCTTCAA	CATTGGCCTT	1560
AACCATTGAT	CTGTTTATTA	TTTCAAGGTC	ATCTTTTCCA	AGACTCTTAA	AAGGCTTTCT	1620
GTAGGGGAAA	CGACCACGGC	TTACAAGATC	AGCTACTGTT	ATTGATTCAG	GGATTATTGG	1680
AGATTGAGGT	AATATAGCTA	TGTGTTTTGC	TAAATCTTTT	TCTTTATAAG	AATTAATTGA	1740

1199

TTTATTATCA	AGCAATACTT	CTCCCTCTAA	TGGCTTTATA	AGTCGAGACA	AGGTTTTAAT	1800
GAGTGTTGAT	TTCCCACAAC	CATTTGACCC	AATAATAACT	GATATTTTTT	CTTCAGGTAT	1860
TTTTATATTT	ATATTTTCCA	AGATTATTTT	TTCATCATAA	CCGCAGGTAA	GATTATTTGA	1920
CCACAGACCT	TTCATTATAT	ATTCCTCCTG	TTCATTTTTA	TTAGTAAGTA	TATTAAGTAT	1980
GGTGAACCTA	ACAAGCCAGT	TACAACACCT	ACTGGATATC	TAGCTGGTAA	AATATTTTGA	2040
GAGAATATGT	CTGATAACAA	AACTAGTAAA	ATTCCAACCA	ATCCAGCTAA	TATTGGGCTT	2100
CTTTTCTTGC	CAATATTTAA	GGCTATGGGA	CCAGCTAAAA	AAGATATACA	AGCTATTGGT	2160
CCTGTAATTG	AAGTAGAAAA	AGCAGTTAAA	GATACAGCGC	AAAAAATTAA	AACAAGCCTT	2220
GAAAGCTCGG	GATTTGCTCC	AAGTCCGATT	GCTATTTCTT	CACCAAGTTC	AATAATTTCT	2280
AGTCTTTTAT	TAAAAAATAA	AACTAATATA	GTAGCAATAA	TACTTACTAT	TAGAACAAGA	2340
GGTATGTCAT	CTAACTTTGT	AAAAGATAAA	GAGCCACTGA	GCCATCTCAT	AACTTCTTGT	2400
AATTCATATC	TTGCTACTTT	CAACAATAAA	AATGAGGTGC	CTGCTCTTGT	GACAGCTTGA	2460
AAACCAATAC	CTAATATTAT	CAGTCTTGCT	GCTGAAAAAC	CATCTTTTTT	AGCTAGTAAA	2520
AATAATATTA	AAGATGATGT	TAGTCCACAA	GTTATTGAAA	TAATTCCAGT	AGTTAAACTA	2580
TTTGTTTTTA	ATACCAATAT	GCAAAAGACC	GCTGCAATAG	ATGAAGAACT	TGTGACACCG	2640
ATTATATCAG	GACTTGCAAG	AGGATTTCTT	AACATAGTTT	GAAAGATAAA	TCCTGCCAAT	2700
CCAAAAGACC	AGCCAGCTAT	AATTCCTGCT	AATAATTTTG	GTAATCTAAT	TTCCATAATC	2760
GAAAACTAG	CTCCAGGAAC	AGTTTCACTA	TTTAAGACTT	TAATCAAAGT	TGAAAAAGAA	2820
TAACTTTCAT	CTCCGATAAG	TAAAATGAAA	AATGATAGAC	TGATTATTAT	TAATAAAAAAT	2880
AGTGAGGAAA	ATAGTGTTAT	TCTATTTTTT	CTTTTTTGAA	TACCTATAAT	TAAATTTTGC	2940
ATTAGTTATT	AACCCCTCTA	TTTTTTCATAG	TTACATAAAT	AAGTACTGGA	CCCCGATTA	3000
TTGCAGTAAT	TATCCCTACT	TCAATTTCAC	CTGGTTTACC	TAACATACGG	CCGATTATAT	3060
CACATATAAG	CAAGAGCTCT	GCACCTATAA	AAGATGAAGA	AATGGTCATT	GTGCGTATAT	3120
CTTTGCTTAT	AAATAAGCCA	CAAAAGTGAG	GAACATAAAG	ACCTACGAAG	CCAATAGGTC	3180
CACCAATTGC	AGTAATACTT	GAACATAAAA	GCACACTTGC	AATTATTGCA	AGTGATCTTA	3240
TCCTATTAAAC	ATTAACCTCA	AGACCAACAG	CCATTTTCATC	ACCCATAGcT	AAAGCGTTTA	3300
AATCTGATGA	AATAAATATA	GCTATCAAGT	GACCTAAAAT	TATAAAAGGT	AGTAGTGTAG	3360
ATATAGAAGA	TAATGTAGCT	GCTCCAAGGC	TACCTATTTG	CCAAAATCTA	AATTTGTCTA	3420
AGACGTTATT	ATTCGGTAAA	ATTAAAAAAC	TTACAAAAC	GCTTAAAGCC	ATACTAACAC	3480

1200

AAGTTCCTGA TAAGGCAAGT TTTATAGGGG TAAGGCCTGC TTTTCCGTTA CAGCAATCGC	3540
GTATACAAAA ATTGCACTTA CTAAGCCACC AATGATTGCG	3580

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

CCAAATTGCT CCACAATTAT TATGGAGTCG TCGTTTGGCA GATGGGCGTG ATATGTGTGC	60
TCAAGAATGG TTGACAGGCA AGATATTGAC CCCCTATGAT ATGAATCGTA AGCAAATCGT	120
CAATATTTTA ACCCGTCTTC ATCGCTCAGC TCCGTTGATG ACACAATTGA GTCGTTTGGG	180
CTATGCCATG GAAACACCTG TAGATTTACT ACAGTCTTGG CAGGAAACGG CTCCAGATGC	240
TTTGCGTAAA AATCATTTTA TCAGTGAAGT GATGGCTGAT TTACGTCAGA CTATTCCAGG	300
ATTTAGAGAG GACCATGCGA CCATTGTCCA TGGAGATGTA CGACATAGTA ATTGGATTGA	360
GACAGATAGT GGCTTGATTT ATTTAGTAGA TTGGGATTCG GTTCGCTTGA CCGATCGCAT	420
GTTTGATGTG GCCCATATGC TCTGCCATTA TATTTTCAGAA CATCAGTGGA AGGAATGGTT	480
GACCTACTAC GGTTACAAGT ACAATCAAAC GGTATTAAGT AAATTGTATT GGTATGGTCA	540
ATTGTCTTAT TTGAGTCAGA TTTCCAAGTA TTATATGAAC CAAGATTTAG AAAATGTCAA	600
TCGGGAGATT CATGGTTTGC GTCATTTCCG AGACAAGTAT GGAAAGAGAA GATGAGAGTT	660
AGAAATCGTA AAGGGGCAAC AGAATTACTA GAGGCAAATC CCCAGTATGT GGTCTCAAT	720
CCCTTGGAAG CCAAGGCAAA ATGGCGGGAC TTGTTTGGCA ATGATAATCC CATTCATGTG	780
GAAGTTGGAA GTGGAAAGGG TGCCTTTGTT TCAGGTATGG CCAAGCAAAA CCCTGACATC	840
AACTATATCG GGATTGATAT TCAAAAGTCT GTTTTGAGCT ACGCTTTGGA CAAGGTGCTT	900
GAAGTTGGAG TGCCTAACAT CAAGCTCTTG TGGGTAGATG GTTCTGACTT AACTGACTAC	960
TTTGAAGACG GTGAGATTGA TCGCTTGATC CTGAACTTTT CAGATCCATG GCCGAAAAAA	1020
CGCCATGAAA AGCGTCGTTT GACCTACAAG ACCTTCTTGG ATACCTTCAA ACGTATCTTG	1080
CCTGAAAATG GAGAAATTCA TTTCAAGACG GATAACCGTG GCTTGTTTGA GTACAGTTTA	1140
GTGAGCTTTT CTCAATATGG CATGAAACTC AATGGTGTCT GGTAGATTT GCATGCCAGT	1200
GATTTTGAAG GCAATGTCAT GACAGAATAC GAGCAAAAAT TCTCAAACAA GGGGCAAGTT	1260
ATCTACCGAG TTGAGGCAGA ATTTTAAGAG ATAACCTAAA ATTAGGCTGT ACAAGTGCTT	1320

1201

TTGCTTTACA	TAAGTTGGCA	AACGTGCTAT	ACTGATAGTA	AGAATATGAA	AAGTGAGGCG	1380
GGGAAATATC	TTCGCCTCTT	GCTTATGAGG	AGGTGGACGC	AATCGCAACA	ATCGTAGAAT	1440
TAGTCAGAGA	AGTTGTAGAA	CCTGTCATAG	AAGCTCCTTT	TGAACTCGTG	GATATCGAGT	1500
ATGGAAAGAT	TGGCAGTGAC	ATGATTCTCA	GTATTTTGT	AGATAAACCC	GAAGAATTAC	1560
CTTGAACGAC	ACGGCAGACT	TGACAGAAAT	TATCAGTCCT	GTCCTAGACA	CCATCAAGCC	1620
AGATCCCTTC	CCAGAACAAT	ATTTCCTAGA	AATTACCAGT	CCAGGTTTGG	AACGTCCTTT	1680
GAAAACCAAG	GATGCCGTCG	CTGGAGCGGT	TGGAAAATAC	ATCCATGTCG	GGCTCTACCA	1740
AGCCATCGAT	AAGCAAAAGG	TCTTTGAAGG	AACCTTGTTG	GCCTTCGAAG	AGGACGAGTT	1800
GA CTATGGAA	TATATGGACA	AGACGCGTAA	GAAAACCGTC	CAAATTCCAT	ACAGTTTAGT	1860
ATCAAAAGCA	CGTTTAGCAG	TTAAATTATA	GAAAAAGAAA	GGATAGCTTT	TGAGGATTCA	1920
AAAGTGAAGA	AAACATGAGT	AAAGAAATGC	TAGAGGCCTT	CCGCATTTTG	GAAGAAGACA	1980
AGGGAATCAA	AAAAGAAGAT	ATCATCGACG	CAGTAGTAGA	GTCGCTTCGT	TCCGCTTATC	2040
GCAGACGCTA	TGGTCAGTCA	GACAGCGTAG	CTATTGACTT	CAACGAAAAA	ACAGGTGACT	2100
TTACAGTTTA	TACTGTCCGT	GAAGTTGTTG	ATGAAGTATT	TGATAGCCGT	TTGGAAATCA	2160
GCTTGAAAGA	TGCTCTTGCC	ATTAATTCAG	CTTATGAACT	TGGAGACAAA	ATCAAGTTTG	2220
AAGAAGCACC	AGCTGAGTTT	GGTCGTGTAG	CAGCCCAATC	TGCCAAACAA	ACCATCATGG	2280
AAAAAATGCG	CAAGCAAACA	CGTGCCATCA	CTTACAATAC	TTACAAAGAA	CATGAGCAAG	2340
AAATCATGTC	TGGTACAGTA	GAACGCTTTG	ACAACCGCTT	TATCTATGTC	AACCTTGGTA	2400
GCATCGAAGC	CCAATTGTCA	AAACAAGACC	AAATTCCTGG	AGAAGTTTTT	GCTTCTCATG	2460
ATCGTATCGA	AGTTTATGTT	TACAAGGTTG	AAGACAACCC	TCGTGGTGTG	AACGTCTTTG	2520
TTAGCCGTAG	TCATCCAGAA	ATGATCAAAC	GTTTAATGGA	GCAAGAAATT	CCAGAAGTTT	2580
ATGATGGAAC	TGTTGAAATC	ATGAGCGTGG	CTCGTGAAGC	AGGTGACCGT	ACGAAGGTTG	2640
CTGTTCTGTAG	CCACAATCCA	AACGTGGATG	CTATCGGTAC	AATCGTTGGA	CGTGGTGGTG	2700
CTAATATCAA	GAAGATTACT	AGCAAATTCC	ACCCAGCTCG	TTACGATGCT	AAAAATGACC	2760
GCATGGTACC	AATCGAAGAA	AATATCGATG	TTATCGAGTG	GGTAGCAGAT	CCAGCTGAAT	2820
TTATCTACAA	TGCCATCGCT	CCTGCTGAGG	TTGACCAAGT	TATCTTTGAT	GAAAACGACA	2880
GCAAACGTGC	CTTGGTGGTT	GTTCCAGATA	ACAAGCTTTC	TCTTGCCATT	GGTCGTCTGT	2940
GACAAAACGT	GCGCTTGGCG	GCTCACTTGA	CTGGTTACCG	TATCGATATC	AAGTCTGCTA	3000
GCGAATTTGA	AGCCATGGAA	GACGCTGCTT	CAGTAGAGTT	GGAAGTAGAA	AACGATACTG	3060

1202

TAGAAGAATA	AAAGCTGCTA	GAGGAGGGAA	AGATGAAAAC	AAGAAAAATC	CCTTTGCGCA	3120
AGTCTGTTGT	GTCTAACGAA	GTGATTGATA	AGCGTGATTT	GCTCCGCATT	GTCAAGAACA	3180
AGGAAGGACA	AGTCTTTATT	GATcCTACGG	GCAAGGCCAA	TGGCCGCGGC	GCTTATATCA	3240
AACTAGACAA	TGCAGAAGCC	CTAGAGGCCA	AAAAGAAGAA	GGTCTTTAAC	CGCAGCTTTA	3300
GCATGGAAGT	GGAAGAAAGC	TTTTATGACG	AGTTGATCGC	TTATGTGGAT	CACAAAGTGA	3360
AAAGAAGAGA	GTTGGGACTT	GAATAAGCAA	AAGATAAGTA	ATCTCTTGGG	GCTTGCTCAG	3420
CGAGCAGGGC	GCATCATATC	GGGTGAAGAA	TTGGTGGTCA	AGGCCATTCA	AGACGGCAAG	3480
GCCAAGTTGG	TCTTTCTAGC	TCATGATGCT	GGACCCAATC	TGACCAAGAA	GATTCAAGAT	3540
AAAAGTCATT	ATTATCAAGT	AGAAATTGTA	ACCGTGTTTT	CAACACTGGA	ATTAAGCATA	3600
GCAGTCGGGA	AATCGAGAAA	GGTTTTGGCT	GTAACAGATG	CTGGATTTAC	AAAGAAAATG	3660
AGGTCTCTTA	TGGAATAGAA	GAGGAGGACA	TGATTTGTCT	AAGAAAAGAT	TGTACGAAAT	3720
CGCAAAAGAA	CTTGGAAGAG	AAAGTAAAGA	AGTTGTAGCG	CGTGCAAAAG	AGTTGGGCTT	3780
GGATGTGAAA	AGCCACTCAT	CAAGTGTGGA	AGAAGCTGTC	GCTGCAAAAA	TTGCTGCCAG	3840
CTTTAAGCCT	GCAGCTGCTC	CGAAAGTAGA	AGCAAAACCT	GCAGCCCCAA	AAGTAAGTGC	3900
AGAAAAGAAA	GCCGAAAAAT	CTGAGCCAGC	TAAACCAGCT	GTAGCTAAGG	AAGAGGCAAA	3960
ACCTGCAGCC	CCAAAAGCAA	GTGCAGAAAA	GAAAGCCGAA	AAGTCTGAAC	CAGTAAAACC	4020
AGCTGTAGCC	AAGGAAGAGG	CAAAACCAGC	TGAGCCAGTC	ACTCCGAAAA	CAGAAAAAGT	4080
AGCGGCTAAA	CCGCAAAGTC	GTAATTTCAA	GGCTGAGCGT	GAAGCACGTG	CTAAAGAGCA	4140
GGCAGAGCGA	CGCAAGCAAA	ATAAGGGCAA	TAACCGTGAC	CAACAACAAA	ACGGAAACCG	4200
TCAGAAAAAC	GACGGCCGTA	ATGGTGGAAG	ACAAGGTCAA	AGCAACCGCG	ACAATCGTCG	4260
CTTTAATGAC	CAAGCTAAGA	AGCAGCAAGG	TCAGCAAAAA	CGTAGAAATG	AGCGCCGTCA	4320
GCAAGAGGAT	AAACGTTCAA	ATCAAGCGGC	TCCACGTATT	GACTTTAAAG	CCCGTGCAGC	4380
AGCCCTAAAA	GCAGAGCAAA	ATGCAGAGTA	CGCTCGTTCA	AGTGAGGAAC	GCTTCAAGCA	4440
GTATCAGGCT	GCTAAAGAAG	CCTTGGCTCA	AGCTAACAAA	CGCAAGGAAC	CAGAGGAAAT	4500
CTTTGAAGAA	GCGGCTAAGT	TAGCTGAACA	AGCACAGCAA	GTTCAAGCAG	TGGTTGAAGT	4560
CGTCCCTGAG	AAAAAAGAAC	CTGCAGTGGA	TACACGTCGT	AAAAACAAG	CTCGACCAGA	4620
CAAAAATCGT	GACGATTATG	ATCATGAAGA	AGATGGTCCT	AGAAAACAAC	AAAAGAATCG	4680
AAGTAGTCAA	AATCAAGTGA	GAAATCAAAA	GAATAGTAAC	TGGAATAACA	ACAAAAAGAA	4740
CAAAAAGGC	AATAACAAGA	ACAACCGTAA	TCAGACTCCA	AAACCTGTTA	CGGAGCGTAA	4800
ATTCCATGAA	TTGCCAACAG	AATTTGAATA	TACAGATGGT	ATGACCGTTG	CGGAAATCGC	4860

1203

AAAACGTATC	AAACGTGAAC	CAGCTGAAAT	TGTTAAGAAA	CTTTTCATGA	TGGGTGTCAT	4920
GGCCACACAA	AACCAATCCT	TGGATGGGGA	AACAATTGAA	CTCCTCATGG	TGGATTACGG	4980
TATCGAAGCC	AAACAAAAGG	TTGAAGTGGA	TAATGCTGAC	ATCGAACGTT	TCTTTGTCGA	5040
AGATGGTTAT	CTCAATGAAG	ATGAATTGGT	TGAGCGTCCA	CCAGTTGTTA	CTATCATGGG	5100
ACACGTTGAC	CACGGTAAAA	CAACCCTTTT	GGATACTCTT	CGTAACTCAC	GTGTTGCGAC	5160
AGGTGAAGCA	GGTGGTATTA	CTCAGCATAT	CGGTGCCTAC	CAAATCGTGG	AAAATGGTAA	5220
GAAGATTACC	TTCCTTGATA	CACCAGGACA	CGCGGCCCTT	ACATCAATGC	GTGCGCGTGG	5280
TGCTTCTGTT	ACCGATATTA	CGATCTTGGT	CGTAGCGGCA	GATGACGGGG	TTATGCCTCA	5340
GACTATTGAA	GCCATCAACC	ACTCAAAAGC	AGCTAACGTT	CCAATCATCG	TAGCTATTAA	5400
CAAGATTGAT	AAACCAGGTG	CTAACCCAGA	ACGCGTTATC	GGTGAATTGG	CAGAGCATGG	5460
TGTGATGTCA	ACTGCTTGGG	GTGGAGATTG	TGAATTTGTT	GAAATTTTCGG	CTAAATTCAA	5520
CCAAAATATC	GAAGAATTGT	TGGAAACAGT	CCTTCTTGTT	GCTGAAATCC	AAGAACTCAA	5580
AGCAGACCCA	ACAGTTCGTG	CGATCGGTAC	GGTTATCGAA	GCGCGCTTGG	ATAAAGGAAA	5640
AGGTGCGGTC	GCAACCCTTC	TTGTACAACA	AGGTACCTTG	AATGTTCAAG	ACCCAATCGT	5700
TGTCGGAAAT	ACCTTCGGTC	GTGTCCGTGC	TATGACCAAC	GACCTTGGTC	GTCTGTGTTAA	5760
AGTTGCTGGA	CCATCAACAC	CAGTCTCTAT	CACAGGTTTG	AACGAAGCAC	CGATGGCGGG	5820
TGACCACTTT	GCCGTTTACG	AGGATGAAAA	ATCTGCGCGT	GCAGCAGGTG	AAGAGCGTGC	5880
CAAACGTGCC	CTCATGAAAC	AACGTCAAGC	TACCCAACGT	GTTAGCCTTG	AAAACCTCTT	5940
TGATACCCTT	AAAGCTGGGG	AACTCAAATC	TGTTAATGTT	ATCATCAAGG	CTGATGTACA	6000
AGGTTCTGTT	GAAGCCCTTT	CTGCCTCACT	TCAAAAGATT	GACGTGGAAG	GTGTCAAAGT	6060
GACTATCGTC	CACTCAGCGG	TCGGTGCTAT	CAACGAATCA	GACGTGACCC	TTGCCGAAGC	6120
TTCAAATGCC	TTTATCGTTG	GTTTCAACGT	ACGCCCTACA	CCACAAGCTC	GTCAACAAGC	6180
AGAAGCTGAC	GATGTGGAAG	TCCGTCTTCA	CAGCATTATC	TACAAGGTTA	TCGAAGAGAT	6240
GGAAGAAGCT	ATGAAAGGGA	TGCTTGATCC	AGAATTTGAA	GAAAAAGTTA	TTGGTGAAGC	6300
GGTTATCCGT	GAAACCTTCA	AGGTGTCTAA	AGTGGGAACT	ATCGGTGGAT	TTATGGTTAT	6360
CAACGGTAAG	GTTGCCCCGTG	ACTCTAAAGT	CCGTGTTATC	CGTGATGGTG	TCGTTATCTA	6420
TGATGGTGAA	CTCGCAAGCT	TGAAACACTA	TAAAGACGAC	GTGAAAGAAG	TGACAAACGG	6480
TCGTGAAGGT	GGATTGATGA	TCGACGGCTA	CAATGATATT	AAGATGGATG	ATGTGATTGA	6540
GGCGTATGTC	ATGGAAGAAA	TCAAGAGATA	AGATTTTTTG	CTCCTTTCTT	AGGTGGTGAG	6600

1204

GGACGCAAGC	AAACCGATGG	TTTCATTGCT	TATTTTGTGAG	CCTAGGGTCT	CAAAAATCCC	6660
CTGTGATGGG	ACTGATAAAT	CAGTTCCATC	ACTTTCACCA	CGGCGAAAGA	AGCAGATGAC	6720
TTCAAATTGA	ACTTCGTTTC	AATTTAAACT	GAAAATCAAG	AAGTTTAAAA	TAGCTAGGTC	6780
TGCTGGCCTA	GCTTTTGGTT	CAAAGTAGAG	AAAGGAATAT	CATGGCAAAT	CATTTCCGTA	6840
CAGATCGTGT	GGGCATGGAA	ATCAAGCGTG	AAGTCAATGA	GATTTTGCAA	AAGAAAGTCC	6900
GTGATCCACG	TGTCCAAGGT	GTGACCATCA	TAGATGTTCA	GATGCTGGGT	GACTTGTCTG	6960
TTGCCAAGGT	TTATTACACC	ATTTTGAGTA	ACCTTGCTTC	GGATAACCAA	AAAGCCCCAA	7020
TCGGGCTTGA	AAAAGCAACT	GGTACCATCA	AACGTGAACT	TGGTCGCAAT	TTGAAATTGT	7080
ACAAAATCCC	AGATTTGACC	TTCGTCAAAG	ACGAGTCCAT	CGAGTATGGA	AACAAGATTG	7140
ACGAGATGCT	ACGCAATCTG	GATAAGAACT	AAAGAAGAGG	GGTTGCCCCCT	CTTTTTTGGT	7200
GGAGGAAAAT	AGGTTGAATT	TGAAATGGAA	AAATATTCTT	TTATAATAGA	TTGAAACTAG	7260
AATAGTACGC	CTCTACTTCT	AAAATATTGT	TAGAAATCGA	TTTGACTGTC	CTGATCGATT	7320
TGTCCTGTTC	TTGTTTCATT	TTAATATAAA	AAAGGGATTC	TGTATTTTTT	AATGTTATCT	7380
AATTAGAAAA	TGCTTTTTTT	GTAGGAAATA	TAATATGATA	AGGTGCAAAA	AAGAAATAAG	7440
GAGTTTGTAT	ATGGCTGAAC	AAGACTTAGC	TATGCAAGTA	TTGCAACAAG	TGGTGAAACT	7500
ACCTGTTGTT	AAGGTTGATC	GTTCGAAATT	TTTAGTGGAT	AAGTTTCCA	AAGAATTGGA	7560
TCCAAAAGAT	ATTCCTACCT	TATTGGAACA	AGGTCCAACG	ACTCTTCTAT	CTCAAGAAAT	7620
ATTAGATCGT	GTAGCTAATG	CTTGATATCG	GGACAATGTA	TTATTAGCGA	GTGGGACTTC	7680
TGTTTTGGCA	GGATTACCTG	GAGGGCTTGC	TATGGCAATT	ACCATTCCAG	CTGATGTGGC	7740
TCAATTTTAT	GCTTTCTCTC	TGAAATTGGC	TCAAGAATTA	GGTTATATTT	ATGGTTATGA	7800
GGATCTTTGG	GCTTCACGAG	AGGAGTTGAG	TGAAGATGCT	CAAAATACCC	TCTTGCTTTA	7860
TCTAGGCGTA	ATGTTAGGGG	TGAATGGAAC	CGCTGCTTTG	CTACGTGTTG	GTAGTATAAC	7920
AATTGCCAAA	CAGGTAATGA	AAATAGTGCC	TAATAAAGCT	TTAACAAAGA	CGCTTTGGTA	7980
CCCTATTTTG	AAAAAAGTCT	TAAAAATATT	TGGTGTGAAT	CTTACCAAGG	GAGGGTTGGC	8040
CAAAGGAATG	GGGAAATTTA	TTCCTATCTT	GGGTGGTATC	ATTTTCAGGTG	GTTTAACCTT	8100
TGCAACTATG	AAACCAATGG	GGGAAAGCTT	GCAGAAAGAA	TTATCCAAGC	TAGTCAACTA	8160
TAGTGAAGTT	CAATATCAAG	AAGATGTTGA	AACAATCCGA	AAAGAGGCTG	AAATCATCAA	8220
AGGAGAGTAA	TATGAATCCT	ATCAAAGCTT	TTGCTAAAAT	TTATGGTAAT	TACTTTTTGA	8280
CCGTGCAAGG	TGTAAAAGTG	ATGAAAACGA	TAAAGAAAGC	TGACCATGTC	GTTGTTGGTC	8340
TGGGGAAACT	TTTTATTGCC	GACAAGTTAA	TGGATACGGC	TCGGTGGCTC	ATTAAGCCAG	8400

1205

AGGAGAGAGA	ATGAAATTTT	TTTGGTCTTC	TTGCTATTCT	TTTTATCAAA	CCGATTATTG	8460
GGATTGTGAA	ATTCTTTTGG	ATGATCATCT	CTTTTGCAGT	CCAATTGCTG	TTTTACAAGA	8520
TAGTGTTTAA	GATATTGGAT	TGGCTCTTTA	AACTTATCTA	GATGGTAATC	CAAGTTGCAG	8580
AGAACTAGCA	GGAAGTCCAC	TGCTAGTTTT	TTATTCTCTT	TCCATATGGT	ATAATATAAG	8640
CAGTAAAATC	ATTTTATACT	CTTCGAAAAT	CTCTTCAAAC	CACGTCAGCT	TCACCTTGCA	8700
GTATATATGT	TACTGACTTC	GTCAGTTCTA	TCCACAACCT	CAAAACGGTG	TTTTGAGCTG	8760
ACTTCGTCAG	TTCTATCTAC	AACCTCAAAA	CACTGTTTTG	AGCAACCTGC	GGCTAGCTTC	8820
CTAGTTTGCT	CTTTGATTTT	CATTGAGTAT	TAGAACATAC	AATGGAGGTC	GTCATGGACA	8880
ATATCATCGA	TGTGTCAATT	CCTGTTGCAG	AAGTGGTGGA	CAAGCATCCA	GAAGTCTTGG	8940
AAATTCTAGT	GGAGTTGGGT	TTTAAACCCC	TTGCCAATCC	CTTAATGCGC	AATACAGTTG	9000
GTCGTAAAGT	ATCACTTAAA	CAGGGTTCTA	AGCTAGCAGG	AACTCCTATG	GACAAGATTG	9060
TACGCACACT	GGAAGCGAAT	GGCTACGAAG	TGATTGGATT	AGACTAATGA	CAGATGAACG	9120
GATTCATATC	CTACGGGATA	TTTTGTTAGA	ATTGCACAAT	GGCGCCTCTC	CTGAGTCGGT	9180
TCAAGATCGC	TTTGATGCGA	CCTTTACGGG	CGTGTGAGCC	ATCGAGATTT	CCCTTATGGA	9240
GCACGAGCTG	ATGAACTCGG	ATTCGGGCGT	CACTTTTGAA	GATGTTATGG	AACTCTGTGA	9300
TGTCCATGCC	AATCTTTTTA	AAAATGCTAT	CAAAGGTGTC	GAAGTTTCAG	ATACTGAGCA	9360
TCCAGGTCAC	CCAGTTCGTG	TCTTCAAAGA	AGAAAATCTG	GCTCTCCGTG	CGGCCTTGAT	9420
TCGCATTTCG	AGATTGTTAG	ATACCTATGA	GTCTATGGAA	GACGAGGAAA	TGCTGGCGGA	9480
GATGCGTAAG	GGTTTGGTGC	GTCAGATGGG	ACTTGTGGGT	CAATTTGACA	TCCATTACCA	9540
ACGTAAGGAA	GAACTCTTCT	TTCCTATCAT	GGAGCGCTAT	GGACACGATT	CACCTCCCAA	9600
AGTTATGTGG	GGAGTGGATG	ATCAGATTAG	GGAAGTCTTT	CAAACAGCTC	TAACGACAGC	9660
CAAGTCACTA	CCAGAAGTGT	CAATTAGCAG	TGTAAAGGAA	GCTTTTGAAG	CTTTTGCGAC	9720
AGAGTTTGAA	AGTATGATTT	TCAAGGAAGA	GTCCATCCTC	CTCATGATTC	TCCTTGAGTC	9780
TTTTACTCAG	GATGACTGGC	TTCAGATTGC	GGAGGAGAGC	GATGCCTATG	GCTATGCCAT	9840
CATCCGTCCG	TCAGAGAAAT	GGGTGCCAGA	ACGACAGAGC	TTTATTGAGG	AAAAGATTGC	9900
AGAGGAGCCT	GTACAGCTAG	ATACGGCAGA	AGGTCAAGTT	CAACAAGTCA	TAGATACGCC	9960
AGAAGGCCAT	TTTACCATTA	CCTTTACCCC	TAAGGAAAAG	GAAGCTGTGC	TGGACCGCCA	10020
TAGTCAACAG	GCTTTTGGTA	ATGGCTATCT	TTCAGTCGAG	CAGGCCAATC	TCATCCTCAA	10080
TCATCTCCCT	ATGGAGATTA	CCTTTGTCAA	TAAAGAAGAT	ATTTTCCAGT	ATTACAATGA	10140

1206

CAATACGCCA GCTGATGAGA TGATTTTCAA ACGGACGCCG TCCCAAGTCG GCGCAATGT	10200
CGAACTCTGC CATCCGCCTA AGTACTTGGA CAAGGTCAAA ACTATCATGA AGGGGCTTCG	10260
TGAGGGAAGC AAAGACAAGT ATGAAATGTG GTTCAAGTCT GAGTCGCGAG GTAAGTTTGT	10320
CCACATCACC TATGCTGCAG TACACGATGA AGACGGAGAA TTCCAAGGAG TGTGAGTA	10380
TGTTCAAGGAT ATCCAGCCCT ACCGTGAGAT TGATACGGAC TATTTTCGTG GATTAGAATA	10440
AGGAGAAAAA ATGAGTTACG AACAAGAATT TATGAAGGAA TTTGAAGCTT GGGTCAATAC	10500
CCAAATCATG ATTAACGACA TGGCGCACAA GGAAAGCCAA AAAGTTTACG AAGAAGACCA	10560
GGACGAGCGT GCCAAAGATG CCATGATTCG CTACGAGAGT CGCTTGGATG CTTATCAGTT	10620
CTTGCTTGGT AAGTTTGAAA ACTTCAAAGT AGGCAAGGGA TTCCATGATT TGCCAGAAGG	10680
CTTGTTTGGT GAGCGAAATT ATTAACGAG AAAGATTCTT GATTTTTCAC TAAAATCTTG	10740
ATAGAATGTT TATGTTAAAT CCTTGTCAGA GCAGGGATTT TTTATTGAAA GGATTTTATC	10800
ATGTCAAAGA AACTCAATCG TAAAAACAA TTACGAAATG GCCTCCGTCG CGCAGGTGCC	10860
TTTTCAAGTA CGGTGACTAA GGTGTAGAT GAGACAAAAA AAGTCGTGAA GCGTGCAGAA	10920
CAGTCAGCAA GCGCAGCTGG TAAGGCTGTT TCTAAAAAAG TTGAACAAGC AGTAGAAGCT	10980
ACCAAAGAGC AAGCTCAAAA AGTAGCTAAT TCTGTAGAAG ATTTTGCAGC AAATTTGGGT	11040
GGACTTCCAC TTGATCGTGC CAAGACTTTC TATGATGAAG GAATCAAGTC TGCTTCAGAT	11100
TTCAAAAAC TGGACTGAAAA AGAACTCCTT GCCTTGAAAG GAATCGGCCC AGCTACCATC	11160
AAGAAATTGA AAGAAAATGG CATCAAGTTC AAGTAATTTT TCTTGAGCCT TGCATTTCCG	11220
AAAAAATCTT GCTACAATAG AGCCATTAGA GGTGTTTTGA ATCCACATT TTACAGAAAG	11280
TGGCGGCGCT GAGAAGTCCA CAAATGTGTC AAAACTGGTT GCTAATGGAT GAAAAATTGA	11340
AATAAAAGTG TCTTTTGTCT TTAAAGACGA GAGTTGCG	11378

(2) INFORMATION FOR SEQ ID NO: 211:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

CCGCGAGCCA CGGCGAATTT GCTGCGGGTA TTCATCAGTC AGGATCTATG ATCTTTGGTG	60
AACAAGAAAA GGTTCAGTT GTGACCTTA TGCCAAATGA AGGTCCTGAT GATCTATACG	120
CTAAGTTTAA TAACGCTGTT GCTGCATTTG ACGCAGAAGA TGAGGTTCTA GTTTTGGCTG	180

1207

ACCTTTGGAG TGGTTCTCCA TTTAACCAAG CTAGTCGCGT GATGGGAGAA AATCCTGAGC	240
GTAAGTTTGC CATCATCACA GGACTTAACT TACCGATGTT GATTCAAGCC TACACAGAGC	300
GCCTCATGGA CGCTGCTGCA GGTGTAGAAA AAGTCGCTGC TAATATCATT AAAGAAGCCA	360
AAGATGGCAT CAAAGCTCTT CCAGAAGAGC TAAATCCAGT CGAAGAAGTT GCAAGCGCTG	420
CAGCTGCTCC AGTTGCCCAA ACTGCTATCC CAGAAGGAAC TGTATATCGGA GACGGTAAAT	480
TGAAAATCAA TCTTGCCCCG CTTGACACAC GTCTACTTCA CGGTCAGGTT GCAACTGCTT	540
GGACTCCAGA TTCAAAGCA AATCGTATCA TCGTTGCTTC AGATAACGTG GCTAAAGACG	600
ACCTTCGTAA AGAATTGATT AAACAAGCAG CTCCAGGTAA TGTCAAGGCT AACGTGGTTC	660
CAATTCAAAA ACTGATTGAG ATTTCAAAAAG ACCCACGTTT TGGAGAAACA CATGCCCTTA	720
TCTTGTTTGA AACACCTCAA GATGCCCTTC GTGCCATCGA AGGCGGCGTG CCAATCAAGA	780
CTCTTAATGT TGGTTCTATG GCTCACTCAA CAGGTAAAAC ATTGGTCAAT ACCGTTTTGT	840
CTATGGACAA AGAAGACGTT GCTACATTTG AAAAAATGCG TGAATTGGGT GTTGAATTTG	900
ATGTCCGTAA AGTACCAAAT GATTCTAAAA AAGATTTGTT TGAATTGATT AACAAAGCCA	960
ATGTCAAATA AGCCATTATT TATGAAAGGA TTTTAAACAT GTCTATTATT TCTATGGTTT	1020
TAGTAGTCGT TGTAGCCTTC TTTGCAGGTC TTGAAGGCAT CCTCGACCAG TTCCAATTTT	1080
ACCAACCACT TGTAGCCTGT ACCCTTATTG GGCTTGTAAC AGGTCACCTG GAAGCAGGGA	1140
TTATCCTCGG TGGATCGCTT CAAATGATTG CCCTTGCTTG GTCAAATATC GGTGCTGCTA	1200
TCGCTCCTGA TGCTGCACTT GCTTCTGTCTG CTGCTGCCAT TATCATGGTT CTTGGTGGTG	1260
ACTTTACCAA GACTGGTATC GGTGTTGCCC AAGCGGTTGC TATCCCTCTT GCTGTAGCTG	1320
GACTTTTCTT GACAATGATT GTTCGTACAA TTTCAGTTGG TTTGGTTCAT ACTGCAGATG	1380
CTGCCGCTAA AAAAGGTGAC TTCGGCGCTG TGGAGCGTGC GCATTTTCATC GCGCTACTTT	1440
TCCAAGGACT TCGTATCGCG CTTCTGTCAG CTCTTCTCCT TATGGTACCA ACTGAAACTG	1500
TACAAAGTAT CCTTAGTGCC ATGCCAGACT GGCTCAAAGA TGGTATGGCT ATCGGTGGTG	1560
GTATGGTCGT TGCCGTTGGT TACGCCATGG TTATCAACAT GATGGCAACT CGTGAAGTAT	1620
GGCCATTCTT CGCTCTTGGT TTCGTTCTCG CTGCTGTGTC AGATATTACT CTAATCGGAT	1680
TCGGTGCTAT CGGCGTTGCT ATCGCTCTTA TCTACCTTCA CCTTTCTAAA ACTGGTGGAA	1740
ATGGTGGCGG AGGAGCCGCA ACTTCTAACG ACCCAATCGG CGATATCCTA GAAGACTACT	1800
AAGATAAGAA AGGACTGAAA ACATCATGAC TGAAAAACTT CAATTAAC TAATCAGATCG	1860
TAAAAAAGTT TGGTGGCGTT CAACCTTCTT ACAAGGGTCT TGGAACCTTG AACGGATGCA	1920

1208

AAACTTGGGC	TGGGCTTATA	CACTCATTCC	AGCTATCAAA	AAACTCTATA	CTAAAAAAGA	1980
AGATCAAATC	GCTGCTCTTG	AGCGTCACCT	TGAGTTCTTC	AACACTCATC	CATACGTAGC	2040
TGCTCCAGTC	ATGGGGGTTA	CTCTTGCGCT	TGAAGAAGAA	CGTGCTAACG	GTGTGGAAAT	2100
CGATGACGCT	GCTATCCAAG	GGGTAAAAAT	CGGTATGATG	GGACCTCTTG	CTGGTATCGG	2160
TGACCCAGTA	TTCTGGTTTA	CAGTACGCCC	AATCCTTGGA	TCTCTCGGTG	CTTCACTTGC	2220
CCTTACTGGC	AATATCTTGG	GGCCACTCCT	CTTCTTTGTT	GCATGGAACT	TGATTCGTAT	2280
GTCATTCTTG	TGGTATGTTT	AAGAGATTGG	ATACAAGGCT	GGATCAGAAA	TCACTAAAGA	2340
TATGTCTGGT	GGTATCCTTC	AAGATATCAC	TAAAGGAGCT	TCTATCCTTG	GGATGTTCAT	2400
TCTTGCTGTC	CTTGTTCAAC	GCTGGGTAAA	TATTAAATTT	GCTTTCGATG	TTTCTAAAGT	2460
TCAACTAGAT	GAAAAGGCTT	ATATCCATTG	GGATAAATTG	CCAGAAGGGT	CTAAAGGTAT	2520
CCAAGAAGCA	TTGCACAAAG	TAGGACAAGG	ATTGTCTCAA	ACTCCTGAAA	AAGTTACTAC	2580
TTTCCAACAA	AACTTGGATA	TGTTGATTCC	TGGATTATCA	GGACTACTCC	TTACTTTACT	2640
TTGCATGTAC	TTACTTAAGA	AAAAAGTATC	TCCAATCACT	ATTATCCTTG	CCCTCTTCGC	2700
AGTGGGTATT	GTGGCACATG	TTCTTCACAT	CATGTAATCA	AGCAACTAAA	AAGGAACCAG	2760
GTTCTAAAAT	CTGATTCCTT	TTTTCTATGC	TTTTATTGAG	CCAAGGCTCC	CATTGGATCC	2820
CATGGTGCAA	GTACGATTGG	TTCTGCTCCA	TAGGCAGCTT	GTTCTTCTGC	TGTCAGCAAT	2880
TCCTTACGAA	CAACGATTTG	GTATGTGTAT	TCGTCCATCC	AAGCGTCTGA	GGCAACAAAG	2940
TAACCATCTG	TACCGACCTT	GTCTCCCCAT	GAGTTTTCAA	CCTTCCACTT	GGTTGATTTA	3000
CCATTTTCGT	CCAAGTCAAC	ACCTGTCAAG	ACCATGGCGT	GGGTCATCAA	GCTTTCAC TA	3060
TAGTCCAAAC	GTCCAGCCTT	GTCTTGAGTA	AGTTTAATGT	CCATGCTTGA	TTCAAAGTCA	3120
TAAACATCTG	TCGCAAGGAT	GCCAGCTTAC	GGTTGCTGAG	CTGGCCGACA	TCAGAACCAA	3180
ACCAAACAGT	CTCACCTGCT	TGCATTTGGG	CAATCGCCAA	TTCTTTCAAG	CGCTCCATTG	3240
GAACGTTGAT	GTAGCGAACT	GCACGGCTAC	CAACCACATT	CCCCAACATC	TCAACTGTGT	3300
AAGATTTTCC	GTAAGGTTTA	TCAGCAGTTG	GAGCATTGAT	AACAGAAACG	TAGTCTTCTA	3360
AAGGAAGATT	GACATATTTT	TTGTAAAACT	CTTGTGGTGT	GATTCCTTTT	TCACTTTTGT	3420
AGTTGTTATC	TTTATCGCGA	TAAGCAAAGT	CAAACTTGCG	TGGTGGAAGT	CCTAATGACA	3480
TAGCAAGAAA	GTTAAAGATT	TCTTGCAAGA	GGTCTTCTTT	CTTAGCTTGA	ACAGTCGCTT	3540
GATCTGCACC	AGAAACAAGC	AAGTCACGCA	AGATTTGAGC	ATCTTGACGA	AGCAATTTAT	3600
TAAGGATCGC	ATTTAGCTCA	CGACTGCTGC	TAGATGAAAC	AGACTCAGGA	TAAACTGACT	3660
TAGGCACGAC	ACCGTATTTT	TCAAAGAGGG	AAACGACCAT	ATCCCATTGA	CCGCCATCTT	3720

1209

GTTGAGGTGT TTGGAGTAAG AAGCTAACTT GCGGCTAGTC AATTCTTGGT CTGAAGTCGC	3780
AATGACTTGC TCCAAGAACC AGTTTGATTT CTCATACTTA TCCCAGAAGA AAGTGTGGGC	3840
TTGTGACAAC TCAAAGTTCT CCAATTTGTA TTGCGAGATG AGTTTGTGGC GGAAGGTGTT	3900
GAGAGCCGCA AACATCCAGC AACGACCAGA CGCTTCTGG TTAGTGACCT TGTCTTGGT	3960
TAAATCCAAT GAGAAAACAG GTGTGTTGTC TACATGGCTT TGGCGACGTT CCAGAGCTGC	4020
AAAAATTCCG TTGTGGCTGG CAGCATTTTC AATCGCTTGG TATTTTACAT TTGCTTCATA	4080
GTTGGCAAAT AGTTTATCAG TAAATGATTC TTGAATCGCG TTCATAGATT CCTCCTTTTA	4140
GTCTACAGTG TATTGG	4156

(2) INFORMATION FOR SEQ ID NO: 212:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3902 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

AAAAACAACA AAATAAAACA AAAACAAAAA TATCGAGGTT TATTTTCAA ACTTTCGATA	60
TTTTTATTAA GTTATTATTT TGTGTTTTCT AGTTTACTTT TTGATGGTTA AGAGTGGTGG	120
AGAATTATAC TCAATGAAAA TCAAAGAGCA AACTAGGAAG CTAGCCGCAG GCTGTACTTG	180
AGTACGGCAA GGCGAAGCTG ACGTGTTTGG AATTTGATTT TCGAAGAGTA TTAGTGCAAA	240
CCGTAGTTGT AGTCATCATC TTGCATGGCT TCAACTTCGC CAAGAAGGTA ACCATTTCCG	300
ACTTGAGAGA AGAAGTCATG GTTGGAAGTT CCTGTTGAAA TACCGTTCAT AACGATTGGG	360
TTGACATCTT CAGCTGAATC TGGGAAAAGT GGATCTTGTC CCATGTTTCAT GAGAGCTTTA	420
TTGGCATTGT AGCGAAGGAA GGTTTTAACC TCTTCAGTCC AACCAACACC GTCATAAAGA	480
CTCTCTGTGT AGCCTTCTTC ATTTTCATAA AGAGTATAGA GTAGGTCGTA CATCCATTCT	540
TTGAGTTTTT CTTGCTCTTC TTCAGGTAAT TCATTGAAAC CAAGTTGGAA TTTGTAACCA	600
ATGTAGGTTT CGTGAACAGA CTCGTCACGA ATAATCAATT TAATGATTTT TGCAACGTTG	660
GCAAGTTTGT TGTTACCGAG ATAGTAGAGG GGAGTGAAGA AACCAGAGTA GAAGAGGAAG	720
GTTTCGAGGA AGACGCTGGC AACTTCTTTT TCAAGTGGGC TGCCGTTTAG GTAGATTTTCG	780
TTGACAATCT CAGCCTTCTT TTGTAGGTAA GGATTGGTAT TGGTCCATTC GAAAATTTCT	840
TCAATCTCAG CCTTAGTATT CAAGGTAGAA AAGATTGATG AGTAAGATTT AGCGTGGACA	900

1210

GATTCCATAA	ATTGGATGTT	ATTGAAGACA	GCTTCCTCAT	GTGGTGTACG	GATGTCTGCG	960
CGAAGGGCTT	GAACCCAGT	TTCAGATTGC	ATAGTGTCAA	GAAGGGTTAA	ACCACCAAAA	1020
ACTTTTCCGA	CCAAGTCTTT	CTCTTTGTTA	GATAGCTTTC	TCCAGTCATC	CAAGTCGTTT	1080
GATAAGGGAA	TACGTGTATC	GAGCCAAAAT	TGCTCCGTCA	GTTTTTCCCA	AGTTGATTTG	1140
TCGATGACAT	CTTCGATGGC	ATTCCAGTTA	ATGGCTTTGT	AGTAAGTTTC	CATTTAAAAT	1200
CTCTTTCTGT	GTTTAGTATT	GCGAACTCAC	AATTATTTCT	ACTTTACCAT	AATTCTATAG	1260
GAGTATCGCA	CAAAAAGTCG	GAAGCCCGAC	TTTTAAAATG	TTACATAAAT	TATGTTATGA	1320
CATAGTAGAT	TTGATTTTAT	CAGTGCTGCT	TAGGGAAAAA	TAGTGTTCCT	ATGCTAGAAA	1380
CTAAATCACA	CAGCTTTCAC	ATTGGTTGGC	GCCGACTTCT	CCACCGTCAT	CTGTAAAGGT	1440
ACGGACGTAG	TAGATAGACT	TGATTCCCTT	GTTAAAGGCA	TAGTTACGAA	GGATGGACAA	1500
GTCACGTGTC	GTTTGTTTAT	TTTCCCTCTT	CCATTTCGTAA	AGGCCTTTTG	GAATGTCACT	1560
GCGCATGAAG	AGGGTGAGTG	AAAGTCCTTG	ATCCACGTGT	TCAGTCGCAG	CAGCGTAAAC	1620
ATCGATGACT	TTACGCATAT	CCATATCGTA	GGCAGAAAGTG	TAGTAAGGAA	TGGTTTCTGT	1680
AGACAAGCCA	GCAGCAGGGT	AATAGATTTT	ACCAATTTTC	TTCTCTTGGC	GTTCTTCGAT	1740
ACGTTGCGTA	ATCGGGTGGA	TAGAAGCAGA	AACGTCGTTG	ATATAGCTGA	TAGAACCATT	1800
TGGCGCTACA	GCAAGGCGAT	TTTGGTGGTA	AAGACCATCT	TCTTGAACCT	TGTCGCGAAG	1860
TTCAGCCCAA	TCAGCAACAC	CAGGGATAAA	GACATTTTTG	AAGAGTTCTT	TAACACGGTC	1920
TGATGTTGGA	ACAAATTCAC	CAGTTACATA	CTTGTCAAAG	TAACCTCCGT	TAGCATAGTC	1980
TGATTTTTCA	AAGTTGTGGA	AGGTAATACC	ACGTTACAGT	GCAATATTGT	TTGACTCTAC	2040
CAAGGTCCAG	TAGTTCATAA	GCATAAAGTA	GATGCTTGTA	AATTCAACAG	ACTCAGGTGA	2100
ACCATATTCA	ATGAGTTGTT	GGGCAAGGTA	GCTGTGCAGT	CCCATGGCAC	CGAGACCAAA	2160
GGTGTGGGCT	TGGCTATTTT	CATGGTCAAT	CGTTGGTACA	GCTACGATAT	GTGAACTATC	2220
TGTAACGAAA	GTAAGGGCAC	GAACCATAGC	ACGGATAGAA	CGACCAAAAT	CAGGTGAAGT	2280
CATCATGTTA	ACCACGTTGG	TTGAACCCAG	GTTACATGAA	ACATCTGTTC	CCATTTGAAG	2340
GAATTCTTGA	GCATCGTTGA	TCAAGCTTGG	TTCTTGAACT	TGAAGAATCT	CAGAACACAA	2400
GTTACTCATG	ATAATCTTTC	CATCAACAGG	ATTTGCACGG	TTAGCCGTAT	CGATGTTGAC	2460
TACATAAGGA	TAGCCAGACT	CTTGTTGCAA	TTTAGAGATT	TCAGTTTCCA	AATCCCGCGC	2520
CTTGATTTTT	GTCTTGCGAA	TATTTGGATT	TGCGACCAAT	TCATCGTATT	TTTCAGTAAT	2580
GTCGATGTAA	TTGAATGGCA	CACCGTATTC	TTTTTCTACA	GAGTAAGGGC	TGAAGAGGTA	2640
CATTTCTTCA	TTTTTACGAG	CCAATTCGTA	GAATTTATCA	GGTACTACAA	CACCAAGTGA	2700

1211

TAGAGTCTTG ACACGTACTT TTTCATCAGC GTTTTCTTTC TTAGTTGAAA GGAAAGCGAT	2760
GATATCTGGG TGAAAGACGT TGAGGTAGAC AACACCAGCA CCTTGACGTT GCCCCAATTG	2820
GTTGGAGTAA GAGAAGCTGT CTTCAAAAAG CTTCATAACA GGAACGACAC CTGAAGCAGC	2880
TCCTTCATAG CCTTTGATAG GTGCACCAGC TTCACGAAGG TTGCTGAGGG TAATTCCCAC	2940
ACCACCACCA ATACGTGAAA GTTGAAGAGC TGAGTTGATA GAACGCCCGA TAGAGTTCAT	3000
ATCATCCGTC ACTTGGATTA GGAAACAAGA TACCAACTCC CCACGACGAG CACGTCCAGC	3060
ATTCAAGAAG GAAGGAGTAG CAGGTTGGTA GCGTTGGTGG ATGATTTCAT TGGCAATATC	3120
GATTGCAACA GCTTCATTCC CATCAGCGAA ATAAAGGGCA TTGAAGAAGA CACGGTCTTC	3180
CATATTTTCA AGATAGTATT CACCGTCATT AGTCTTTAAG GCATATTGAT TGTAAAATTT	3240
ATAAGCTGCC ATGAATGACT TGAATTGGAA GTTTTGGTCT TTGATAAATT GAGCTAATTC	3300
TTCCAAGAAC TCTGGACGGT ATTTCTTGAT AAAGGCTGTT TCGATGTAGT TGTGTTCAAT	3360
GAGGTAATTG ATTTTGTCTT TGATTGAATC AAAAACCATA GTGTTTGGAA CTACATTTTC	3420
TTTAAAGAAA GCATCCAAGG CTTCCTTGTC TTTATGAAGC ATGATTGTGC CATTAACAGG	3480
ACGGTTAATT TCGTTATTAA GACGGAAGTA AGTCACGTCT TCAAGATGTT TTAATCCCAT	3540
AAAATTTCCC TTATCTAATT ACAAAGAAA GGCTTCTAAG TTAGCCCTAA AAGCAGTTTC	3600
TTCTGGATGA TGTACTAAGA TTATGCTAAT TGTTTCAGTT TTCCTGGTTG GAAACCTGAA	3660
AAGACTTCAG TTGGTGTTTG GATAACAGGA GCTGCGCTAA AACCGAGCTC TTAACTTGA	3720
TCGACGTACT CAGGTTGCTC ATCAAGATTG ATTTACGAT AAGAGACATT ATTACTGTCC	3780
AAGAAACGCT TGGTCATTTT ACATTGGACA CAATTGTTTT TAGAATAAAC GGTTACCATT	3840
GTGTAACCTC TCTTCAAAAT TTAATACTAT CTTAGTATAT CAGAAAATAA AATTTTGTCTG	3900
GG	3902

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

TATTGAAGCT ATTGTAGACT ACAAAGATAA GGATTTGCAG TTAGTAGGCG GTGAGACTCA	60
CTGATAACCT AAAAAGGATA GTCAATTATG CTTGTTTACT AACTATTAAC TATGCTAAAT	120

1212						
CAATTGAGGT	TGTTTACATA	AAACTCTATA	TCAGAGAAGC	CTGATATAGA	GTTTTTTCTT	180
GCTAGTTTTA	GGATTTTTTT	GTAAAATAGA	AAAAGTGAAG	AGAGGTATGA	AATGAGCAAG	240
AAAGATAAAA	AAATCGAAAT	TCAAGTAGCG	GATGCCAAAG	TTAATGTTGG	TAAAGACAGT	300
TTTGAAGGTT	ATACATTGAC	TATCGGTAAA	AAAGTTATCG	GAGAAATTGC	CGAATTAGAC	360
GGACAATTTG	CCATTATAAA	GAATGGGAAT	GTCGATAGTT	TTTATAAAAA	ATTGGAAAAA	420
GCTGTGGAAA	TTTTGATTGA	AAATTATAAT	TTAGCAAAAT	AAGTCTTGTT	TTTTTGAAAT	480
TTTCATGATA	TAATAGTCCA	TGTTGATTGT	AGGAGAGATA	GCGAAGAGGC	TAAACGCGGC	540
GGACTGTAAA	TCCGCCCCTT	CGGGTTCGGG	GGTTCGAATC	CCTCTCTCTC	CATTTCATTA	600
ATGGGGTATA	GCCAAGCGGT	AAGGCAAGGG	ACTTTGACTC	CCTCATGCGT	TGGTTCGAAT	660
CCAGCTACCC	CAGTTCTTAG	GTAATAATCA	AGATAGAAAG	CAAAATATCT	TAGGGTATTT	720
TATTTTTATA	ATTGAAAGAC	GTGAATGATA	TGAACATGTC	CTTGCGGGTG	CTTAGGAAAA	780
AAATTATAAG	TATGTCAAGT	TTAAGAAAAA	CTTGATTGTT	GGAGGATTTT	TTAGATGAAC	840
GAATTTGAAG	ATTTGCTAAA	TAGCGTTAGT	CAAGTTGAGA	CTGGTGATGT	TGTTAGTGCT	900
GAAGTATTGA	CAGTTGATGC	GACTCAAGCT	AACGTTGCAA	TCTCTGGAAC	TGGTGTTGAA	960
GGTGTCTTGA	CTCTTCGCGA	ATTGACAAAC	GATCGTGATG	CAGATATCAA	TGACTTTGTT	1020
AAAGTAGGAG	AAGTATTGGA	TGTTCTTGTA	CTTCGTCAAG	TAGTTGGTAA	AGATACTGAT	1080
ACAGTTACAT	ACCTTGTATC	TAAAAAACGC	CTTGAAGCTC	GCAAAGCATG	GGACAAACTT	1140
GTTGGTCGCG	AAGAAGAAGT	TGTTACTGTT	AAAGGAACGC	GTGCCGTTAA	AGGTGGACTT	1200
TCAGTAGAAT	TTGAAGGTGT	TCGTGGATTT	ATCCCAGCTT	CAATGTTGGA	TACTCGTTTC	1260
GTACGTAACG	CTGAGCGTTT	TGTAGGTCAA	GAATTTGATA	CTAAAATCAA	AGAAGTTAAC	1320
GCTAAAGAAA	ACCGCTTCAT	CCTTTCACGT	CGTGAAGTTG	TTGAAGCAGC	TACTGCAGCA	1380
GCTCGCGCTG	AAGTATTCGG	TAAATTGGCT	GTTGGTGATG	TTGTAAGTGG	TAAAGTTGCT	1440
CGTATCACAA	GCTTCGGCGC	TTTCGTGAC	CTTGGTGCTG	TTGACGGATT	GGTTCACTTG	1500
ACTGAATTGT	CACATGAACG	TAATGTATCA	CCAAAATCAG	TTGTAAGTGT	TGGTGAAGAA	1560
ATTGAAGTGA	AAATCCTTGA	TCTTAACGAA	GAAGAAGGAC	GTGTATCACT	TTCACTTAAA	1620
GCAACAGTAC	CAGGACCATG	GGATGGCGTT	GAGCAAAAAT	TGGCTAAAGG	TGATGTAGTA	1680
GAAGGAACAG	TTAAACGTTT	GACTGACTTC	GGTGCATTTG	TTGAAGTATT	GCCAGGTATC	1740
GATGGACTTG	TTCACGTATC	ACAAATTTCA	CACAAACGGA	TTGAAAATCC	AAAAGAAGCT	1800
CTTAAAGTTG	GTCAAGAAGT	TCAAGTAAAA	GTTCTTGAAG	TTAACGCAGA	TGCAGAACGC	1860
GTGTCACTTT	CTATTAAAGC	TCTTGAAGAA	CGTCCAGCCC	AAGAAGAAGG	ACAAAAAGAA	1920

1213

GAAAAACGTG CTGCTCGTCC ACGTCGTCCA AGACGTCAAG AAAAGCGTGA TTTCGAACTT	1980
CCAGAAACAC AAACAGGATT TTCAATGGCT GATTTGTTTG GTGATATCGA ACTTTAATCA	2040
AATTGAAAAT TCACAAAATC CTTTGTTTAC TAAACAAGGG ATTTTCTGG CTCTTTGTCA	2100
ACTGTAGTGG GTTGAAGAAA AGCTAAGCTC GAGAAAGGAC AAATTTTGTC CTTTCTTTTT	2160
TGATATTCAG AGCGATAAAA ATCCGTTTTT TGAAGTTTTC AAAGTTCCGA AAACCAAAGG	2220
CATTGCGCTT GATAAGTTTG ATGAGATTAT TGGTCGCTTC CAGTTTGGCG TTAGAATAGT	2280
GTAGTTGAAG GGTGTTGACA AGCTTTTCTT TATCTTTGAG GAAGGTTTTA AAGACAGTCT	2340
GAAAAATAGG ATGAACCTGC TTAAGATTGT CCTCAATAAG TCCGAAAAAT TTCTCCGGTT	2400
CCTTATTCTG AAAGTGAAAC AGCAAGAGTT GATAGAGCTG ATAGTGGTGT TTCAGG	2456

(2) INFORMATION FOR SEQ ID NO: 214:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10974 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

AAATAGGATA TAGAGACATC CTTCTGATCT GCTTTTwACA AAGTCCAATT ATATGCGGAT	60
CTATACCTCC ACAATGTCCA TTATTATmCC TAACTATAAT ATGAGCCGAA AACACTATAT	120
CCTTAATGTC TCCATATCCA TCAGGGATAT TAATATTTAT TTTTCCACAA CTATATTGCA	180
TTGTAACCAT CTCCTTAAAC GACGCATTAT GATATTTGAT AGAGAAATTT TTATGAATAA	240
CTCAATAATT TTATAGTAAA TCATGCTTAT ATCTCAAAGA TACCTATTTT ATCTTGCTCTC	300
GACCTTCTCC AAAGAATTGC TATAATACTA TTACAAATCC ATCTGCACTA CACTTCAAAT	360
TTTAGCACTG TATAAAAACG TTTCAATACA CTAACTTCAA GAAAACTTCC ACTATTAATT	420
GAAAAAATTG ATAGAGATAA ATTAAAAATC TATATTGAAA CTCATCCCGA TGCTTATTTG	480
ACTGAAATAG CTGCTGAATT CAACTGTCCT CCAACAAC TAATTACGC TCTAAAGGCT	540
ATGGGATATA GTCTAAAAAA GAGCCGTACC TACTGCGAAC AAGACCCAGA AAAAGTAAAT	600
CGGTTCTTA AAGAATTGAA TCACTTAAGC TACCTGACTC CTATTTATAT TTATGAGACA	660
GGGGTTGAGA CCTATTTT TA TCTCGAATAT GATCGAGCCT TGAGCAGGCA GTTAGTCTCT	720
CTGGAAGAAG ATATAATTAT TTGAATTAAG ATCGAGACAA CGCACACCAG AGATTGCGAT	780
ACTGTTATAG AAGTACTAAT GCCCTTTTTT GTTTCAATAT ACTATGGCTC CGATGACCTA	840

1214

TAAAGATACG	ATGACGAGTG	ACTTTTTTCGA	AGCTTGCTTC	CAAAAATTCT	TACTACCTAC	900
TTTAGATACA	CCATCCCTTA	TCATTATGGA	CAATGCAAGG	TTTCACAGAA	TGAACATGTG	960
TAAGGAGCAG	GGCATAGACT	GTTACCACTT	CCTACCTATT	CACCCGAGTA	TAATCCCATT	1020
GAGAAAATAT	GGGCTTACAT	CAAAAACATC	TCAGAATAAT	ATTGTCAAAT	TACGATGCTT	1080
TTCTTGAGGC	ACTTTTGTCC	TATTCTTGTT	TCAGCCGACT	ATACTCCGTT	ATTGGGCAGC	1140
TACGGAACAG	TCGATGGGAC	GATGGGGGGA	CATAAAAAAA	TCCTCCAGTT	TTGTTTTTTA	1200
TAACAGTATA	CTGGAGAATT	GACAATCTCG	GTAGATACCT	CGTTATAGCG	CGGTTACTTA	1260
TTAGGCAGTT	ACAAAACAAC	TGTGAACAGA	AAACATTCCA	GAGTCAGACA	AGACTTTGGA	1320
ATGTTTTTGGC	TCTATAATTT	CTGTAGTGGG	TAATCCCACC	CCAGGAATTA	TAGGGTCGTT	1380
TCTTGTAGAA	AAAAAGCCCC	ATATGACCTA	TAATGAAAAG	CGTCTAACCA	ACTCATTAGA	1440
AAGGGTTCAT	ATGGAACAAC	TTAAGAATAC	CACAGATTTG	CTCGGATTGG	AAGACAAAAA	1500
TATCAAAATC	TTGTCTGTTC	TGAAATACCA	AACCCATCTA	GTCGTTCAGG	CAAAGTTGGA	1560
TTCCCCCGCT	CCTCCTTGTC	CTCATTTGTC	AGGGAAGATG	ATCAAATACG	ACTTCCAGAA	1620
AGCCTCTAAA	ATCCCGCTTC	TCGACTGTCA	GGGTTTACCC	ACGGTACTGC	ATCTCAAAAA	1680
GCGCCGCTTT	CAGTGCAAGA	ATTGCCTTAA	GGTGGTCGTT	TCTCAAACAT	CCATTGTCAA	1740
GAAAAATTGC	CAGATTTCCA	ACATGGTGAG	ACAAAAAATC	GCTCAGCTCC	TCCTTGAAAA	1800
GCAGTCTATG	ACTGAGATTG	CCCACAGATT	GGCGGTCTCA	ACTTCCACCG	TCATCCGAAA	1860
ACTGAGGGAA	TTTAAGTTTG	AAACCGATTG	GACCAAGTTG	CCAAAAGTTA	TGAGTTGGGA	1920
TGAGTATAGC	TTCAAAAAGA	GCAAAATGAG	CTTCATTGCC	CAAGATTTTG	AGTCCAAATC	1980
CATCCTCGCA	ATTTTAGACG	GGCGAACTCA	TGCGGTGATT	CGAAACCATT	TCCAACGCTA	2040
TCAGAGAGAG	GTTCGGGAGC	TGGTCGAGGT	CATCACCATG	GACATGTACA	GCCCTTATTA	2100
TCGGCTCGCT	AAGCAACTCT	TTCCAAAGGC	GAAGATTGTT	CTTGACCGCT	TCCACATTGT	2160
CCAACATCTG	AGCCGAGCTA	TGAACCGAGT	ACGAATCCAA	ATCATGAACC	AATTTGACCG	2220
AAAATCCTTG	GAGTATCGGG	CGCTCAAGCG	CTTTTGGAAC	CCTCGCTTTT	TCGTTTCTAG	2280
GCTCGGGCTA	AATCAGTCCA	CTGGACTGAT	TTACTACACC	AGTATAGCTT	CAAGCTCTGT	2340
CAGAAACGAT	TCTATCAGCC	CACGTTTTCGA	ATGCACTTAA	CCCATCGGGA	AGTACGAGAT	2400
AAGCTGCTTT	CTTACTCTGA	GGGATTACAG	GTTCACTACG	AACTCTATCA	ACTCCTGCTC	2460
TTTCATTTTC	AAGAGAAGAA	TGCCGACCAT	TTCTTTGGAT	TGATTGAGCA	AGAACTGCCA	2520
ACGGTTCATC	CGCTTTTTCA	AACGGTCTTT	TGGACTTTTT	TAAGGGATAG	AGATAAGATT	2580
ATCAACGCAC	TTAAGCTGCC	TTATTCCAAC	GCTAAACTTG	AAGCGACCAA	TAATTTGATT	2640

1215

AAGATTATCA	AGCGCAAAGC	CTTTGGTTTC	CGGAACTTTA	ACAATTTTAA	AAAACGGATT	2700
TTGATGACTT	TGAACATCAA	AAAAGAGAGT	ACGAATTTTCG	TACTCTCCAG	ATTGCAGCTT	2760
TTCGCCTACC	CACTACACTT	GACAAAGAGC	CACTCTTTAT	TCCATGGTAT	CAAAGGCAAG	2820
ACTTGGTTTG	GCATTGAGGT	CCCAGCCTGC	GAAGTTTCT	TTGTTCCACT	CGCTGACGCT	2880
GGCATAGGCA	ATCATACCTG	CATTGTCTCC	GCAGAGTCGC	AGAGGGGGGA	TGATAACCTT	2940
GACATCTGTG	ATTTTCGGCTG	CTAGGCGTTC	TCTGAGACCT	TTATTGGCTG	CCACACCACC	3000
TGCCACAAC	AGGATTTTAA	CAGGATATTT	CTCCAAAGCC	TTCTTGGTTT	TTGCCATGAG	3060
AATGTCCATA	ACTGCTGCTT	GGAAGGAAGC	ACACAAATCT	TCTGTAGACA	GGCTTTCTCC	3120
CTTTTGCTCG	GCATTGTGAT	GAAGATTGAT	AAAGGCAGAT	TTCAAACCTG	AGAAGGAGAA	3180
CTCCAGATTA	TCTTCCTTAA	TCATGGCAGC	GGGGAAATCA	TAAATATCCT	GCCCCTGATG	3240
AGCCAGCTCG	TCAATCTCAC	GACCTGCAGG	ATAGGTCAAG	CCCATGACAC	GGCCGACCTT	3300
ATCATAAGCC	TCACCAACCG	CATCATCACG	GGTTTCCCCA	ACAATCTTAT	AATCTCCTGC	3360
CTCCGAAACA	TAAACCAACT	CTGTGTGTCC	GCCGCTGACC	AAGAGGGCTA	GCAAGGGAAA	3420
CTCCAAAGGC	TCCACACTCT	GAGCTGCCAT	GAGGTGCCCA	GCCATGTGAT	TAACAGGAAT	3480
CAGTGGAAGT	CCGTGAGCCC	AAGCAAAGGC	CTTGGCAGCT	GACAAACCAA	CTAGCAAGGC	3540
TCCGACCAAG	CCTGGTCCGT	AGGTAACCGC	AACAGCTGTC	ACGTCCCTCT	CGGTAATCCC	3600
TGCTTCTGCC	AATGCCTCCT	CGATACAGGC	TGTAATGACC	TCGACATGGT	GACGACTGGC	3660
TACTTCGGGC	ACTACGCCAC	CAAAACGTTT	GTGACTCTCA	ATTTGACTAG	CAATGACATT	3720
GGACAAGAGC	TCATCGTCGT	TTTTCAAGAC	GGCGACACTG	GTCTCATCAC	AGGATGTCTC	3780
AAATGCTAAA	ATATATCTAT	CCTTCATCTA	TTTCTCTCTT	CATGATAATG	GCGTCCTCGA	3840
CTGGGTCATG	GTAGTAGGCC	TTTCGCTCAG	CGATAACTGT	CATCTTTTCT	TTCTTGTAAG	3900
ATGCTTGCGC	TCGTTGATTT	GACTGTCTGA	CTTCGAGGAA	AATTTCCCTG	TCTGTCGGCA	3960
ATTGAGCAAA	CAAGGCTGAC	GCAATCCCCCT	GACCCTGATA	AGCTCCCTTG	ACAGCGATTT	4020
GCAGGACTTC	TGCTTCAAAA	AGATTCTCCT	GCACAGCTAG	AAATCCAATC	ACTTCTGCCC	4080
CATCATAAGC	CAATGCATAC	CAAGTCTGGT	CTTGGGACAG	ATCTGCTTGG	ATTTGCTCCA	4140
GAGTCCAAGG	ACTGACTAGG	TAAACAGCTG	CCATAACAGC	GTAGATGGCT	TGAGCTAGGT	4200
CAGGCTGTTG	TTGAATTCGC	TTGATTTCTA	TCATAGGCGT	TTAATGTAAG	ACTCGCCAGA	4260
CTCGGTATGG	TTCTTGAGCC	AGTTTTCCTC	AGCCTCGACT	CGTTTGAGGT	AATTCGGCAC	4320
AAAATCATGC	AAGGAGTCTG	CTTCCTTGTC	CCAGGCCAAA	AGAGCTAGAT	TAGCTGCATT	4380

1216

GGGCAATGTT	TCTTTGTAAT	CAGTCCTTGG	CAAGTGTTTT	TGAATCTGCT	CAACAAAGGG	4440
GCCAACTTCT	CCGACAAAGG	TTACCTGACT	AGTACCCTTG	ACTTTTTCTA	GCACCTCTTC	4500
AAAAGATAGG	TGCGCTTCTG	CCATGACAGG	TTTGGCATT	TCATAAAATC	CTGCATAAAC	4560
ATTATTGCGA	CGCGCATCCA	TCAAGGGGAC	AAACAAACCT	TCTTGTTGAT	GGGGCACCAG	4620
AGCCAAGAGA	CTCGACATAC	CAACCAACTC	GATGTTTCAGG	GTGTGAGCTA	AGGTCTTAGC	4680
AGTTGCTACC	GCAATTCGCA	AGCCTGTATA	GCTACCCGGC	CCTTCAGCTA	CCACGATTCCG	4740
GTCCAAATCC	TTGGGTGTCC	AATCCAAACT	TGCCATCAAA	AAATCGATGG	CAGGCATAAG	4800
AGTAATACTG	TGATTTTTCT	TAATATTAAT	CGTCGTCTCG	GCAAGAACCT	GCTTATCCTC	4860
TAAAATAGCC	AGAGAAAGAG	CCTTGCTGGA	CGTATCAAAA	GCTAATACTT	TCATAACACA	4920
TTCCATATCTT	TTTGTCTGCT	TACTATTATA	CTACAAAAGC	TGGCACATGG	GAATTTTCTT	4980
TGCCCCCAGA	CAAGAGTGCC	CTCACTTAAC	TAAAAATAAT	TTAAAAAAT	GCTCACTTTT	5040
CCTTTTCTTT	TCCGAATATA	AAAGTGAACA	AGAAAAAAGG	AGGAAAGTTC	AATGACAAAT	5100
TTTGACATTC	TTGACAATCA	ATTTTTATCC	TTATCTGAAA	ATGAATTATC	AGATATTGAT	5160
GGCGGTCTCG	CTCCCTTGGT	TATCTTTGGA	GTAGCAGTAT	CTTGGAAGGC	TATTGCAGGT	5220
GGAACAGCAC	TTATAGGTTC	TGGTTTGGCA	GCTGGTTATT	TTTTAGGAGG	AGATTAATAT	5280
GATGAAAGAT	TTGAACAATT	ATCGTGAAAT	TTCTAATAAG	GAATTGCAAG	AAATCAAGGG	5340
TGGCTTTGGT	GTCGGTGTTG	GTATCGCTTT	ATTTATGGCA	GGTTATACCA	TTGGAAAAGA	5400
CCTTCGTAAA	AAGTTTGGTA	AGTCATGCTA	GATAAGAAAC	ACATTTTTAG	AAGGATAAAT	5460
TTTATTGTCT	TCATCTCTTA	CAGTTTGCTC	AGCATCTCA	ATGATTTGAA	CATTACTACC	5520
ATCCCTTTAC	CATTCGATTT	ATCTGTTTGT	ATTGTTTTAT	TTTTATGCTT	CAACTCTATT	5580
TTTGATCAGA	ACAATGACTC	CCATAAAAAT	AATAAGCTTT	GAAAATTCCA	TTGTCATGTC	5640
ATGTTAGAAA	AATGCAAAGA	CCACCTCATC	TTGATAGATG	GGGTGGAATT	TTCGTGTCGT	5700
AAATCTACTA	TCTCTACATT	CCCAAACAAA	AAACCCAGC	ATAAGCAGGG	CATCTAAGCA	5760
TTTAATTCAA	AGTAAAATAC	AAACCAAACG	ACATAGGTCA	CGAGGAGGAG	AAAAAGCGAG	5820
TAGAGAGTCA	CAAAGGTCAT	TTTCCACAAG	AACTTGGTTT	GTCGTCGTTC	CAGTTTGGCA	5880
AATAGAAGAT	TCCCCGCATA	AACGCAAGCA	ACAAAAACAA	TAAAAGCTAC	CAAGCGAGCT	5940
CCGATAGCAA	AAGCAAATAA	GTTATACATA	GGGCAACCTC	CTTGACTTAA	AATCTATATG	6000
GAATTATGAC	AAGCAATAAA	TTTCACTTCC	GTTATCAACA	TAATACATTT	TCTTTATTTT	6060
TGAAAACGCT	TACCAAAGAA	ATCGTCCCCT	AACTTCTCG	TTTCCGTCTT	TTACTAATTT	6120
TTCATTTTGT	GGTATAATTG	AAATAATTGT	AACGAATCAA	GGTCAATCTA	GACACAAAAT	6180

1217

GGAATGAAAT	CAAGCAAATA	TCTGCTAAAA	GTTTGGAATA	AGCTGACCTG	TAAATAGAAA	6240
GGAACTATAT	GATTTACAAA	GTTTTTTATC	AAGAAACAAA	AGAACGTAGC	CCACGCCGTG	6300
AAACAACACG	CACGCTTTAC	CTAGACATCG	ATGCCAGCTC	AGAACTTGAG	GGCCGTATCA	6360
CTGCTCGCCA	ACTTGTCGAA	GAAAATCGCC	CAGAGTACAA	TATCGAGTAT	ATCGAACTCT	6420
TGTCTGACAA	ATTGCTCGAT	TACGAAAAAG	AAACTGGCGC	CTTCGAAATT	ACGGAGTTCT	6480
AATATGGCCT	ACACTCTTAA	ACCTGAAGAA	GTCGGCGTTT	TTGCCATCGG	TGGTCTAGGA	6540
GAAATCGGGA	AAAACACTTA	CGGAATTGAA	TACCAAGACG	AGATTATCAT	CGTCGATGCT	6600
GGGATTAAAT	TCCCAGAAGA	TGACTTGCTT	GGTATCGACT	ATGTCATTCC	TGACTACTCT	6660
TACATCGTGG	ACAATATCGA	CCGCGTCAAG	GCTGTTTTAA	TCACACACGG	ACACGAGGAC	6720
CACATTGGTG	GGATTCCGTT	CCTACTCAAG	CAAGCAAATG	TCCCTATTTA	TGCTGGACCG	6780
CTTGCCCTTG	CTTTGATCCG	TGGGAAACTC	GAAGAACACG	GCCTCTTGCG	CAACGCCAAA	6840
CTTTACGAAA	TCAACCACAA	CACCGAGTTG	ACCTTTAAAA	ATCTCAAGGC	AACTTTCTTT	6900
AGAACGACTC	ACTCTATTCC	AGAGCCTTTG	GGGATTGTCA	TTCATACTCC	TCAAGGGAAA	6960
ATCGTCTGTA	CGGGTGACTT	TAAGTTCGAC	TTTACTCCAG	TTGGAGAACC	TGCGGACTTG	7020
CATCGTATGG	CTGCGCTTGG	TGAAGAAGGC	GTGCTCTGTC	TCCTGTCTGA	CTCGACAAAT	7080
GCGGAAGTAC	CAACCTTTAC	CAACTCTGAA	AAAGTCGTTG	GTCAGTCCAT	TATGAAGATT	7140
ATCCAAGGTA	TTGAAGGACG	TATCATCTTT	GCATCCTTTG	CCTCAAATAT	CTTCCGTCTC	7200
CAGCAGGCAA	CAGAAGCTGC	TGTTAAGACT	GGACGCAAGA	TTGCGGTCTT	TGGTCGTTCT	7260
ATGGAAAAGG	CCATTGTCAA	CGGAATCGAT	CTTGGCTACA	TCAAAGCTCC	TAAGGGAACC	7320
TTTATCGAGC	CAAATGAAAT	CAAAGATTAT	CCTGCAGGAG	AAGTTCTTAT	CCTCTGTACA	7380
GGTAGTCAGG	GTGAGCCTAT	GGCAGCCCTC	TCTCGTATCG	CCAACGGAAC	CCACCGTCAA	7440
GTACAATTAC	AACCAGGTGA	TACCGTTATC	TTCTCTTCTA	GTCCCATCCC	TGGAAACACT	7500
ACTAGTGTCA	ACAAGCTGAT	TAACATCATT	TCTGAAGCTG	GTGTCGAAGT	TATCCACGGT	7560
AAAGTGAACA	ATATCCATAC	ATCTGGACAC	GGTGGTCAGC	AAGAGCAAAA	ACTCATGCTC	7620
TGCTTGATTA	AGCCAAAATA	CTTCATGCCT	GTCCACGGTG	AATACCGCAT	GCAAAAAGTC	7680
CACGCTGGAC	TAGCAGTGGA	TACTGGTGTT	GAGAAGGACA	ATATCTTTAT	CATGAGCAAT	7740
GGCGATGTGC	TTGCCCTTAC	TGCTGACTCA	GCTCGTATCG	CAGGTCATTT	CAACGCCCAA	7800
GATATCTATG	TCGATGGAAA	TCGTATCGGT	GAAATTGGCG	CAGCTGTCCT	CAAAGATCGT	7860
CGCGATCTAT	CTGAAGACGG	TGTCGTTCTG	GCAGTTGCAA	CTGTTGACTT	CAAATCGCAG	7920

1218

ATGATTCTAT	CTGGTCCAGA	CATCCTCAGC	CGAGGCTTTG	TCTACATGAG	AGAGTCTGGC	7980
GACTTGATTC	GCCAAAGCCA	GCGTATCCTC	TTCAATGCCA	TTCGTATCGC	ACTGAAAAAT	8040
AAGGATGCTA	GCGTGCAATC	TGTCAATGGT	GCCATTGTCA	ACGCTATTCTG	CCCCCTCCTC	8100
TATGAAAATA	CCGAACGTGA	ACCGATCATC	ATCCCGATGA	TCCTCACACC	AGATGAAGAA	8160
TAAAGCAAGA	AAACAGCCCC	GTCCTCGGAG	CTGTTTTTCT	CTATGCTTTC	TTTTGAGATT	8220
AAAACTCATA	CTCAATGAAA	ATCAAAGAGC	AAACTAGGAA	GCTAGCCGTA	GGTTGCTCAA	8280
AGCACTGCTT	TGAGGTTGTA	GATAGAACTG	ACGAAGTCAG	TAGCCATACC	TACGGCAAGG	8340
CGACGTTGAC	GCGGTTTGAA	GAGATTTTCG	AAGAGTATCA	ATAAAAAATCG	AAATCAGACT	8400
AGAAGGCTAA	GCGAAAGCAT	AACTTGAGTT	AGCTCCCATA	GTTCCGGGAAA	CTATGGGAGG	8460
CTGGAGATGA	ATCAAAGCCA	AGCTTTGAAC	TCATTTCGTAA	GAAGCCGACG	ACGTATCATT	8520
TTGATTTTTG	AAGAGTTTTA	GAAATACTAC	GATTTTTTACC	TTCCAGATAC	ACCATCAAAA	8580
TAGAAATATC	TGCTGGGTTT	ACTCCCGAAA	TACGGCTGGC	TTGGCCGATG	GTTTCTGGAT	8640
TGATGAGTTT	GAACCTCTGA	CGGGCTTCGG	TTGCGATAGA	ATCAATGTCA	TCCCAGTCGA	8700
TATTGGCCGG	AATGCGTTTT	TCTTCCATGC	GTTTCATCTT	GGCAACCTGG	TCCATGGCTT	8760
TGGAAATATA	GCCTTCATAC	TTGATTTCTG	TTTCAATCAA	TTGATAATC	TTGTCATCCA	8820
AGTCTTCTGC	AGCTGGTCCG	ATGAAGGCCA	CCACATCTTG	GTAAGAAACT	TCTGGACGGC	8880
GAAGGAATTC	CTTGGCTGTC	ACTGCATCGG	TCAAGGGTTT	GAAGCCCATC	TCCTCAACCT	8940
TGGCATTGGT	TTCCTTGACT	GGCTTGAGTT	TGATACTGTC	TAGGCGCTTC	ATCTCATTAT	9000
CAAATTGATT	TTTCTTGATT	TCAAAACGAG	CCCAGCGTTC	ATCGTCCACA	AGGCCAATCT	9060
CGCGTCCCAT	CTCAGTCAAG	CGCATATCAG	CATTGTCTATG	ACGAAGAATG	AGACGGTATT	9120
CAGCACGACT	GGTCAAGAGA	CGGTAGGGTT	CAATGGTTCC	CTTGGTCACC	AAGTCGTCTGA	9180
TCATCACCCC	GATATAACCA	TCACTGCGCT	TCAAAATCAA	TTGAGGCTTG	CCTTGGATTT	9240
TCAGAGCCGC	ATTGATACCC	GCGATAATCC	CTTGGCCTGC	TGCCTCTTCG	TAACCTGATG	9300
TTCCATTTGT	CTGACCAGCA	GTGAAGAGAC	CTGAGATTTT	CTTGGTTTCC	AAAGTCGCAC	9360
GCAACTGATG	AGGCAAGACC	ATATCATACT	CAATAGCATA	ACCTGTCCGC	ATCATCTCTG	9420
CATTTTCCAA	ACCTTTGATG	GAATGCACCA	AGTCACGCTG	GACATCCTCA	GGCAGACTGG	9480
TTGAAAGTCC	TTGCACATAG	ACTTCCTCAG	TATTGCGCCC	TTCTGGCTCA	AGGAAGAGTT	9540
GGTGACGTTT	CTTGTCCGCA	AAGCGCACAA	TCTTGTCTTC	AATCGACGGA	CAGTAACGAG	9600
GCCCCACTCC	CTTGACCACA	CCTGTAAACA	TAGGCGCACG	GTGGAGGTTG	TTTTGGATAA	9660
TCTCATGACT	GGTACCATTG	GTATAGGTCA	ACCAGCATGG	TACTTGGTCC	TTGACATAAT	9720

1219

CCTCATCACG TGAAGTGTAT GAGAAATGAT TAGGCACTTC GTCTCCTGGC TGAATTTCTG	9780
TCACATCGTA ATTGATAGAA GAAGCCTTGA CACGTGGAGG GGTTCCTGTC TTGAAACGAC	9840
CGATTTTCGAG ACCCAGTTCC TTGAGATTGT CAGCTAGGTT AATAGAAGCC AAGCTGTGGT	9900
TAGGACCTGA TGAGTACTTG AGGTCTCCGA TGATAATTC CCCACGGAGA GCAGTCCCTG	9960
TCGTCACAAT AACAGCCTTA GCAGCATATT CTTGATGGGT GGCTGTACGC ACACCGACAA	10020
CCTTGCCATC TTCCACCAA ATCTCATCAA TCATGGTTTG ACGAAGGGTC AGATTTTCTT	10080
GGTTTTCAAC CGTCTTGCGC ATCTCCTTAG AGTAAAGTTC CTTGTCAGCC TGCGCACGAA	10140
GGGCACGGAC AGCTGGCCCC TTCCCTGTGT TTAGCATCTT CATCTGGATG TAAGTCTTGT	10200
CAATGGTTTT GGCCATCTCG CCACCGAGGG CATCGACTTC ACGCACGACA ATCCCCTTGG	10260
CAGAACCACC GATAGAGGGA TTACAAGGCA TGAAAGCCAG CATTTCAATA TTGATGGTCG	10320
CAAGCAGGAC CTTACAGCCC ATACGGCTAG CGGCCAAGGA AGCCTCAACC CCAGCGTGTC	10380
CCGCACCAAT TACAATAATA TCGTATTCTT CAGTAAAATG ATAAGTCATG TTTCTCTCCT	10440
ATTCCTCAAG ATGAATGTGT CTTAGTTGGC CTTCCCAATC TGGTAGGGCT GTTTTTAAAA	10500
AGACTGGAAC TAGCTGGATA TTCTGGAGCT TATCCAAGTC AATCCACTCA CAGGGCTGCC	10560
TTTTCTCATC TTCCTGCATG GTCAACGGGG CATCTTCAAG CAAATCCACC AGATAATGAA	10620
ACTCGATATT GTGATAGGAA ACGCCGTCCA CTTCAAAACG ATTTTCAACC AAAAAAGCTA	10680
GCTGCCCAGC TTGAGCTTTG ACACCCAGTT CTTCTTCAC TTCACGGACT ACCGCGTCTT	10740
CCGTGCTTTC ATTGACTTGA ATCGCACCTC CAATAGTGTA ATACTTGCCC TTGTCTTTGG	10800
TAAC TAGAAG CTTGTGATTT TGGACAATCA AGGCTGTAGC CCGAACACCA AAAACCGTAT	10860
TGTCTACTTT TGTCCGAAAG TCTTGTGAG TCATTCTTGT CCTTTCCTT AAACGACACA	10920
AAAACAGTCA AACTACAAA GAAGTGCAGG AAAAAAAGC CTGCAACATC CAGG	10974

(2) INFORMATION FOR SEQ ID NO: 215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 987 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

CCCGTTATGA TTATGGATAG CGCTTTCAAA TTTTAAACT CCTATCCCAT CCTTTTATCT	60
ATATAATAAG TGAAAATATA ATAAGTGTCA AGTAACTGAA GTGAATTTTA TAAAAAATT	120

1220

ACAAGCCAAA TTTGTAAAGT TTACACTAAG CCGCTAGgCA ATCGTCTATC AGAATATCCG	180
TTTATTTGTC AATAATCCGA GAAAATCTTG CAACGCTTAG AAGTCTATAA AAACATCAA	240
CATTTATATG ACTTGCGAAT AGCAATCCTG CTAAACCTTT CCACACTCTA TCTATACAAT	300
CAAGATAAAA ACATGTGTAA GCAAATCTGC TACACTTTAC TGGAGGACGC CAAGAATAAG	360
AAAAGCTACG ATAGGCTTGC TATCTGCTAT GTCCGTATTG GGATTTGTAC AGACGATTCT	420
AAACTTATCC AAAAAGGGTT CTCCCTTCTG GAGCTGACCG AGGAAACTTC TATGCTGTCT	480
CATCTCAAAA AAGAAGTAGA GACCCATTAT CAACCAAAGA AATTATAAAA AAAGTCGAGG	540
GAGCTCCTCG ACCTTTTCAT AGAATCGCCG AACGATTTAA CGAGAAAGTA TGAATTTTAC	600
GTTTATCCCA ACTCAATTAT GACATTTTTT TCAAAAGTCA ATATATCTCA CTTTTTCAAC	660
GACAAGAAAG AGGCTGATAA TCTACCAACC TCTTATTCTG AACCCATCAC TCCATCACTT	720
TTTAGCTTCA TTCGCTTTCT TAGCGACTGC AATCTGGTAT TCGACTTGGT CATTCCCCTT	780
ACCGGTACAA CCATGAGCAA TTGTAGTCGC TCCTATCTGA TCGGCTATTT CAACCAATTT	840
TTTAGAAATC AGAGGGCGGC TCAAGGCAGA TACCAAGAGA TACTTTTGTT CATAATAGGC	900
ATGTGACTGA TGAGCCACTA GCACATAATC TGTAGCAAAT TCGTCCTTAA CATCAATGAC	960
ATAAGATTCT ACTGCCAAA CCTTAAG	987

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

CTGGGTCTTG TTCATAGTAG GTGTGGTtCT TTTTTTCGAG TGTAGCCCAT AGCTTTGAGC	60
GCATAGTGGA TGGTAGTTGG ATGACAGCCA AAGTCAGAAG CTATTTTCAGT CAAATAAGCA	120
TCTGGATTGT CAGTAAGATA GTTTTTAAGT CTATCTCTAT CAACTTTTCT TGGTTTTGTT	180
CCTTTTACTT GGTGGTTT TAG CTCTCCTGTT TTCTCTTTTA GCTTTAACCA GCCATAAATG	240
GTATTACGTG AGATTTGGAA AACGTGTGAT GCTTCTGTTA TACTACCTAT TCGCTCACAA	300
TAAGAGAGAA CTTTTTTACG AAAATCTATT GAATATGCCA TAAGAAGATT ATACCACATT	360
GTGTACTATT TTTGGTTCAT TTTACTATAT TTTATAAGTT ATAGTGTAGC ATTCCAACCTT	420
CAAAGCACTA TAAAGTAAAT TGAAACAAGA ACAATACAAA CAATTCTCGT AAACGGATTG	480
CAACCACAAA AAAGCAAGCA TTCACAAGAA TACTTACCTA TCATGGGAGG AACAACCGTT	540

1221

CCTCTTTTTT	ATTACTAAAA	TTCAAAGAAT	TCCAATGCTT	TTTTCAAGAG	CAAATCCGTA	600
TATTCTGGAT	CTTCTTGGGC	TACTTCTATT	TCCCGCTGAA	CTTTTTCCAA	ATCATCTGTA	660
ATCACTCCAT	CTACTCCTAA	GTGAAGAGAT	TTGCTGATAG	CTTCTGAATC	ATTGACAGTC	720
CAGACATAAA	GTTTCTGATC	CGTTGTCCAT	AGTTTGCTTA	CAAAATATTC	ATCCAAGGTT	780
GAGTACTCCA	TAGTATATCC	TGTCGCTCTT	GTTTTAGGAA	AGACAGAATT	GTAGGGCATG	840
ATGAAATAAA	CTGGTAGTTC	GGCATCATAC	TGTCTTACTT	TTTCGACAAC	ATGGTAGTCT	900
AAAGACTGGA	TTTGATGTCC	ATAAATCTTG	AGCTTTGCAG	CATAACGGGC	TAAAAAGCGG	960
TTCATCATGT	CTGGACTATC	TTTTTTACTG	GTTTTAATTT	CAATTAGTAA	TTTTTGACCA	1020
AGTTCGTTGG	CTCGACTGAG	ATAATCTTCA	AAGCTTGAAA	TTTTAGTCTG	GTAGCCATTT	1080
TCAAAAATAT	CAATCCCTTT	AAGCTCCTCC	AAGTTTAAGT	CTTGAGGACT	TTTATTGATA	1140
CCTGCTAGAT	TTTTCAAGTT	AGCATCATGC	ATCATGACAA	ACTGCCCATC	TTTTGTTTCC	1200
TGCACGTCCG	TCTCCACCAA	GTCTGGTTTG	AGTTGTGCTG	TAGTTTCCAA	GGACTCTACT	1260
GTATTTTGAA	TCCCATTTGC	ATTGGAAACC	CCTCGGTGAG	AAATAAGTTG	AGGTAGATGA	1320
ACCATGGGAG	CCTCCAGATA	AATATAACCT	TCTAAGGCAA	AGAAAAGACT	GGCACAAGTC	1380
ATGACACCCC	ATCGCACGAT	GTGATCTTTT	TCTCTCCTAG	GAAGCATATC	CAGCTCCTTT	1440
CCTGTCAAAA	ATGAAACAAA	TTTAACCAAA	AAATAAGTCA	GAGCCATATA	ATAGAGATTT	1500
TTAATCACGA	CAAAATTCAA	AATACCAAGA	ATCAGAGACT	CTCTCTGAGT	GATATCATCT	1560
ACCAAAGTTT	GAGCCAATAA	TAAAGGAATC	AAAGGAAGAT	AATAATAATA	ATGTGCTTTG	1620
AGCAAGATGT	AAAATAAATT	CCAAGCATAA	AAAGTAACTC	TCTTCTTGGT	TTTCTCCAAG	1680
CTAAACATCA	CTGCTTCTCG	AACAGTCAGC	TGATCATATA	CAATCTTCGG	AAGGGCAAAC	1740
ATCAATCTGA	CAGAGACATA	GAGAAAGATA	AGAGATAGAA	GTAGGATGCT	CAGCCACCAC	1800
ATCCAATATC	TATCTTCTAA	ATAAGCTTGG	ATAAACTCTG	GAATGACGAT	TTTATTAAGA	1860
TAATAAATCT	TCAGCATTTT	CCGTATAAAA	GGAAACAGCA	TAGCTATATA	GAAAAAGATA	1920
AACAAGGCTT	TAGCGCAAGT	TAGCTTTTTT	ATAAATCCAA	AACTTTCATG	GAAAACCTTG	1980
CGGATATACT	CAATTAGCCT	TCGCTTTTCA	TTATAGAGGA	GATGACGAGC	ACCAATAAAG	2040
AGGAGTCCTA	TTTGAAAATA	AGCAACCAGA	AGGTTAATTA	CAATCAAGGC	TAAAAAAGCT	2100
AGACTAATCA	ATGGAGAATG	AGTAAGGATG	GCTAAGACAT	TGTTATAGGA	AATAAAAAGA	2160
TAACCTGTCT	GATCTAATAA	GAAGCTAGCC	AACCATGAAT	TGAATGGTAC	CCACAAATAC	2220
TCCACTATCA	TAAAAATCAA	GAAAAATAGA	AAGAGGATTT	TATCAAGATC	GAGGTAAATC	2280

1222

TGTTTAAGAC CCAATTTTTT AGGTTTTTCA GGTTCATAG GCACTCCTAG TCAAATAATT	2340
GAGACAAGTC CAAGCCACCA AAAGGATTGT TTGATAAGCT ACTTCTGTGTC TCTAACAATT	2400
CCCTAGCTTG ATCCGACTCT AAGAAGGATT CGTAAACACG CGCCGTCATC CGAGCATCCT	2460
CTAAACTATT ATGAGACTGA CCTTGAAATC CAAGAAATGA GGCAACAGTT TGCAATTTGA	2520
GATTGGCAAT ACCATGTAAA TCTGAACTCC GACGTTCAAA AGCTTCATCA TACAAATCCA	2580
CCTTGTA CTG TTGGCTATAG TCTAAACCAT GCTCTGCTAA AATAGGTAAA TCACTTTTAG	2640
CAGCATTGTA G	2651

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5638 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

CGTTATAATA AACTTGTGAA AAAATTAACA AAGGATATCG TTCCTTGAAA GCTATGGAGG	60
AAAATATGGC TGATAAAAAA ACTGTGACAC CAGAGGAAAA GAAACTCGTT GCTGAAAAAC	120
ACGTAGATGA GTTGGTTCAA AAAGCTCTAG TTGCCCTTGA AGAAATGCGT AAATTGGATC	180
AAGAACAAGT TGA CTACATC GTTGCCAAAG CATCAGTAGC AGCTTTGGAT GCCCACGGAG	240
AATTGGCTTT ACATGCCTTT GAAGAAACAG GACGTGGTGT ATTTGAAGAC AAAGCAACTA	300
AGAACTTGTT TGCCTGTGAA CACGTAGTAA ACAACATGCG CCACACTAAG ACAGTTGGCG	360
TTATCGAAGA AGACGATGTA ACAGGATTGA CTCTTATTGC TGAACCAGTT GGTGTTGTTT	420
GTGGTATTAC TCCAACAACA AACCCAACAT CAACAGCAAT CTTCAAATCA TTGATTTTCAT	480
TGAAGACACG TAACCCAATC GTCTTTGCCT TCCATCCATC AGCACAAGAA TCATCTGCTC	540
ATGCAGCTCG TATCGTCCGC GATGCAGCTA TCGCAGCTGG TGCTCCTGAA AACTGTGTGC	600
AATGGATTAC TCAACCATCT ATGGAAGCAA CAAGTGCCCT TATGAACCAC GAAGGTGTTG	660
CGACAATCCT TGCAACAGGT GGTAATGCCA TGGTTAAGGC GGCTTATTCA TGTGGTAAAC	720
CAGCTCTTGG GG TAGGTGCC GGAAACGTT CAGCTTATGT TGAAAAATCA GCAAACATTC	780
GTCAAGCAGC ACACGATATC GTCATGTCTA AATCATTTGA TAACGGTATG GTCTGTGCAT	840
CTGAACAAGC AGTTATCATT GATAAAGAAA TTTACGATGA ATTTGTAGCA GAGTTCAAAT	900
CTTACCACAC TTA CTTTGTA AACAAAAAAG AAAAAGCTCT TCTTGAAGAG TTCTGCTTCG	960
GCGTCAAAGC AAACAGCAAA AACTGTGCTG GTGCAAAATT GAACGCTGAC ATCGTTGGTA	1020

1223

AACCAGCAAC	TTGGATTGCA	GAACAAGCAG	GATTTACAGT	TCCAGAAGGA	ACAAACATTC	1080
TTGCTGCAGA	ATGTAAAGAA	GTTGGCGAAA	ATGAGCCATT	GACTCGTGAA	AAATTGTCAC	1140
CAGTTATTGC	AGTTTGTAAA	TCTGAAAGCC	GTGAAGATGG	TATTACTAAG	GCTCGTCAAA	1200
TGGTTGAATT	TAACGGTCTT	GGACACTCAG	CAGCTATCCA	CACAGCTGAC	GAAGAATTGA	1260
CTAAAGAATT	TGGTAAAGCT	GTTAAAGCTA	TTCGTGTTAT	CTGTAACCTA	CCTTCTACTT	1320
TTGGTGGTAT	CGGGGACGTT	TACAATGCCT	TCTTGCCATC	ATTGACACTT	GGATGTGGTT	1380
CTTACGGACG	CAACTCAGTT	GGGGATAACG	TTAGTGCCAT	TAACCTCTTG	AATATCAAAA	1440
AAGTCGGAAG	ACGGAGAAAT	AACATGCAAT	GGATGAAACT	TCCTTCAAAA	ACATACTTTG	1500
AACGTGATTC	AATTCAATAC	CTTCAAAAAT	GTCGTGACGT	TGAACGTGTC	ATGATCGTTA	1560
CTGACCATGC	CATGGTAGAG	CTTGGTTTCC	TTGATCGTAT	CATCGAACAA	CTGGACCTTC	1620
GTCGCAATAA	GGTTGTTTAC	CAAATCTTTG	CGGATGTAGA	ACCGGATCCA	GATATCACAA	1680
CTGTAAACCG	TGGTACTGAG	ATTATGCGTG	CCTTCAAACC	AGATACCATC	ATCGCACTCG	1740
GTGGTGGGTC	TCCAATGGAT	GCTGCCAAAG	TAATGTGGCT	CTTCTACGAG	CAACCAGAAG	1800
TGGACTTCCG	TGACCTTGTC	CAAAAATTCA	TGGATATCCG	TAAACGTGCC	TTCAAGTTCC	1860
CATTGCTTGG	TAAGAAGACT	AAATTCATCG	CGATTCCAAC	TACATCTGGT	ACAGGATCTG	1920
AAGTAACACC	ATTTGCCGTT	ATCTCTGATA	AAGCAAACAA	CCGTAAATAC	CCAATCGCTG	1980
ACTACTCATT	GACACCAACT	GTGGCAATCG	TAGATCCTGC	TTTGGTATTG	ACAGTTCCAG	2040
GATTTGTTGC	TGCTGATACT	GGTATGGACG	TATTGACTCA	CGCGACAGAA	GCATACGTAT	2100
CACAAATGGC	TAGTGACTAC	ACTGATGGTT	TAGCACTTCA	AGCCATTAAA	TTGGTCTTTG	2160
AAAATCTCGA	AAGCTCAGTT	AAGAATGCAG	ACTTCCACTC	ACGTGAGAAA	ATGCATAACG	2220
CTTCAACAAT	CGCTGGTATG	GCCTTTGCCA	ATGCCTTCCT	AGGTATTTCT	CACTCAATGG	2280
CCCATAAGAT	TGGTGCGCAA	TTCCACACAA	TCCACGGTCG	TACAAATGCT	ATCTTGCTTC	2340
CATACGTTAT	CCGTTACAAC	GGTACACGTC	CAGCTAAGAC	AGCAACATGG	CCTAAGTACA	2400
ACTACTACCG	TGCAGATGAA	AAATACCAAG	ATATCGCACG	CATGCTTGGA	CTTCCAGCTT	2460
CTACTCCAGA	AGAAGGGGTT	GAATCTTACG	CAAAAGCTGT	CTACGAACTC	GGTGAACGTA	2520
TTGGGATCCA	AATGAATTTT	AGAGACCAAG	GAATTGACGA	AAAAGAATGG	AAAGAACATT	2580
CTCGTAAATT	AGCCTTCCTG	GCTTATGAAG	ACCAATGTTT	ACCAGCTAAC	CCACGTCTTC	2640
CAATGGTAGA	CCATATGCAA	GAAATCATCG	AAGATGCATA	CTATGGCTAC	AAAGAAAGAC	2700
CAGGACGCCG	TAAATAATTG	TTTATCAGTC	TAGAAGCAAG	ACAAAAACTC	AATTTGAGGG	2760

1224

AAAGATCCAG	TAATTTTTCT	ATGATAAAAG	GCATCCTATC	AAGGTTTTTG	AACACCTGAT	2820
AGGATGCCTT	TTTATGATAT	TGAGGCCTTT	TTGCCCTTTT	TGAAAACTA	GAATAGAAAC	2880
AAAATATATA	ATAGATTGAA	ACTAGAATAG	TACATATCTG	CTTCTAAAC	ATTGTTAGAA	2940
TTCGATTTGA	CTGTCCTGAT	CGATTTGTCC	TGTTCTTATT	TCATTTTGAT	ATATAAAAAA	3000
TATAGTATAG	TAGACTGAAT	CTAAAATAGT	ACGAAACAAT	TGCTAAAACA	TTTATAGAAA	3060
TTAATTTTAC	TTTTCTGATA	GAGTTGTTCA	CATCTTATTT	CAATTCACCTA	TAGTTTAATT	3120
TAAGAGTAGT	ATTTACTAAG	GCCCAATTAA	AATCAAAGAG	CAAACTAGAA	AACGAGTGCC	3180
ATTCAGCTCA	AAACACTGAT	TTGAGATTGC	AGATAAGACT	AGCCCCCTCA	TTAACAGATT	3240
TACGATAAAA	CGATGACAAG	GTGTGTTGCT	TTTTGATTTC	TAAAGAGTAT	AATGATAGAT	3300
CTCTATAAAA	TAAGTGCGAA	GGAAATGAGC	TTTTATAGTC	CTTTCGTTTT	AAAATACTAT	3360
CTCAGATATT	CTTATATCGA	CAAGAAGTTT	TTGAGTCATT	CCCTCATCAT	ACATATTAAA	3420
TAAATAGTGG	CTCATTCAAT	TTTTCACTAG	AATAATAAGC	TAGTATAGTA	AACTGAAATA	3480
AGATATAAAC	AAATAAATTG	GAGCTTAACA	TCCATTTCCA	GCAATTTTTT	AGAACTACA	3540
GTGGACTATT	CTAGATTCAA	CATATTATAA	AAACTAGAGT	AAAAGAAAAG	GATTGGATCT	3600
TGTGTAATGC	AGGATCCAAT	CCTTTCAATC	ATTTTGTCCA	ACTTTTGGAG	GTTCCCTACAA	3660
TGTAGTCGTC	ATTAATAAAG	ACAGATGGGA	ATGACAGTGT	TCCTATTTAT	TTTGATAGAG	3720
ATCGATGAAT	TCTTTAGATA	GCAACTGAAT	AATCTCTGTT	GAAGCCATTT	GGTCTTCTGC	3780
ATGCATAAAT	AGCAAGGAGA	ATCCTATTTT	TTCTCCAGTA	GCTTCTTTTT	GTATGAGATT	3840
AGAGTGAATC	TTGTGCGCTT	CTACTAAGGA	GTCTTCCGCT	TCTTCAACTT	TAATTTTCGC	3900
TTCTTTTAAA	TTTCCTGCCT	TAGCTAGTTG	GATGGCTTCA	ATAAAGGATG	ATTTGGCTGC	3960
TCCACTATTG	GCAATGAGCT	GAAAACAGAT	ATATTCCATT	TCTTCTGTCA	TCTTATTTCT	4020
CCTATCCATG	CAAGTGCTTG	TTCCAGAACT	TTTGCTCCAT	TCATCATTC	GTAATCCCGC	4080
ATATCAATGG	TATCTACAGG	GATATTTCC	GCAATTTCTT	TCACAGCAAG	TAACTCATAA	4140
CGAATTTGTG	GCCCAATTAG	AATGACATCT	GCTTCATGGA	TATTCTTTTT	AGCTTCTGTC	4200
ATTGATTTTG	CTTGGATAGA	GATTTCAATC	CCACGTTTCA	TCGCACTTTG	TTGCATTTTT	4260
TTAACAAGCA	TACTTGTCGA	CATTCCCGCA	TTACATACTA	ATAAAATTTG	TTTCATAATC	4320
TTAACCTTCC	ATTTCTTGTT	CAACAACCTT	GTCATTAAC	TTGATAAATG	GAATGTATAG	4380
AAGAACTCCA	AGTGCAAAGA	TGATGAATTG	AACTAGAACT	GCTCTCACGT	CCCCTGCTGT	4440
TGCTAACCAT	GCATTTAAGA	ATACTGGTGT	AGTCCAAGGA	ACTTGTATAA	ATGCAGGACT	4500
CATGAATTCT	GTAACCTGTT	CTAAGTAGCT	GATTAAAATA	CCAAGGACTG	GAACTGTGAT	4560

1225

AAATGGAATA GCTAATGAAA TGTTATAAAC GATTGGGTAA CCGAATAATA CTGGTTCATT	4620
GATATTGAAG ATACCAGGTC CAAAAGATAA TTTAGCCACG TTTTGTAGAGA CAGCATTGCG	4680
ACTCACTAAG AATGTTGCTA TTAATAAACA TAATGTAGAT CCACTACCAC CCATTAAAGC	4740
GAATGTTTGT ATTTGTGATA GGTGATGAT GTGTGGAATG GCTTGTCCAT TATTTGCTGC	4800
AGTGATGTTT TCAGTAATGT TAATTAATAG TAATGGTTCT AGGATGGCAC TGTAATAAAC	4860
TGCTTGGTGA ATACCAAATA GCCATAACAT ATTCCTAAA GAGTAAATAA TAATGACCCC	4920
GATTAAGCTT GTACCAATAT GACGAATTGG TTCTTGAATA AAGATTGTAA TGATTGAGAT	4980
TAAGTTCATT CCAGTTATAT TGAATAATAA TGCTGAAACA ACCCCAAATA AGGAGATGAC	5040
GGTCATGACT GGAAGTAATA CGCTAAATGA TCTACTACA GCTGGTGGAA TATTTTCACC	5100
AAGGTTTATT TGTAAGCTT TAACGTTTGA TAATTCAATG AATAATTCTG TTGCAATAAT	5160
CGTACGATAA CCCC GGCGAA CATTGCGCCT GTACCTGTGT TGTTGAATGA AAGAACACCT	5220
GAAATGTTTA CCGCATCTTT TGCTCCGTCA GGAACACAG AAAGTGTATT TGGCATCATC	5280
ACAATTAAAG AAATAATGA TAGCATTGAT GCTGCTAACG GGTTTTCGAA ATCTCTGTTT	5340
TTAGCTAAGA AATAACCAAC CATTACAGCA ATAATCATAC CTGAAATACT TAAAGTACCG	5400
TTTGCAATTG TTATTCCCCA ATATTGGAAT CTTGTTAATG TATCCCCTTG GAAAATCCAC	5460
TTAAATACCG TGTTGTTCAA AAGAACGATT AAACCTGCCA AAATATATAA TGGCATTACT	5520
GTTACGAATG CATCTCTTAG GGTTTTAAA TGAATTGGT TCCCTAGTTT ACCAGCAAAG	5580
GATGGCAAAA AAATTTTTTT GGGGGGGGG GTTATTAAAC CCCCCTTTT AAAAAAA	5638

(2) INFORMATION FOR SEQ ID NO: 218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4745 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

CCGGAAGCTG TTGCCCTTGG AACTCCAAAT GAAGAAACAG CCTTTGTCTT GAACTATTTT	60
GGTGTGGAAG CACCACGTGT TATCACTTCT GCCAAAGCAG AGGGGGCAGA GCAAGTTATC	120
TTGACTGACC ACAATGAATT CCAACAATCT GTATCAGATA TCGCTGAAGT AGAAGTTTAC	180
GGTGTGTAG ACCACCACCG TGTGGCTAAC TTTGAAACTG CAAGCCCACT TTACATGCGT	240
TTGGAGCCAG TTGGATCAGC GTCTTCAATC GTTTACCGTA TGTTCAAAGA ACATGGTGTA	300

1226

GCTGTGCCTA	AAGAGATTGC	AGGTTTGATG	CTTTCAGGTT	TGATTTTCAGA	TACCCCTTCTT	360
TTGAAATCAC	CAACAACACA	CCCAACAGAT	AAAATCATTG	CTCCTGAATT	GGCTGAATTG	420
GCTGGTGTGA	ACTTGGAAGA	ATATGGTTTG	GCAATGTTGA	AAGCTGGTAC	CAACTTGGCT	480
AGCAAATCTG	CTGAAGAATT	GATTGATATC	GATGCTAAGA	CTTTTGAACT	CAACGGAAAT	540
AATGTCCGTG	TTGCCCAAGT	GAACACAGTT	GACATCGCTG	AAGTTTTGGA	ACGCCAAGCA	600
GAAATTGAAG	CTGCAATGCA	AGCTGCCAAC	GAATCAAACG	GCTACTCTGA	CTTTGTCTTG	660
ATGATTACAG	ATATCGTCAA	CTCAAACCTCA	GAAATCTTGG	CTCTTGGTGC	CAATATGGAC	720
AAGGTCGAAG	CGGCTTTCAA	CTTCAAACCTT	GAAAACAATC	ATGCCTTCCT	TGCTGGTGCC	780
GTTTCACGTA	AGAAACAAGT	GGTACCTCAA	TTGACTGAAA	GCTTTAATGC	GTAAGATTTT	840
GGGTGTCAGC	TCAAAATCGG	AAAGTCTAGT	TTGCCTTATA	TCGCAAGGAG	TTTCGGCTCC	900
TTTTTTCTAG	GAGTGAAGTA	TGTTAGAAAA	TGGCGATTTG	ATTTTTGTGA	GAGATGGGTC	960
AGACATGGGA	CAGGCCATCC	AGACTTCCAC	AGGTAACAT	AGCCATGTTG	CCATTTATTT	1020
GGATGGGATG	ATTTATCATG	CTAGTGGACA	GGCTGGTGTT	GTCTGTCAAG	AACCGGCAGA	1080
CTTCTTTGAG	TCCAATCATT	TATACGACCT	CTATGTTTAC	CCAGAAATGG	ATATCCAGTC	1140
GGTGAAGGAA	AGAGCTTGCA	AACATCTTGG	AGCACCTAC	AATGCTTCTT	TCTATCCAGA	1200
TGCAGCTGGT	TTTTACTGCT	CCCAGTATAT	AGCAGAAATC	CTACCTATTT	TTGAAACTAT	1260
TCCTATGAAA	TTTGAGwTG	GGGAGCAGGA	GATTAGTGAT	TTTTTGAGGG	AGTATTACAT	1320
AGAAGTAGGT	CTGCCTGTTT	CTCTGAACCA	AGCTGGTACC	AATCCTAGTC	AGTTGGCAGC	1380
ATCGCCTCTG	TTACAATGTA	AAGAAAGGAA	TCTTCATGAT	TCAGATTTTT	AATCCATCTC	1440
GTTTGACGAG	ACAGCCATTT	TTGGAGAATT	GATCCGCTAT	CTGGATCAGT	ATGAGGATGT	1500
GATTCTACGG	GAAATTAAGG	CTCAATTTCC	AGATGTTGCA	GTTGATAAAC	TCATGGAAGA	1560
GTATATAAAG	GCAGGCTTGA	TTCTACGTGA	AAATAAGCGC	TATTACCTCA	ATTTTCCTAC	1620
GCTTGAATCA	CTTGATAGTC	TTGAACTGGA	TCAAGAGATT	TTTGTGAGAG	AAGCTAGTCC	1680
GGTCTATCAA	GCCTTGTTGG	AGCAGAGTTT	TGAGACGGAA	TTGCGCAATC	AAATCAATGC	1740
AGCTATTTTA	GTTGAAAAGA	CGGACTTTGC	GCGCATTAAT	ATGACCCTGT	CCAATTATTT	1800
TTACAAGGTC	AAACAGCAGT	ATCCTTTGAC	AGAAAAACAG	CAGGAGCTCT	ATGACATTTT	1860
AGGAGATGTT	AATCCTGAGT	ATGCCCTCAA	GTATATGACG	GCTTTTTTGT	TGAAATTTCT	1920
CAAAAAAGAC	CAGCTTATGC	AGAAATGCCG	TGATATCTTT	GTGGACAGTT	AGGTTGTCTT	1980
AGGCTATATT	GTGCAAAATG	AAGATGGAAA	GTATGAGTTG	GCTATCGATT	TTGATAAGGA	2040
GAGGTTAACT	TTCTACTTAG	CGTGATTTCT	TGTTTCTGAG	TACATTGTTT	GACTTTCCTT	2100

1227

AGTATTTCGGT	ATAAACTATA	TGTAACCGGT	AACACATATC	GGAATAAACT	AAAGGAGACA	2160
ATCATATGTC	ACTTGAAAAC	AAATTGGAAC	AAGCAACAGG	CGCTGTCAAA	GAAGGTTTGT	2220
GTAAAGTTAC	TGGAGACAGC	AAGACAGAAC	TTGAAGGAGC	TGTTGAAAAA	ACAGTTGCTA	2280
AGGCAAAAGA	CGTTGTAGAA	GACGCAAAAG	GTGCTGTAGA	AGGTGCCGTT	GAAGGTTTGA	2340
AAAACGTTTT	TACTAAAGAA	TAGGAAAAAA	TCAAGGGTTT	CATTTTCCCT	TGATTTTTTC	2400
TATTCTTATA	AATAATTTTC	TGCGACGGCT	GTATCTCCTG	GGTAGGATTC	TTTCTTGCCC	2460
TGGATGATTT	GGTAACAATC	GGCTCCCTTA	CCCGCAATAA	TAAGTGCATC	TAATTCGTGA	2520
TTTGTGATAG	CCATTGCCGC	CTTGATGGCT	TCTTGGCGAT	CCGCAATCTT	TTCAACAGGA	2580
TGATTGATGT	AGCTACTAAT	TTCATCTGCA	ATGGCCATTG	GGTCTTCATA	GTTAGGGTCA	2640
TCAGCAGTCA	GAAAGACTTG	AATCTCAGGG	TGTTGATTGA	GGAGGAGGCC	AAAGTCCTTA	2700
CGACGACTTT	CTCCCTTGTT	TCCTGTTGAT	CCCAGAACCA	GAGCAATCTT	TCCGGTTTGA	2760
TGAGTTTCAA	CCACATTGAT	GAGTTTTTTC	AGACTATCCC	CATTGTGGGC	ATAGTCGATG	2820
AAGACCTTGG	CTCCATTTT	CTGAGTGAGG	ACTTCCATAC	GACCAGGAAC	GCGGGTTGCA	2880
GCGATGCCTT	TTTTGATGTC	CTCAAGACTT	GCTCCGAGAC	GGAGACAAGC	AAGTCCAGCA	2940
GCAACTGCAT	TTTCTTGTT	GAAGTTGCCA	ATGAGTTGAA	TATCATAATC	TCCAGCGAGT	3000
TTACCCGTAG	CTGAAAAGCT	AAAGGCTTTG	GAATTCTCGA	TTTGGTTATC	AAATTGGCTA	3060
CCATAGAAAT	CATGGTCTTG	ATCTTCAACC	TGTTCTTTCA	AGACTGAGAA	GTGGTCCATG	3120
TCACTGTAA	TGATGACTGC	TCGGCTCTTT	TCCATCAAGA	GACGCTTGTG	GTAGAAATAG	3180
TCTTCAAAGC	TAGGGTGTTT	AATCGGGCCG	ATATGGTCTG	GGCTGATATT	TAGGAAAAC	3240
CCCACATCAA	AGGTTAGACC	ATAGACACGT	TTGACCAGAT	AGGCTTGACT	GGAGACTTCC	3300
ATGATGAGGT	GGGTACGGTC	ATTTTGCACA	GCCTGATTCA	TCATGTCAAA	GAGGTCAATA	3360
CTCTCAGGGG	TTGTCAACGC	TGACTTAAAG	AAAGTCTCGC	CATCAAGAGT	TGTGTTTCATG	3420
GTCGACAACA	TAGCAGGTCT	ATGCCCTTGA	GATAAGATGT	TATAGGCGAA	ATAGGCTGCT	3480
GTTGTCTTAC	CCTTAGTACC	AGTAAAGGCA	AGGAGTTTGA	GTTTTTCCTG	TGGATTACCA	3540
TAGAACTCCA	TGGCAATCAA	ACTCATGGCT	TTCTTTATAT	CGTTCACAAT	GATGACAGGG	3600
ATACCGACTT	CGTAGTCCTT	TTCAGCTACA	TACCAAGCTA	ATCCTTGTGT	TATAGCAGAA	3660
AGAAGGTATT	CTTTTTTAAA	GGCAGCGCCT	TTTGCGAAAA	AAAGAGTGTC	TTCTGTTACT	3720
TTTCGGCTGT	CGTAGCTGAT	GCTATCAAAA	ATAACTTTGC	TGTAGTTGTA	GTGGTAATGA	3780
CCTTGGTCAA	TAATTTTCGCG	AAAAAGGCCA	TCTTTCTTTA	AAATATCTAA	TACGGTTTCA	3840

1228

ATCTTAATCA TACTTTCTAT TGTAACCGA AAGTCGTAAA TTTACAAGTA ACAAGGAAAA	3900
GTTTATAATG GAAGATAAGG AGTTTTTCCT AGTTATCAAA ATTGAATGAG GAATCTATGT	3960
CGCACGAAAA CAATCACCAG CAGGCCCAGA TGTTACGGGG GACTGCTTGG CTAACGGCTA	4020
GTAACCTTAT CAGTCGCCTA CTCGGGGCTG TTTACATTAT CCCTTGGTAC ATCTGGATGG	4080
GGGCTTATGC AGCTAAGGCA AATGGTCTCT TTACCATGGG TTACAATATC TATGCTTGGT	4140
TCTTGTTGGT TTCAACAGCG GGGATTCCAG TTGCGGTGGC CAAGCAAGTT GCCAAGTATA	4200
ATACCATGCG AGAAGAAGAG CATAGCTTTG CCCTGATTCG GAGCTTCTTA GGCTTTATGA	4260
CAGGACTAGG CCTGGTTTTT GCTTTAGTCT TGTATGTCTT TGCTCCTTGG CTAGCAGACT	4320
TGTCTGGCGT GGGCAAAGAC TTGATCCCAA TCATGCAAAG CTTGGCTTGG GGAGTCTTGA	4380
TTTTCCCGTC TATGAGTGTT ATCCGAGGAT TTTTCCAAGG GATGAATAAC CTCAAACCCT	4440
ATGCCATGAG CCAAATTGCT GAGCAGGTCA TTCGTGTTAT CTGGATGCTC CTAGCAACCT	4500
TTATCATTAT GAAGCTCGGT TCAGGAGATT ATCTAGCAGC CGTTACCCAA TCAACCTTTG	4560
CTGCCTTTGT CGGTATGGTA GCCAGTTTTG CAGTCTTGAT TTATTTCCCTT GCCCAAGAAG	4620
GTTCACTCAA AAGAATCTTT GAAACAGGAG ATAAGATTAA CAGTAAGCGT CTCTTGGTTG	4680
ATACCATTAA GGAAGCCATT CCTTTTATCC TGACAGGGTC TGCCATCCAG CTCTTCCAGA	4740
TTTTG	4745

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

CCTGATTGAC CTTATAATAA GGAACAAAAC ACAATGCACT ACCTTTTCAA CAAAAGAGTT	60
GCTGCTTGAT TAAAACCATC ACACCAGTTA TACCATTTTG CTTCATACCC ATCTTGAGCT	120
AGGATACGAT CTTCTAAATC AAAACAGAG TAAATCTTTC TTTCCCTCGCA AGCTTGCGCA	180
TAGAGATGAT ATAGTTCATC ACCACCATCT CTATCCCACT CAGCAGAAAT CGTATCCCGA	240
CCTGCCAATA AAGCCTGATA AGCCCTGTGA TGCCCATCTG TAATCAGCAA ACAATCTCCA	300
AAGGCAAGAA TACTGATTGG ATCGACTTGG ATTGTTTCTG CCGACTGGTA AAGCATCTGA	360
ATATCTTGCA ACTTCTTTTC TGATAAATAT AGTTGAGTCA GATGAAGATC TGCTATATTG	420
ACTTTCATTT CTTTCTCCTC AAGGGAATTC GATACTCACT TCTGTTTGCC TTTAAATCGC	480

1229

CATTGGAAGC	GGAgCTTGTC	ATAAAAGGGA	AACTCGATAA	ACAGGACTCC	CAAGCCCACA	540
CAGAGACTGG	CAAGGACGTC	TGATGGGTAA	TGAACTCCCA	GATAGACTCT	TGATACCAGC	600
AACTGACTA	GGTAGAGGCC	AAGGACGATT	TGTACGATTT	TTCTCCAGAC	CTGATCTTTA	660
ATCCGCTGAC	TAAGAATAAC	AATCAAAGTC	CCTACCATCA	GCGTTACAGC	TAGAGAATGC	720
CCACTTGGA	AGGAAAATCC	CTTCTCCTCC	ACCAGATGTA	AAATAGCTGG	TCGTGGGCGC	780
TGGTAGATAT	TTTTAAAGGT	CACGATTAAA	AGACCTGCCA	AAGCCAGATT	TCCCAGCATG	840
AAGAACTTT	CTATCTTCCA	TCGCTTACGA	TAAAAGACAA	AAGCTGTAAT	GACAACCCAA	900
GTGATAATCA	CTGGGATATC	AATCAGACGT	GTGAGGGCTC	GAAAAAGAAT	AGTCAAATAA	960
TCTGGTAAGT	CTCCTCGAAT	GGCAGTCTGA	ATCGATTGGT	CAAATTGAC	CAACATTTCA	1020
GGGTAAATTT	TGACCATGTA	GCCAAGAATA	ACGAAAAGTA	AAAGGGCAAA	ACTGCCCTTC	1080
ATTAAAAATG	TTTGTTTATC	TCTCATAATG	TTTTAAGGTT	GGTTTCAAGA	GAACATACAA	1140
CAACCAGAAT	GAAACGGAAA	AGATAACACC	TTCAATCAAG	TTAAAAGGTA	ATACCATGGT	1200
CATTAGGTAG	TTGGAAAGTC	CCAAAATTTT	TCCAATATCA	AAGTTAGCAA	ACTTAGCGTA	1260
CAAAGGAACA	GCATAAACAT	AGTTGAGAAC	CAACATGGCC	AAGGTAAAC	CAATAGTTCC	1320
AGCTAGAGAG	CCTAGTAGGA	AACGAAGGGT	TGTCCGTTCC	TTTTTCCAAA	TCAAAGCAAA	1380
TACGATGACA	AAACTCCCA	AAGCTACGAT	ATTCATCGGC	AAACCAATGT	AAGTATTCAC	1440
TCCTTGCTG	TTAAGAAGCA	ATTTCAAGAG	TGAGCGAAGC	AAGAGCACTC	CTAGAGmCsC	1500
AGGCAAATCC	ATGACCACCA	GACCCACAAG	GACTGGCAAG	ATACTAAATT	CGATCTTGAG	1560
GAAAGATGCC	GCTGGTAAAA	GCGGAAAGTC	AAAGTACATC	AGCACAAATG	AGATGGCTGA	1620
TAGAATTGCA	ATGGTCGAAA	GTCGACGTGT	GTTTGTCATA	ACAGGTTCCCT	CCAATTTTCT	1680
ATAAAATCAG	AAGAAGTTGG	AAAGGATTCC	TCTATCTATT	CTCACTTTTT	ATATCCCAAA	1740
AGTTCCCTCT	TACTCTATTA	AAGAAAAACA	AAGCAAGTGG	TTACAATCCG	GCTATAAATC	1800
TATCAAAACA	GACAAGGCTA	TTCTTTTCGTC	TTCTCCCATC	CAGACTATAC	TGTCGGTTGT	1860
GGAATCTCAC	CACATCACGT	TGCGCTCACG	GACTTCTTTA			1900

(2) INFORMATION FOR SEQ ID NO: 220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4692 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

GGTTTTCCAG CAGGAGCTTC TCCTTTATCA GAATGACCAT CCCATCTGCT CACGATAGAT	60
GAATAATGAT ATTTTTTACC ATGATAGTAA TTTGAAAAAG CCTAACCACC TCCTGAACCT	120
TCTCCATATG TCCATACTCC TCCATCTGGA TATTATACAG CAGCTGATGC AGCTCCCAAT	180
AATGTAAAAC TTGAAATAAG AGCTAGAGCA AGTAATCTAT GTTTTTTCGT TTTCATTTTA	240
TTTTTTCTTT CAAAAAAGC ACACCTTGAG CAACAATGCA ACAAATAAA TCCTCCTCTC	300
TCTTTTATTG AAACCGCTTT CTTATGTGAT AAGAATAACT TTTTATtAT TTGTTGTCAA	360
GGAAAAATC GAATTTTTTA GATATTTTAC TATATTACCT CTGTGAATAA TATTATATAG	420
TAGTTTTATT TCAAATAAT ATGCAACCAG TACTAACCAA ATATAAAATA GATGCCATTA	480
ACGAATTTTA TTCAAGTTTT TCCCATTCAT ACTATACAAG TAAAAGAGAT GGTGTAACT	540
AAAAAGCAAT TCAAACTATT GTAAAATTCC TAGCAAAAAG AGAGCCGAAA CTCTCTTTTT	600
TATCTTCTTT TACTTTTTTT GACTGGCATG AGTGTGATGT CTCTAACACT AAAGTAAGCT	660
AGGATCAACA TGGCTATTGC TAGGAATATT TCTGTTGGTA ATTGAAAAAT TTTCAGAAAA	720
GATAGAACCA ATAAATCAA GAGTGCCACT AAAATACATA CCATAGCGAC GATATTGACA	780
GTCCCTTTAA TGCTTTCTGG TGTCGCAAAT ACATAGAGTA GGAGCAGTAA AATTCCTAGG	840
ACTAAATAGA CCATCTTTCT CTCTTTCTAG CTCTTATTCA GCTGATTTTT TCTTCTTGTT	900
AGCTTTCTCA CGCTCTGCTT TGTTAAGGAT TTGTTTACGC AAACGGATAG ACTCAGGCGT	960
TACTTCCATG TACTCATCGT CGTTCAAGAA CTCAAGAGAC TCTTCAAGTG TCAAGATACG	1020
AGGCGTCTTG ATAACAGCTG TTTGGTCCTT AGTAGCTGAA CGAACGTTGG TCATTTGTTT	1080
TGCCTTCGTG ATGTTAACTG TCAAGTCATT TTCACGAGAG TTTTCACCGA TGATCATTC	1140
TTCATAAACC TCAGTACCTG GGTGACAAA GATCGTACCA CGTTCTTCGA TAGACATGAT	1200
TGAGTAAGTT GTAGCCTTAC CAGCATCGAT AGAAACAAGG GCACCACGGT GACGTCCACC	1260
AATTTCCCCT GGAATCAATG GCAAGTATTG GTCGAAGGTA TGGTTCATGA TACCGTAACC	1320
ACGAGTCATT GATAAGAACT CAGTTGAGTA TCCAATCAAA CCACGCGCTG GAACAAGGAA	1380
GACCAAACGA GTTTGACCAT TACCAGTTGA AATCATATCC AACATTTTAC CTTTACGTTT	1440
AGAAAGGCTT TGGATAACAG ACCCTTGGTA TTCTTCTGGA GTGTCGATTT GTACACGTTT	1500
AAATGGTTCA CATTTAATAC CGTCGATTTT TTTTACGATA ACTTCTGGAC GAGATACTTG	1560
AAGTTCATAG CCCTCACGAC GCATTGTTTC GATAAGGATT GACAAGTGCA ATTCTCCACG	1620
TCCTGAAACA GTCCATTTAT CTGGTGAATC AGTTGGGTCA ACACGAAGGG AAACGTCTGT	1680
TTGCAATTCT GCCTGCAAGC GTTCTTCCAC CTTACGAGAA GTTACCCATT TACCTTCTTT	1740

1231

ACCAGCAAAT	GGTGAGTTGT	TGACCAAGAA	AGTCATTTGA	AGAGTTGGCT	CATCGATGTG	1800
TAGGATTGGA	AGAGCTTCTA	CTGCATCTGT	CGGAGTGATG	GTTTCACCGA	CAAAGATGTC	1860
TTCCATACCT	GAAACGGCAA	TCAAGTCACC	CGCTTTGGCT	TCTTGGATTT	CACGACGTTT	1920
CAAACCAAAG	AAACCGAAGA	GTTTTGTAAC	ACGGAAGTTT	TTAGTTGTAC	CGTCAAGTTT	1980
AGAAAGGGTA	ACTTGGTCCC	CAACCTTAAC	TGTACCACGG	AAGACACGAC	CGATACCGAT	2040
ACGTCCAACG	AAGTCATTGT	AGTCCAAAAG	TGACACTTGG	AACTGCAAAG	GCTCATCTGA	2100
GTTATCTACT	GGAGCTGGGA	TATGGTCGAT	AATCGTGTC	AAGATTGGTG	CCATAGTCGC	2160
TTCTTGGTCA	GCTGGATCAT	CTGACAATGA	AGAAGTTCCG	TTGATCGCTG	AAGCATAAAC	2220
CACTGGGAAA	TCAAGCTGGT	CGTCATCTGC	ACCAAGCTCG	ATGAAAAGTT	CCAAGACTTC	2280
ATCCACTACT	TCTGCTGGAC	GAGCTGATGG	CTTATCGATT	TTGTTAACAA	CCACGATTGG	2340
GACAAGGTCT	TGTTCCAAGG	CTTTTTTCAA	TACGAAACGA	GTTTGTGGCA	TGGTTCCTTC	2400
ATAGGCATCT	ACGACCAAGA	CAACACCGTC	AACCATTTTC	ATGATACGCT	CAACTTCTCC	2460
ACCAAAGTCC	GCGTGTCCTG	GTGTGTCCAT	AATGTTGATA	CGAGTTCGGT	TGTAAGCAAC	2520
GGCAGTATTT	TTAGCAAGGA	TGGTAATTCC	ACGCTCTTTT	TCGATATCGT	TTGAGTCCAT	2580
AGCACGCTCT	GCCAATTCAG	TCCGTGCATC	AAGCGTTTCT	GATTGTTTCA	ATAATTCGTC	2640
AACCAGGGTT	GTTTACCCTG	GGTCAACGTG	GGCGATAATC	GCAAATGTTAC	GGATATCTTC	2700
TCTTAATTTT	GTCATGATTT	CCTCTATAAT	ATTCAAAATT	TATTTTCTAA	CTGAACGATT	2760
ATACCATAAT	TTCAAATAAA	TAACATAACT	CAAGCAAGTG	TAAATGTTTT	CACTCTGCTT	2820
TTCTTTTCAC	GTCAAGCCTT	TTCAAAGCGA	GCGACTTATG	ATAAGATAGG	CACAGTATGC	2880
GTTTAGATAA	TTTATTAGCT	CAAGAAAAAA	TCAGCCGAAA	GGCCATGAAG	CAAGCACTCC	2940
TCAGAGGGGA	AATTCTAGTC	GATGGTTGCC	CAGCCCGCTC	CCTAGCTCAA	AATATCGATA	3000
CAGGACTACA	AGAACTCCTT	TTTCAGGATC	GAATCATTTA	AGGCTATGAA	CACACCTATC	3060
TTATGCTTCA	TAAACCTGCT	GGTGCCGTTA	CAGCCAACAA	AGACAAGGAA	CTTCCGACCG	3120
TCATGGACCT	GCTTCCATCT	AACATCCAGT	CTGACAAGCT	CTATGCCGTT	GGCCGACTGG	3180
ACCGAGATAC	AACGGGACTC	CTCCTCTTGA	CCGATAACGG	TCCCTTGGGC	TTTCAGCTCC	3240
TCCATCCCCA	ATATCATGTC	GATAAGACTT	ACCAAGTTGA	GGTTAATGGA	CTTCTAACAC	3300
CTGACCATAT	CCAAACCTTT	CAAAAAGGAA	TTGTCTTTTT	AGATGACACT	GTCTGTAAAC	3360
CCGCAAAACT	AGAGATTCTA	TCTGCAAGTC	sCTCCCTCAG	TCAAGCCTCT	ATCACCATTT	3420
CAGAAGGAAA	ATTTTCATCA	ATCAAGAAAA	TGTTCCCTCT	GGTTGGTGTT	AAGGTGACTA	3480

1232

GCCTCAAAAG AATCCAATTT GGGGACTTCA CATTTGAACCC AGATTTTAGCA GAAGGTAAC	3540
ACCGCCCTTT GAACCAAAAA GAGTTACAAA TCATTAAAAA CTATTTAGAG ATGAGTCGAT	3600
AAAACAAAAA AAGCTTTTAA ACTAAAGCTT TTTTCTTTTA TTTACCGAAA AATTAAGGCG	3660
ATTGCTACAA TCCAGTTAAC TACAGAAATC ACAATTCCTA AGATATTAAG AATCTTTTCT	3720
ATTTTATAGT CTAATTGTGA CTCTTTTGG TATGAAATAG CCAAGACCAA TCCTATGATA	3780
CCCAAAATCA GGCCTACAAT TGGAAATAAC AAACCAAGAA TAATCGACAA GATACCCACA	3840
AAAAGTGGAT TTTTCTTCTT TTCTTTTATG TTCTAAGAAC TCCTTAAATT TTATACAAAT	3900
TAATTATACT ATAAAACAAT AGCTTCATCC TATCATTCGA CTAATTTGGA AATAAGGTTA	3960
GCTAGTCTTC ACTTTCCTT TCCAAGAATC CAAGCCATAA GAAAGGATAT AAATCTCAGA	4020
AAAACCTTGT TTTTCAAGT AAAGAGCTGC ATTTGTAAC CGTTGCGCAC GTTGGTTTTT	4080
GTAGAGAAGG ACAGGTTTAT CTTTACGAAG GGCTGCAAGA CTAGTTTTCA ACTGACTTGA	4140
AGGAATATTG CGTGCACCAA GGATATGTTT TCTGTGGAAT TCTGCTGGGT CGCGCAAATC	4200
AATCAATTGA CCCGTACGAA TCAAGGCTTC AAATCCTCA TTGTCCACAA TTTTAGCCGC	4260
ACGGCGAATA CGAAGATAGT TAAAGCCCAT CCACGCCAAC ATTGCTAGTA TAAGTGCCCA	4320
CAAAATCCAA GTAACCATTA GTTCTTTTCT CCATTTTCT CAATATAATC CAATTCTACC	4380
TTGTGCTCTC TGCGAAGAAC TGCTTCTGCC TCTAGATAGT CTAATTTATC CATCAACCCT	4440
GCATCGTAAA TCCGAGATAG TTCCAACCTC ATCAGTTCAA TATCATATAA GCGTTTTCCC	4500
ATGTAAACAA TAATACCAA TCGTTTGAGG AATTGCTGCA CATCATAGAA TGTTTTCATA	4560
AGACTCATTC TAGCAAAATT TTGTGTTTTT TTCAAGAAGA GACTCACACA ATGCTCCTTA	4620
TTTTCTATC TTCTTAGCG ATTCTAAGGC AAGTATGGTA CAATAAAAAC ATGGGGATTC	4680
AACAATTACA TT	4692

(2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 706 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

GCTAAAAAGC TGATAATCTT CGACTCCTGT ATATGATGTG TCTTTTCATG TAAGACACGC	60
GCCGCCAGAA TCATGGCAAG AGCTGCAAGA CTGGCAAGTA AGAAGCCGAT AAGATAGGCA	120
AAAAGATAAG TGAATTTGAC AAAGAAAGTC AAAAGAACTA GGAAACCAA GCCTCCTCCA	180

1233

AAAAC	TACCA	AAGTC	TTTCG	TAAAT	CCCAG	ATTTT	TATCCA	ACTGC	TTGAC	GAGGG	AAGTC	240
GTCTG	ACGAA	CGCCT	TACAAT	AGTTG	CTAAC	ATACT	TCCTA	AAAAG	AATGG	ATAGAC	ATGA	300
GTTAA	ACTGG	AGAAAT	AATAC	AGAGG	AATAA	GAGGT	CACTA	GAAAA	CTACC	AATAA	ACATG	360
GAGAAG	AAAC	TGATCA	AAGAA	GGCAAC	AGCA	GATAAG	AGAA	AGACCA	TCCC	CTTCA	ACTGA	420
CCATTT	GATT	TAGCT	TGTTT	GGATA	AGAAC	CAAAC	TGCCA	ATCCCC	AAAAG	AATATA	GTAG	480
TGAAC	CTCA	CTGCC	AAACT	CCAATT	TATGA	ACAAAC	AAAT	GAGGA	ATGAA	CTGAG	ATTCA	540
TAAC	TCCCAC	CTGTT	AGGAG	TTCATA	GAAG	TTGGT	CATAA	AGCCT	AAGAC	GCCCG	CAATC	600
TGGCC	ACCAA	TTCCAG	CAAC	ATAGT	CTTGG	CGAAC	CAAGA	AAGTA	AAAAG	CATGG	TCACC	660
AAGAC	CATCA	AAACC	ACAGG	TGGCA	CAATC	TCGATA	AAAAG	CGTCTT				706

(2) INFORMATION FOR SEQ ID NO: 222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

CAGCTG	ATGG	GCAAT	ATCAG	TCATA	GAAAT	TTTTT	CAATT	AAC	TTTTG	GAG	CAAT	TTTTTTG	60
GTTGAT	GATA	CGAGG	GATTT	GGTGAT	TTTTT	CTTTA	CCAGG	GGAGT	CTCAG	CAACC	ATCAT	120	
TTTTGA	ACAG	TGATAG	CACT	TGAAAC	GGCG	TTTTCT	AAGG	AGAAT	TCTAG	AAGGC	ATACC	180	
AGTTGT	TTTCG	AGGTA	AGGGA	TCTTAG	ACGG	TTTTTG	AAAG	TCATA	TTTCT	TCATT	AGACT	240	
TCCACA	ATCA	GGGCA	AGATG	GAGCCT	CATA	ATCCAG	CTTA	GCGATA	AATTT	CTTTG	TGGGT	300	
ATCCAT	ATTG	ATGAT	ATCTA	GAATCT	TGAT	GTTTGG	GTCT	TTAAT	ATCGA	GCAGT	TTTTGT	360	
GATAAA	ATGT	AATTGT	TCCA	TATGAT	TCTT	TCTAAT	GAGT	TGTTTT	TGTCG	CTTTT	CATTA	420	
TAGGTC	ATAT	GGGAC	TTTTT	TTCTAC	ACAA	AAATA	AGCTC	CATAAT	ATCC	ATAGG	GGATT	480	
TACCCAC	TAC	AAATAT	TATA	GAGCCC	GAAA	ATATGG	GAAA	ACTGAT	CCTT	GTTTCT	GCCTT	540	
TTGTCT	TATAG	AAGAATA	AATA	AAGATT	TATCT	TCTTCA	AAAT	CTCCG	ATATT	CTCTAA	AGTT	600	
TTGTGCA	AGT	TGCAC	AGAAC	TTGTTT	ATTTT	TTTTGG	TCAT	CTTGCC	ATAG	AAATATA	AAAG	660	
CGTTTT	CATA	TATAAT	TATA	TTATCA	AAAAG	ACAAA	AGGAG	TTCAC	CTCAT	GGTAG	AATTG	720	
AATCTT	AAAA	ATATTT	TACAA	AAAAT	TATCCA	AACAG	CGAAC	ACTATT	CAGT	TGAAG	ATTTT	780	
AACTTGA	ACA	TCAAAG	ATAA	AGAATTT	TATC	GTTTT	CGTAG	GACCTT	CAGG	ATGTGG	TAAA	840	

1234

TCAACTACAC	TCCGTATGAT	TGCTGGTCTT	GAAGACATTA	CAGAAGGTAC	TGCATCTATC	900
GATGGCGTAG	TTGTCAACGA	CGTAGCTCCA	AAAGACCGTG	ATATCGCCAT	GGTATTCCAA	960
AACTACGCTC	TTTACCCACA	CATGACTGTT	TATGACAACA	TGGCTTTCGG	TTTGAAATTG	1020
CGTAAATACA	GCAAAGAAGA	CATTAACAAA	CGTGTTCAAG	AAGCAGCTGA	AATACTTGGA	1080
TTGAAAGAAT	TCTTGGAACG	TAAACCAGCT	GACCTTTCAG	GTGGTCAACG	TCAACGTGTT	1140
GCCATGGGGC	GTGCGATTGT	CCGTGATGCG	AAAGTATTCT	TGATGGACGA	ACCTTTGTCA	1200
AACTTGGATG	CCAAACTTCG	TGTATCAATG	CGTGCTGAAA	TCGCTAAAAT	TCACCGTCGT	1260
ATCGGAGCTA	CAACTATCTA	TGTAACCTCAC	GACCAAACAG	AAGCGATGAC	ACTTGCAGAC	1320
CGTATCGTTA	TTATGTCAGC	TACTAAGAAC	CCTGCTGGTA	CAGGTACTAT	CGGACGTGTA	1380
GAACAAATCG	GTACTCCTCA	AGAAGTTTAC	AAAAATCCAG	TTAACAAATT	CGTTGCAGGA	1440
TTCATCGGAA	GCCCAGCTAT	GAACCTTCATC	ACCGTGAAAT	TGGTTGGTAG	CGAAATTGTT	1500
TCTGACGGTT	TCCGTTTGAA	AGTGCCAGAA	GGAGCATTGA	AAGTTCTTCG	TGAAAAAGGC	1560
TACGAAGGAA	AAGAATTGAT	CTTTGGTATC	CGTCCAGAAG	ACGTGAATGC	AGAACCTGCT	1620
TTCCTTGAAA	CATTCCCAGA	CTGTGTTGTA	AAAGCGACTA	TCTCTGTATC	AGAACTGCTT	1680
GGTTCAGAAT	CTCACCTTTA	CTGTCAAGTT	GGTAAAGACG	AGTTTGTGTC	AAAAGTTGAT	1740
GCTCGTGACT	ACTTGCAAAC	AGGTGCAACA	GTTGAGCTTG	GATTTGACTT	GAACAAAGCA	1800
CACTTCTTCG	ATGTAGAAAC	TGAAAAAACA	ATCTACTAAA	ATAAATAAAA	TTCAAAGCAC	1860
TACAAGAAAA	GATATCTCTT	TATCAATTGT	AGTGGAGAGA	TATCAGTTAA	TCTAGGGAGA	1920
GAAACAAAAT	GCTTCTCTCC	TTTTTGCTAG	AGAAGTCATA	TTATGCATCT	ATATTGTGAT	1980
GCTCTTTAAT	ACTCTTCGAA	AATCTCTTCA	AACCACGTCA	ACGTCGCCTT	GCCGTACGTA	2040
TGATTACTGA	TTTCGTCAGT	TTTATCTGCA	ACCTCAAAGA	TGTACTTTGA	GCAGCTTACG	2100
GCTAGTTTCC	TAGTTTGCTC	TTTGATTTC	ATTGAGTATT	ATTTGTGGGT	ACCATCTACA	2160
AGTGAAGCTA	TATGCGTAAA	CTACGTGAGC	AATTGAATTC	GAAC TAGAGA	GGTAATAATA	2220
AATTTATGCT	ATAGTTATGG	TGACTTGTAT	GCTTTTGATT	CTAGTTTATC	AAATAATAGA	2280
TTAGAATTGT	CAGATAATAT	CATTTTGTGT	TATAATGAAG	AAAAAACAGA	GGTGTTCAAA	2340
TGTCAGAAGC	AGGTCATAAG	TTTTTAGCAA	AATTGGGGAA	AAAACGCTTA	CGTCCAGGTG	2400
GAAAGCGTGC	CACAGATTGG	TTAATTGCAG	AAGGAGGATT	TTCAAAAGAA	AAGAGAATAC	2460
TAGAGGTTGC	GTGTAATAGG	GGAAC TACAG	CAATTGAGTT	GGCACAGCGT	TTTGGTTGCA	2520
AGATAACTGC	TGTTGATATG	GATGCTCAAG	CTTTAGAAGT	GGCTAAAAAA	TCTGCTGGAA	2580
CGGCAGGTGT	TGCTCATTTA	ATCAGTTTTG	AAAGAGCAAA	TGCAATGAAA	CTTCCTTATC	2640

1235

AAGATGCTAG TTTTGATATT GTTATAAATG AAGCTATGCT GACTATGCAA GCCGATCAAG	2700
CTAAGAAAAA ATGTGTAATG GAATATCTAA GGGTATTAAA ACCTGGAGGT CTTCTCTTGA	2760
CACATGATGT GCTTCTTAAG GAAGCTAAAG AGTCTATCAG ACAGGAATTA TCACAAGCAA	2820
TTCATGTAAA TGTAGGTCCT TTAACCTCAAG ATGGTTGGGA ACAGGTGATG ATAGAATCAG	2880
GTTATTGTGA TGTGAAAGCA TTGACTGGTG AAATGACATT AATGAAATTA TCGGGTATGA	2940
TTTATGACGA AGGTTTGCTA GGAACCTTGA AAATTTGTGT AAATGCTTGT AAAAAGGAGA	3000
ATAGAAAGCA GTTTTAACT ATGTATAAAA TGTTTGCTAA GAATAAACAG AAATTGGGCT	3060
TTATTGCGAT GGCTAGTTAT AAATCGTCAA AACGTTAGAT AATTATTGAA GTTAACTTTT	3120
CCTTTTTTCT TTCTTAAAAA ATATGCTATA ATAGAGAGTA AAAAAGTTTG AAAGAAAGAA	3180
AAAGATGAAT TTAAGAGATT ACATTGCAAC AATTGAAAAT TATCCAAAGG GTACCG	3236

(2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2885 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

CCTGACTTTT CAAATTGGTT AGTTTGCCAC ACTTGGTTTA TATGGTCGTG GAAAGCATGG	60
CTATTACTTC TCAAAGGGCG ATTTCTCACC CCATGAAAAG TGTCTATTTT TGTTTAGGTT	120
TGTAAGTTAA TTCATTGTCA CATATTACTC TTTAACTGAT TGAGTGAGTA CCGCTTATAT	180
TTGATGCCAA ACGCCTTAAA AGTGTTACCC TCAAGTCCTT TTAGAATACG GCTATAATTC	240
CGCTCATTGT AAACATCTT AAGCTCATCA CTATCTAGGT TGGTATTAAA AATGGTATTT	300
TCACGATTGT TTAGCACGTC AAAGAGTAAA TCCTGCTCCC AGTCACTCTT AGGCTTAATA	360
ACAGCATTTT TTGCTCCTAA ATCATCAATA ATTAAGTAAT CAACAGACTT CATGAGTTCA	420
GTAGCTTCAA ACTCTGTAAG TGTTGCACCT TTACCATAAT TCCACCCCTC TTTAATTTGT	480
TTGATCATTT CGGTTAGGCT TACAAAAAGC AACTCTTAG GTTCTCCTTT TGTCTTATAC	540
CCCTCATTTA TACCTTTGGC AATAGCAACT GATAAAAGTG TTTTCCCAAT CCCTGTACCT	600
CCTGTGATAA GCGTATTTCC CCTCATGCCA TCAAGATATT TTTGTACCTG ACCTTTTGCA	660
AATTCTAAAA ATCGCTTTTC TTCTGATGTT ACAGCATTA AATCATCAAA AGTTTTAGTT	720
TTAAACTCAT CTGCTACATA GCTCTTATTG CTCATCAACA CATTATAAGT TTGCATATAT	780

1236

AGTTTAGCAT	TCAAATTATC	AGCAATCGCA	TCTTCTTCAT	CTTGCTTTTT	CTGTTCTTCT	840
TGGCATTGTT	CACAATAGGG	TGGGATACAG	CGAACTTCTT	TTATTGCCTC	TCCGTTCTCA	900
TTCCACCCCA	CTACTACATG	TCTTTCTCCT	TTGATTTGTG	TTAGCTGTAT	TTCATGCTTA	960
GGACACAATT	CGTCTAGTTT	AAATGTCTCA	ATATTTCTTA	AACTAGATTG	TAATGATTTT	1020
ATTTTCTGAC	CTCCTAAAAT	GGTTTTTCTT	GTGTTGGTAT	CCAATCTTCA	TAGCTGGTAG	1080
GCTCTAGTTG	ATTGGTTTGC	TGTTTTTTAG	CCTCACGCGC	TGCCCTGCTA	TTTCTAACAA	1140
GTTCCACCGT	CAATAAATTG	TCCTGTTTCC	AACGGTTAAG	GATTACCTTG	ATGTATGCAA	1200
AGTTTGCTTT	ACCCTGACTG	ACAGCCTCTT	TTAACGCCTC	ATGGATAAGC	TCTGGGCTAA	1260
AATCTTCTAG	CATATACTGC	AATCTTGAA	TCTGTAACGG	TGACAATGCT	TTACCTGTCT	1320
CAGCTCGCTT	CATATTCAAC	AAGTCGTCTA	TTTCCACACT	GGTTACTTTT	TTATTTACAA	1380
AATCAGAAAT	CAGTTGAAAA	ATGTTTGGAC	TTGTAGCTG	GATTTAGCC	ATTACCTCAT	1440
CAAATTCTGC	TTGTGTCATG	TTGTCTAAAT	CTAGTGTCAT	TGCATTGCCT	CCTCAAACCT	1500
CTCTATAAGA	CAACTTTTAT	TTGCTTTCTG	AGTTCCATTT	TTAGAGTTAA	AAAGAATATC	1560
TTTTAAGGTT	ACAGTAGCCT	CTAAATACTC	CTTTTCAGCA	TGCTCTATAT	ACGCCTGTTG	1620
CTCTGCTTCG	TTCTCAAAAA	AGTGCTTAGC	TTGGCGTTTA	AAGAATGCTT	TTCGCATAGC	1680
GTCCATTTCA	AAAATACCAG	GGGCGAAAAA	CATTCCCGTA	GTGCTTTTAG	AGACCGCTTC	1740
GATTTTATGG	CTTTCATTCA	ATTGAGGAAG	TTCAATCCAA	AGTAAACGGG	ACAACCTCATC	1800
TTTGATGGAT	TTTGTCTGAC	TTTCCAATAA	AGAAAGGATT	CTTAGGCCAT	TTTCTTCGCT	1860
AATTTCTCGC	ATTTCTGCGC	TAATCTGTGC	TATACGTCTA	GTTAAATTCT	CATATGTTGT	1920
TTCTGTCATG	TTTTTACCTC	TGTTTCTTTG	TTGGTGTGAT	TTTTTAGCTT	ATTTTTTTTAC	1980
TTCTAAACAT	CATTGTCTTA	ATTTCTTGAT	AACTCATTTT	CAATTCAATC	ATAGCTATTG	2040
CCATATCCTC	AAATGCCTGG	TACTGCTCCA	ACTCCTCACT	AGTCAAGCTA	TCGATACCGT	2100
TATAGCCCCC	ACGCTCTTCT	CTTAACCTGCT	TAGCGTTCAT	GTCTGTTACT	GCCTTTAGTA	2160
GCAAGTTGTT	CATGGTGCTA	TGCGCGTGCT	TTGGTGCATT	AGGCCATGTT	TCTATACTGT	2220
CATGCAAGGT	TTTTCTTTTC	GGTTTTTCTA	GCGCCCTCTG	CAGACGAATT	TCAGAAAGTT	2280
CCTCACGCAT	TTCAAAGAAT	GCTTTGACTA	GGTTTAGTTT	GAATTGCCGT	ACTGTTTCGG	2340
TATTCTTTAA	ATAAGTGATC	AGAAAAGTAG	CCTGTTGCTC	GTTGAGAATA	TAGGATTTTT	2400
TAGGTTGTCC	TCTAGTATCT	AATTTATGGA	TTTTAAATCC	AAGTATTCCC	AACTCTTCAA	2460
AGTCAGCCTT	ATTTTCTCTT	ATTAAGCGCG	TGATAGTGTG	GTGTTGTACT	TCAGCACATT	2520
CAGCGATGAT	CTCGCTTGTG	GTGTACGGCT	CTTCTTACC	GTCCATGTAA	ACTAGTTCCA	2580

1237

TTACGGTTCT ACCTCCTGTA TAAATCTGGT TAGCTTACTT TTTAATTGCC TCCTCTAGCC	2640
TCTTTTTTTAG CCTCTAAAAC GGCTTTGGCT AGTGGTTAAT ATTATTTACC ACTTGTCTCT	2700
ATAAACGTGT TAGAGGCCTT TATAACGACT TGTATCGCTG TATCGATATC CTCCGTGGAA	2760
TAGTAGATTT ATTTTCTAAT ATCATTCAAG ACTTGTTTAA CCCATTTCTT GAAAGAAATA	2820
AAATTACATC TTCTTTATCC TTGGCATCTG CTTTGTCTGA GACAAATTAG AATGTCAATA	2880
CTTGG	2885

(2) INFORMATION FOR SEQ ID NO: 224:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

TATCAATCCT TTCCCATTAT AGGAGCAACA GAGTGGGAGT AGTCATCTAA GGACTAATTT	60
ATGTATTTTTT ACGAGTCAGT ATCTTGGGAT ACTGGTTTTT ACTTTTCTAG ACTTTTTGAC	120
TACTTGTTAA AACTGGGATA ATTTTCGACT GTTTAACAGT TATTATGCAA AGTCTAAAAG	180
ATTAGAATTG TCAAAACAAT CCGTCTAGGC TTGATTTTAT CCTTTATTTA CTATAAAATG	240
AGAAGGAAAA ATGTCAAAC TTTATATTGC AAATAGGAGA AATCATGACA AAAACATTAA	300
AACGTCCTGA GGTTTTATCA CCTGCAGGGA CTTTAGAGAA GCTAAAGGTA GCTGTTCACT	360
ATGGAGCAGA TGCTGTCTTT ATCGGTGGTC AGGCCTATGG TCTTCGTAGC CGTGCGGGAA	420
ACTTTACTTT CGAACAGATG GAAGAAGGCG TGCAGTTTGC GGCCAAGTAT GGTGCCAAGG	480
TCTATGTAGC GGCTAATATG GTTATGCACG AAGGAAATGA AGCTGGTGCT GGTGAGTGGT	540
TCCGTAAACT GCGTGATATC GGGATTGCAG CAGTTATCGT ATCTGACCCA GCCTTGATTA	600
TGATTGCAGT GACTGAAGCA CCAGGCCTTG AAATCCACCT TTCTACCCAA GCCAGTGCCA	660
CTAACTATGA AACCCCTGAG TTCTGGAAAG AGCTAGGCTT GACTCGTGTC GTTTTAGCGC	720
GTGAGGTTTC AATGGAAGAA TTAGCTGAGA TCCGCAAACG TACAGATGTT GAAATTGAAG	780
CCTTTGTCCA TGGAGCTATG TGTATTTTCACT ACTCTGGACG TTGTACTCTT TCAAACCACA	840
TGAGTATGCG TGATGCCAAC CGTGGTGGAT GTTCTCAGTC ATGCCGTTGG AAATACGACC	900
TTTACGATAT GCCATTTGGG AAAGAACGTA AGAGTTTGCA GGGTGAGATT CCAGAAGAAT	960
TTTCAATGTC AGCCGTTGAY ATGTCTATGA TTGACCACAT TCcAGATATG ATTGAAAATG	1020

1238

GTGTGGACAG	TCTAAAAATC	GAAGGACGTA	TGrAGTCTAT	TCACTAyGTA	TCAACAGTAA	1080
CCAAC TGCTA	CAAGGCGGCT	GTGGATGCCT	ATCTTGAAAAG	TCCTGAAAAAG	TTTGAAGCTA	1140
TCAAACAAGA	CTTGGTGGAC	GAGATGTGGA	AGGTTGCCCA	ACGTGAACTG	GCTACAGGAT	1200
TTTACTATGG	TACACCATCT	GAAAATGAGC	AGTTGTTTGG	TGCTCGTCGT	AAAATCCCTG	1260
AGTACAAGTT	TGTCGCTGAA	GTGGTTTCTT	ATGATGATGC	GGCACAAACA	GCAACTATTC	1320
GTCAACGAAA	CGTCATTAAC	GAAGGGGACC	AAGTTGAGTT	TTATGGTCCA	GGTTTCCGTC	1380
ATTTTGAAAC	CTATATTGAA	GATTTGCATG	ATGCTAAAGG	CAATAAAATC	GACCGCGCTC	1440
CAAATCCAAT	GGAAC TATTG	ACTATTAAAG	TCCCACAACC	TGTTCAATCA	GGAGACATGG	1500
TTCGAGCTCT	TAAAGAGGGG	CTTATCAATC	TTTATAAGGA	AGATGGAACC	AGCGTCACAG	1560
TTCGTGCTTA	ATGTAGTTGT	TTAGTTTTAA	AAACTATGC	AAAGCTCCAT	ATACAACACT	1620
TAAACGAGAT	TAAAGAATGG	CGAAATCCCT	TGATGCGCAA	GAGATTAGCT	GTCTTTTTTA	1680
TTTTTTAAGT	GATAAAGTCG	GAGTTTAGGC	ATCAAAGCCT	ATCAAATTAA	ACAAAGAAGC	1740
GATGTCTTAG	ATATTTTGAA	AAAAATTAAT	AAGCAGAAAA	CTCTCTATTA	TTTTGTTGTA	1800
GAGAGTTTTT	TGTTAATAAA	ATTTCACAAA	ATGACATTTA	TATATTGCAT	TAAGTTAGAT	1860
ATATGATATA	ATATTGTTAA	AAAGAGGCGC	AACTTTTTAA	AATTAATGAG	AATCAAAGAG	1920
AAAACCAATA	ATATTAATGG	AGGAATAAAA	AATGTAAGTA	AGCATTATGG	TCATTCAATC	1980
ATTCTCAAAG	ATATAAATTT	TGCACTTAAC	AAGGGTGAAA	TTGTTGGTCT	AGCAGGGAGA	2040
AATGGAGTTG	GTAAGAGTAC	GTTGATGAAA	ATTCTTGTTT	AGAATAATCA	ACCGACTTCA	2100
GGTAATATTA	TAAGCAGTGA	TAATGTTGGG	TATTTAATCG	AAGAACCAAA	ATTATTTTTTA	2160
TCTAAAACAG	GTTTAGAGAA	TTTAAAATAT	TTGTCAAATT	TATATGGTGT	TGACTACAAT	2220
CAAGAAAGAT	TTAGATGTTT	GATCCAAGAG	TTAGATTTGA	CTCAGTCTAT	TAATAAAAAA	2280
GTAAAGACCT	ATTCTTTGGG	TACAAAACAA	AAATTAGCTT	TGCTTCTAAC	TCTCGTTACG	2340
GAACCTGATA	TATTGATTTT	AGATGAACCG	ACTAATGGTT	TAGATATTGA	ATCATCACAA	2400
ATAGTTTTAG	CGGTTCTAAA	AAAATTAGCT	TTACATGAAA	ATGTGGGAAT	TTTAATATCG	2460
AGTCATAAAT	TAGAAGACAT	TGAAGAAATT	TGTGAGAGAG	TTCTTTTCTT	GGAGAACGGG	2520
CTTTTGACAT	TTCAAAAAGT	AGGAAAAGAT	AGTCATAATT	TCTTGTTTGA	GATAGCTTTT	2580
TCATCAGCTA	CAGATAGAGA	CATTTTCATT	ACCAAACAAG	AATTTTGGA	TATTGTTTAG	2640
GAAGAGGGAT	TGAGAATTAC	TATGTCTGGG	AATATTCAAA	ATAGTGAGCT	TTTTAAATTT	2700
TTTAACGAAA	ACTCTATTAA	AGTAGTTGAT	TTTGAAACTA	AAAAAGAGAC	GCTTAAAGAT	2760
ATTTACCTAA	ATCGTTCAAA	ATAAAGGAAG	GTTATAATCA	TGAAATTAAA	TAAACAGAAG	2820

1239

AATCGGATGA TTTACGTCTT GTCTAATTTT CTATATGCTA TCTCAGTTTC CATTATTTAT	2880
GCTTTGAATG GCATTGTGTT ACTAGTCATA GTAAGTAAAT TGGGTATTCC AGGTGATTTA	2940
GGATTAAATT TTATAGTAGC TATTGTAGTC AATACAATTT TGTTAGTCCT GTTTTATTTT	3000
CTATTATCTT ACATTTTCTA TTTATACAAA TTGAAAAGTG GCTTGGTATw TGGTATTTTA	3060
GTAGCTTTAC TACTCTTTAT CTCTAATATA TTAAATACGA TGATGATGAA TACTAGTAAT	3120
GATTTGTTTA TCAAAGCAAT TGAA	3144

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

TACGGTATTA TTTTAAAGGA GAAAGAATCA TGAAAATCAA AAAATGGCTT GGTCTAGCAG	60
CCCTTGCTAC AGTCGCAGGT TTGGCTCTTG CAGCTTGCGG AAAGTCAGAA AAGAAAGCAG	120
ACAATGCAAC AACTATCAAA ATCGCAACTG TTAACCGTAG CGTTCTGAA GAAAAACGTT	180
GGGACAAAAT CCAAGAATTG GTTAAAAAAG ACGGAATTAC CTTGGAATTT ACAGAGTTCA	240
CAGACTACTC ACAACCAAAC AAAGCAACTG CTGATGGCGA AGTAGATTTG AACGCTTTCC	300
AACACTATAA CTTCTTGAAC AACTGGAACA AAGAAAACGG AAAAGACCTT GTAGCGATTG	360
CAGATACTTA CATCTCTCCA ATCCGCCTTT ACTCAGGTTT GAATGGAAGT GCCAACAAGT	420
ACACTAAAGT AGAAGACATC CCAGCAAACG GAGAAATCGC TGTACCGAAT GACGCTACAA	480
ACGAAAGCCG TGCGCTTTAT TTGCTTCAAT CAGCTGGCTT GATTAAATTG GATGTTTCTG	540
GAACTGCTCT TGCAACAGTT GCCAACATCA AAGAAAATCC AAAGAAGTTG AAAATCACTG	600
AATTGGACGC TAGCCAAACA GCTCGTTCAT TGTCATCAGT TGACGCTGCC GTTGTAACA	660
ATACCTTCGT TACAGAAGCA AAATTGGACT ACAAGAAATC ACTTTTCAAA GAACAAGCTG	720
ATGAAAACCTC AAAACAATGG TACAACATCA TTGTTGCAAA AAAAGATTGG GAAACATCAC	780
CTAAGGCTGA TGCTATCAAG AAAGTAATCG CAGCTTACCA CACAGATGAC GTGAAAAAAG	840
TTATCGAAGA ATCATCAGAT GGTTTGGATC AACCAGTTTG GTAATAAGAA ACAGGGAGGT	900
GGGAGAGAAA ATTCCACCTC TTGCTTTTGT ATAGAGTATA GATTGTAAAG AAGACTATTC	960
GTTCATAGAA AGGTAGAGAG AATATGGTTT TTCCTAGCGA ACAAGAACAG ATTGAAAAAT	1020

1240						
TTGAAAAGGA	TCATGTAGCC	CAGCATTATT	TTGAGGTTTT	GCGTACCTTG	ATTTCTAAGA	1080
AATCAGTCTT	TGCCCAGCAG	GTTGGACTCA	AGGAAGTCGC	AAATTATCTG	GGTGAGATTT	1140
TCAAGCGTGT	TGGAGCTGAA	GTGGAGATTG	ATGAGAGCTA	TACAGCGCCC	TTTGTCATGG	1200
CACATTTCAA	GAGTTCGCGT	CCAGATGCCA	AGACCTTGAT	TTTCTATAAC	CACTATGACA	1260
CTGTGCCAGC	GGATGGGGAT	CAGGTCTGGA	CAGAGGATCC	kTTTACGCTT	TCGGTCCGCA	1320
ATGGCTTCAT	GTATGGGCGT	GGGGTTGATG	ACGACAAGGG	TCATATCACA	GCTCGCTTGA	1380
GTGCTTTGAG	AAAATATATG	CAGCACCATG	ATGATTTACC	TGTCAATATC	AGCTTTATCA	1440
TGGAGGGAGC	GGAGGAATCG	GCTTCAACAG	ACCTAGATAA	GTATTTGGAA	AAGCATGCAG	1500
ACAAACTCCG	TGGGGCGGAT	TTGTTGGTCT	GGGAACAAGG	GACCAAAAAT	GCCTTGGAAC	1560
AGCTGGAAAT	TTCTGGTGGC	AATAAGGGGA	TTGTGACCTT	TGATGCCAAG	GTAAAAAGCG	1620
CTGATGTGGA	TATCCACTCG	AGTTATGGTG	GTGTTGTGGA	ATCAGCTCCT	TGGTATCTCC	1680
TCCAAGCCTT	ACAGTCTCTT	CGTGCTGCGG	ATGGCCGTAT	CTTGTTGAA	GGCTTGACG	1740
AAGAAGTACA	AGAGCCCAAT	GAACGAGAAA	TGGCCTTGCT	AGAAACTTAT	GGTCAACGAA	1800
ACCCAGAGGA	AGTTAGTCGG	ATTTATGGAT	TGGAGTTGCC	TCTCTTACAG	GAGGAGCGGA	1860
TGGCCTTTCT	AAAACGTTTC	TTTTTCGATC	CAGCGCTTAA	TATCGAAGGA	ATCCAGTCTG	1920
GTTATCAAGG	TCAGGGTGTT	AAGACTATTT	TACCTGCAGA	AGCCAGTGCC	AAGCTAGAGG	1980
TTCGTCTGGT	TCCGGGCCTA	GAACCGCATG	ATGTTCTGGA	AAAAATTCGG	AAACAGCTAG	2040
ACAAAAATGG	CTTTGATAAG	GTAGAATTAT	ACTATACCTT	GGGAGAGATG	AGCTATCGAA	2100
GCGATATGAG	CGCACCAGCC	ATTCTCAATG	TGATCGAGTT	GGCCAAGAAA	TTCTATCCAC	2160
AGGGCGTTTC	AGTCTTGCCG	ACGACAGCGG	GGACAGGACC	TATGCATACG	GTCTTTGATG	2220
CCCTAGAGGT	ACCAATGGTT	GCATTCGGTC	TAGGAAATGC	CAATAGCCGA	GACCACGGTG	2280
GAGATGAAAA	TGTGCGAATC	GCTGATTATT	ACACCCATAT	CGAATTAGTA	GAGGAGCTGA	2340
TTAGAAGCTA	TGAGTAGAGA	TATTATCAAG	TTAGATCAGA	TCGATGTGAC	TTTTCACCAA	2400
AAGAAGAGAA	CCATCACAGC	GGTTAAGGAT	GTGACCATTC	ACATCCAAGA	AGGGGATATC	2460
TACGGAATCG	TTGGATATTC	TGGAGCAGGA	AAATCAACCC	TTGTACGGGT	GATTAATCTC	2520
TTGCAAAAAC	CATCTGCAGG	GAAAATTACC	ATTGACGACG	ATGTGATTTT	TGACGGCAAG	2580
GTGACCTTGA	CGGCAGAGCA	GTTGCGTCGT	AAACGTCAAG	ATATCGGAAT	GATTTTCCAG	2640
CATTTTAACC	TGATGAGCCA	AAAGACAGCA	GAGGAGAATG	TAGCCTTTGC	CCTTAAACAC	2700
TCTGAACTCA	GCAAGGAAGA	AAAGAAGGCT	AAAGTAGCTA	AGTTGTTGGA	CTTGGTTGGT	2760
TTGGCAGATC	GTGCTGAAAA	CTACCCTTCA	CAACTATCTG	GAGGGCAAAA	ACAGCGTGTG	2820

1241

GCAATTGCGC GTGCCTTGGC CAATGATCCA AAAATCTTGA TTTCAGACGA GTCAACTTCT	2880
GCCCTTGATC CGAAGACAAC CAAGCAGATT TTGGCCTTGT TGCAAGATTT GAACCAAAAA	2940
TTAGGCTTGA CTGTTGTCTT GATTACGCAT GAAATGCAGA TTGTCAAAGA CATTGCCAAC	3000
CGTGTTCAG TTATGCAGGA TGGGCATTTG ATTGAAGAGG GTAGTGTGCT TGAAATCTTC	3060
TCAAACCCTA AACAACCTTT GACTCAAGAC TTTATCTCAA CAGCTACAGG TATTGACGAA	3120
GCCATGGTCA AAATCGAGAA GCAAGAAATC GTGGAACACT TGTCTGAAAA CAGTCTCTTG	3180
GTGCAACTCA AGTACGCTGG AGCTTCAACA GACGAGCCAC TTTTGAATGA ATTGTACAAG	3240
CATTACCAAG TAATGGCTAA TATTCTCTAT GGAATATCG AAATTCTCGA TGGTACTCCT	3300
GTTGGAGAAT TGGTGGTGGT TTTGTCAGGT GAAAAAGCAG CGTTGGCAGG TGCCCAAGAA	3360
GCCATTCGTC AAGCAGGTGT ACAACTAAAA GTATTGAAGG GAGTACAGTA AGATGGAATC	3420
ATTGATTCAA ACCTATTTAC CAAATGTCTA TAAGATGGGT TGGGCTGGTC AGGCAGGCTG	3480
GGGAACGGCT ATCTACTTAA CTCTTTATAT GACAGTTCTT TCCTTCATTA TCGGAGGCTT	3540
CTTGGGGCTA GTGGCAGGTC TCTTTCTCGT CTTGACAGCG CCAGGTGGTG TCTTGGAGAA	3600
TAAAGTCGTA TTCTGGATTT TAGACAAAAT TACCTCAATT TTTCGTGCGG TTCCCTTTAT	3660
CATCCTCTTG GCAATCTTGT CACCACTTTC TCACTTGATT GTTAAAACAA GTATCGGGCC	3720
AAATGCAGCC CTTGTCCAC TTTCTTTTGC AGTCTTTGCC TTCTGG	3766

(2) INFORMATION FOR SEQ ID NO: 226:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2520 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

TGTTGCTGAG TTAATCGGTA CGTTCATGTT TGTATTCGTC GGGACAGGAG CTGTTGTTTT	60
TGGAAATGGT CTTGATGGCC TTGGTCACCT TGGAATCGCC TTGCGCTTTG GTTTGGCAAT	120
CGTGGTGGCA GCCTACTCAA TCGGAACTGT TTCAGGTGCT CACTTGAACC CGGCTGTTC	180
GATTGCTATG TTTGTAAACA AACGTTTGTC ATCTTCAGAA CTTGTAAACT ACATCCTTGG	240
TCAGGTTGTT GGAGCTTTCA TCGCTTCTGG CGCTGTCTTC TTCCTCTTGG CTAATCAGG	300
TATGTCAACT GCTAGTCTTG GTGAAAATGC CTTGGCAAAC GGTGTCACTG TCTTTGGTGG	360
TTTCTTGTTT GAAGTCATCG CAACTTTCTT GTTTGTATTG GTTATCATGA CTGTGACTTC	420

1242

AGAAAGCAAG	GGCAATGGCG	CGATTGCTGG	TTTGGTAATC	GGTTTGTCAT	TGATGGCGAT	480
GATTCTTGTC	GGATTGAAGA	TTACTGGACT	TTCAAGTAAAC	CCAGCTCGTA	GCTTGGCACC	540
AGCTGTCTTG	GTAGGCGGCG	CAsCCTTCAA	CAAGTTTGGA	TTTTCATCCT	TGCACCAATC	600
GCTGGTGGAG	TTCTTGCAAG	CCTTGTTGCA	AAAAATTTCC	TTGGAACAGA	AGAATAATTG	660
AAACTCAAAA	AGCCTTGCTC	CTCATCTTGA	GGAACAGGGC	TTTTTCGTAT	GATACTCTTC	720
GAAAATCTCT	TCAAACCACG	TCAGCTTCAT	CTTGCCGTAG	TATGGTTACT	GACTTCGTCA	780
GTTCTATCCA	CAACCTCAAA	ACAGTGTTTT	GATCTGACTT	CGTCAGTTCT	ATCTGCAACC	840
TCAAAACAGT	GTTTTAAGCT	GACTTCGTCA	GTTCTATCTG	CAACCTCAAA	ACAGTGTTTT	900
AAGCTGACTT	CGTCAGTTCT	ATCTGCAACC	TCAAAACAGT	GTTTTAAGCT	GACTTCGTCA	960
GTTCTATCTG	CAACCTCAAA	ACAGTGTTTT	AAGCTGACTT	CGTCAGTTCT	ATCCACAACC	1020
TCAAAACAGT	GTTTTGATCT	GACTTCGTCA	GTTCTATCCA	CAACCTCAAA	ACAGTGTTTT	1080
GATCTGACTT	CGTCAGTTCT	ATCCACAACC	TCAAAACAGT	GCTTTGAGCA	ACcTGCGGCT	1140
AACTTCCTAG	TTTGCTCTTT	GATTTTCATT	GAGTATGACT	TTAGCGGTTG	TCAATTTTCT	1200
CTGGATAAAG	GTCGTGTTGG	AAGAGGCGTT	GTTCTGCCAA	GCCCTCATAC	TTAGTTCCTT	1260
GCTTACCGTA	GTTGTAGTAG	GGGTCGATTG	AAATGCCACC	GCGCGGAGTG	AATTTTCCCC	1320
AGACTTCTAA	ATAGCGAGGG	TCTAGCAAGT	TGACCAAGTC	TTTCCCGATG	GTGTTGATAC	1380
AGTTTTCTGT	GAAATCTCCG	TGGTTTCGGT	AGCTAAATAG	ATATAGTTTG	AGGGATTTTG	1440
ACTCGACACA	GAGCTTGTC	GGAATGTAGG	AAATATGAAT	CGTCGCAAAG	TCTGGCTGAG	1500
CAGTGATTTG	TCCCAGCAGA	GACATATCGA	GGATATGGTG	ACGAATGCCC	TGTTCCCTTAG	1560
CGATTTCTCT	AGTAATTTGA	ATTTTCGAGGT	GATGACGTTG	GCCGTAGGCA	AAGGTGACAG	1620
CTTCGACTGT	TTCATAGTGT	TGCATGACCC	AGAAAAGGCA	GGTTGTTGAA	TCTTGACCAC	1680
CACTAAAGAC	GACCAAGGCT	AATTGACGTT	TCATAGTACT	CCTTCCAAAA	TGGGAAATGT	1740
TCAGAGCACG	CAAAAAGCTC	CCATTAGGGA	GCTAAAAAAT	ACCAAATCGA	GGTTTTTTTA	1800
GCGATGGCAT	ATCCCAAACA	TCGTAATATT	CTACTTATAT	AGTAAAATGA	AATAAGAACA	1860
GGACAAATCG	ATCAGGACAG	TCAAATCGAT	TTCTAACAAT	GTTTTAGAAG	TAGAGGTGTA	1920
CTATTCTAGT	TTCAATCTAC	TATAGTCTAG	CATATTTTTT	GAAAAATGGC	AAAGGGCAAG	1980
AAAAAAGAGA	CCAAAGAAAG	TACTTGGTCT	CTCGTTTGAT	TAGCTCAATT	CAGCAATGAT	2040
GGCCTTGATT	TGTTCTGCTG	TGTGAACACC	TGCAACTTGT	TTGACAACTT	GGCCGTCTTT	2100
TTTGAAGAGA	AGAGTTGGAA	TAGACATGAT	TCCAAAAGCA	CGAGCTGTGT	TTGGATTTTC	2160
ATCAACGTCC	ATTTTAACGA	TTTTCAAGAC	ATCTTCTGAA	AGTTCTTCAG	ACAATTTGTC	2220

1243

CAAGATTGGA CCTTGCATAC GACATGGACC ACACCAAGTT GCCCAGAAGT CTACTAAGAC	2280
CAAACCGTCT TTTGTTTCTT GTTCGAATGT TGCATCTGTA ATTGCTTTTG CCATTGTATT	2340
TCTCCTTTTT TTAGTTATAT TGGCTTAAAT CTTGTTTCAT GAGATAGAAG AAGATATCTC	2400
CATAAGTCCC ATGGTAGTCC AAATTATGAC CCTTGTAAGT TAATTTTTTG ACAGGGTAGT	2460
AkkCTGCGAC GCCGATAAGG CAAGCTTGTT GCGAACGTTT AAAGTCTTCA TAAGACTCGG	2520

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

ACTCAGTTAG ATTTTGTTTT CAAAAACAAC GAAGAAAAAG ACCATGTTGC TCTACTTGGA	60
AGAATTGGCT CCGAACGTGT TTATCGATAT ATTAATAAAA AATATTTAGA TTTACCGGAA	120
ACATTGAAAA ATTATAATGT TTTTGTACCA GAAGCTAATG GAAGTGGTGC CTTAGGTGAA	180
GTCTTATCAA CCCCCCTAAT CGGGGAACCC CTAATCGGGC ATACAGATAC TTTTTTATCT	240
ATTGGTAATT TTAACAACAA ATTTGAAGCC GATGCTTGTA TTAAATTTAT TAAAACTAAA	300
TTCGCTAGAG TATTATTAGG TGTTTTGAAA GTTACTCAGC ATAATTCACG CAAAACCTGG	360
TATTACGTCC CCCTCCAAGA CTTTACGGTC AATTCGGACA TTGATTGGAC ACAATCAGTG	420
ACTGATATTG ACCGCCAGCT TGATCAAAAA TATGACTTTT CCCCTGAAGA AATTGCCTTT	480
ATTGAGAATC ATGTAAGGGA GATGGATTAG AAAAGTATTT TTATTTGACA AATAGTGCTC	540
AATGATCTAA AATGACTATA TAGGATTAGG TCAGGAAGCA TACGATGCCC TGACCCTTTT	600
TGTACTTATG AGATGAGAAA GTCATTTGTT AGATAAATTG ACTCGTTAGC AAACGTTCAA	660
AAAAGGAAAA CTTATGCCAG TAGAAATTAA AACCCTAAA GAAATTCATC CTAAAATCTA	720
TGCCTACACC ACACCGACAG TAACCAGTAA TGAAGGCTGG ATTAAGATTG GGTATACAGA	780
ACGTGATGTC ACACAACGTA TCAAGGAGCA AACGCATACA GCTCATATAG CTACAGATGT	840
CTTATGGACT GGTGATGCAG CTTATACAGA AGAGCCTGAT AAGGGGAAAA CTTTCAAGGA	900
CCATGATTTT CACCATTTCC TTTCTTTCCA TGATGTAGAA CGTCGTCCCA AGACGGAATG	960
GTTCTATTTT AATGGAACTC CTGAAAAATC AAAAAATCTT TTTGATAAGT TTGTTCAGCA	1020
TGATTTGTCT GGTATCAGC CTGGAAAAGG ACAGGACTAT ACTCTGCGAC AAGAGCAAGA	1080

1244

AGAAGCAGTT	GCTAAGACAT	TAGCTTATTT	CCAAGAACAT	GCTGGAGGCA	AGTTTCTCTG	1140
GAATGCCAAG	CCACGCTTTG	GTAAAACCTT	GTCTACCTAT	GACCTAGCTC	GACGGATGGA	1200
AGCTGTCAAT	GTCCTAATTG	TAACAAACCG	CCCTGCCATT	GCTAACTCAT	GGTATGATGA	1260
TTTTGAAACA	TTCATAGCAG	GTCAAACGAC	TTACAAGTTT	GTTTCTGAAT	CAGATAGCCT	1320
TAAGAGTCGT	CCAATCTTGT	CACGACAAGA	ATTTCTTGGT	ATTTTAGCTG	ACGATGTAAG	1380
ACAACTTGCT	TTTATCAGTC	TCCAAGACTT	GAAAGGATCT	GTTTATTTAG	GTGGAGAGCA	1440
CGATAAACTC	AAATGGGTAA	CTGATCTGCA	TTGGGACTTG	TTGGTTATTG	ACGAGGCTCA	1500
TGAAGGAGTT	GATACCTTCA	AGACTGACCA	AGCCTTTAAT	AAGATTCGAC	GAAATTTTAC	1560
TCTGCATTTG	TCAGGTACAT	CATTTAAAGC	ATTGGCTAAA	GGAGATTTTA	CAGAGGAACA	1620
AATCTACAAC	TGGTCTTATG	CTGATGAGCA	GGCTGCTAAG	TATTCGTGGT	CTCTTGAGCA	1680
AGAAGAGGAA	AATCCTTATG	AAAGCTTGCC	TCAGTTGAAT	CTCTTTACCT	ATCAAATGTC	1740
TCAGATGATT	GGCGAAAAGT	TAGAAAAAGG	CGCTCAGATC	GATGGTGAAA	ATATTGACTA	1800
TGTTTTTGAC	TTAAGTGAAT	TTTTCGCTAC	AGATGATAAA	GGGAAATTTA	TTCATGAGCA	1860
TGATGTCAGA	AATTGGTTAG	ATACTCTATC	AAGCAATGAA	AAATATCCAT	TTTCAACCAA	1920
AGAACTCCGT	AATGAACTCA	AGCATACTTT	TTGGCTTTTA	GAACGTGTCG	CTTCGGCCAA	1980
AGCATTAATA	GCCCTACTAG	AAGAACACCC	AATCTATGAA	AACTATGAGA	TCGTTCTAGC	2040
TGCTGGTGAC	GGACGTATGT	CCGAAGAAGA	CGATAAAGTC	AAACTCAAAT	CCTTGGAATT	2100
GGTTAGAAAA	GCGATAGCAG	AGAATGACAA	AACCATTACC	CTATCCGTTG	GTCAGCTGAC	2160
GACAGGTGTC	ACTATCCCTG	AATGGACAGG	TGTATTGATG	TTATCAAATT	TGAAATCACC	2220
AGCTCTTTAT	ATGCAGGCCG	CCTTCCGTGC	TCAAAAATCCT	TACTCATGGA	GCGATAACAA	2280
AGGAAATCAC	TTTCGCAAAG	AAAGAGCCTA	TGTATTTGAC	TTTGCGCCGG	AAAGAACCTT	2340
GATTCTCTTT	GATGAGTTTG	CCAACAACCT	ATTGCTTGTA	ACTGCAGCTG	GTAGAGGAAC	2400
TTCAGCTACA	CGCGAAGAAA	ATATTAGAGA	ATTATTAAAC	TTCTTTCCAA	TTATTGCCGA	2460
AGACCGTGCT	GGTAAGATGG	TTGAAATTGA	TGCAAAGGCA	GTTCTAACCA	CTCCTCGCCA	2520
GATAAAAGCT	AGAGAAGTTC	TTAAACGAGG	TTTTATGTCC	AATCTCTTAT	TTGATAATAT	2580
TAGTGGTATT	TTCCAAGCAA	GTCAAACAGT	TTTAGATATT	TTAAATGAGC	TGCCAGTTGA	2640
AAAGGAAGGG	AAGGTACAAG	ATAGTTCTGA	TTTATTAGAT	TTTTCAGATG	TTACAGTCGA	2700
TGATGAGGGA	AATGCAGTAG	TAGACCATGA	AATTGTAGTT	AATCAGCAAA	TGCGACTTTT	2760
TGGTGAAAAA	GTTTATGGAC	TTGGTGAATC	TGTTGCTGAG	TTAGTCACAA	AAGATGAGGA	2820
ACGAACTCAA	AAACAGCTGG	TCAATGACTT	GAGTAAGACC	GTTTCTTCAG	TGATTGTAGA	2880

1245

GGAATTGAAA	GCAGATTATT	CTCTAAAAAC	AAGGGAAACT	GAGCAAATTA	AGAAACAAAT	2940
TACAGCAACA	CTTGAGAATG	AAATTCGAAA	AAATGATATC	GAAAGAAAAA	TTTCTGAAGC	3000
TCATATCAAG	CAAGAGTTGC	AACAGCAGCT	CAAAGAAGCA	AATGATAAAG	CGCAAAAAGA	3060
TAAGATTCAA	GAAGATTTGG	AAAAACGTTT	AGAAGAAAAT	AAACTCATTC	ATAAAGAAAA	3120
ACTAGAACAA	ACACTCAAAA	AAGAAGTGGA	AAAAATGCCT	GAGAAATTTA	TCGAACAGGT	3180
TGAGATAAAA	CGTGTGGAAC	AGTTGAAACA	ATCAGCTCAA	GATGAAATTC	GTGACCATTT	3240
ACGAGGGTTT	GCAAGAACAA	TTCCAAGTTT	TATTATGGCT	TACGGTGATC	AAACTCTAAC	3300
ACTTGATAAT	TTTGATGCCT	TTGTTCCCTGA	ACATGTTTTT	TATGAAGTAA	CAGGGATTAC	3360
GATTGATCAG	TTTAGATATT	TGCGAGATGG	TGGGCAGGAT	TTTGCAGGGC	ATCTCTTTGA	3420
TAAAGCAACA	TTTGACGAAG	CTATTCAAGA	ATTTCTTCGC	AAGAAAAAGG	AGTTGGCGGA	3480
TTATTTTAAA	GATCAAAAAG	AAGACATTTT	TGACTATATT	CCACCGCAGA	AGACCAACCA	3540
AATTTTCACT	CCTAAACGAG	TGGTGAAAAG	GATGGTAGAT	GATTTGGAAA	AGGAAAATCC	3600
AGGGATTTTT	GATGATCCAT	CTAAGACTTT	TATTGATTTA	TATATGAAGT	CAGGCCTCTA	3660
TATTGCAGAA	CTTGTGAAGC	GGTTATATAA	TAGCAATGGC	TTGAAAGAGG	CCTTTCCAAA	3720
TCCTGAAGAA	CGCTTAAAAC	ATATTTTGGG	AAAGCAAGTT	TATGGATTTG	CTCCGTCTGA	3780
GATTATCTAT	AACATTTCCA	CTAATTTTAT	ATTTGGCAAT	CTTTCCTAAAG	ATATCAGTAG	3840
GAAGAATTTT	GTTTTAGCAG	ATACCATTCC	AGCGGCTAAA	GAAGGGAGCA	TTCAAAAGTT	3900
GGTTGATTCC	TATTTTGAAA	ATAATTAAAA	AGAAGGCCGA	GTCAAAATTC	TTTGAAATCA	3960
GAAAAAACGC	ATAATATTGA	GTGCTTTTGT	ACTGCCCCCC	AAAAGTTAGA	CAGAAAAAAT	4020
CTAACTTTTG	GGGGGCAGTT	CAGACAATCC	TTGGTATTAT	GCGTTTTATT	GTGGGAAGAT	4080
GTATAATGGA	TTGAAATAAG	ATATGAACAA	ATCAATTAGG	AATTTAAAGC	ATTTTATAAC	4140
AACGTTTTAG	AGTAATGGGG	GGCTATTTCA	ACTTCAACCT	ACTATAATAC	AGAAAAAAC	4200
AACTCCCTGA	TAATTCAAGG	AGTTGTCTAT	AGTTAAATTA	GTTTTTAGAA	GCTTCTTGGA	4260
ATTCTGGGTT	TTTCCATGCT	TCGTCAATGA	TAGCTTGTA	TTCTTTAGCA	GATGCTTGCA	4320
TTTTTTGAGT	TTCTGCGTCG	TTCAATGGGA	TATTTACTGG	ACGAACGATA	CCATGTGCAC	4380
CAACAACAGC	TGGTTGACCG	ATAAAGACAT	TCTCAACTCC	GTATTGACCT	TCTTGGAATA	4440
CTGAAAGTGG	AAGTACTGCG	TTTTCATCGT	CAAGGATTGC	TTTAGTGATA	CGAGCAAGGG	4500
CTACTGCGAT	ACCGTAGTAT	GTTGCACCTT	TTTTGTTGAT	GATTGTGTAG	GCTGCATCAC	4560
GAACACCTTC	GAACAATTCA	ATCAATTCAG	CTTCTTGAAC	ATTTTGAGTG	TCTTTAAGGA	4620

1246

ATTCTTCAAG	GTTTACACCA	GCGATGTTAG	CGTGTGACCA	AACAGCGAAC	TCAGAGTCAC	4680
CGTGTTCAAC	CATGATGTAG	GCGTGCACTG	AACGAGCATC	CACATCCAAT	TTTTTCAGCAA	4740
GTGCTTGACG	GAAACGAGCT	GAGTCAAGTG	AAGTACCTGA	ACCGATAACG	CGTTCTTTAG	4800
GGAAACCAGA	GAATTTCCAA	GTTGAGTAAG	TCAAAACGTC	AACTGGGTTA	GCAGCAACAA	4860
GGAAGATACC	TTTGAAACCA	GATTCAACAA	CTTGAGTTAC	GATTGATTTG	TTGATAGCAA	4920
GGTTTTTACC	TACAAGGTCA	AGACGAGTTT	CACCTGGTTT	TTGAGGTGCA	CCTGCAGTGA	4980
TCACAACAAG	GTCAGCGTCT	GCACAGTCAG	AGTATTGAGC	TGCATAGATT	TTTTTAGGTG	5040
AAGTGAAGGC	AAGGGCGTGA	CTAAGGTCAA	GCGCATCACC	AACAGCTTTT	TCATGCAATT	5100
GTGGAATTC	GATAATTCCA	AGCTCTTGTG	CAATTCCTTG	GTTAACAAGT	GCAAAAGCGT	5160
AAGATGAACC	TACAGCACCA	TCACCGACAA	GGATAACTTT	TTTGTGTTGT	TTAGTTGAAG	5220
TCATTGTTTT	AAACATCTCC	TTAATTTTAT	TAGGGGATTT	TCCCTAGACA	ACTTCATT	5278

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1941 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

ATAAGGAATC	TCTAAAAAAT	TTTAAGGAGA	ATCTAGCAAA	TGGATTTTAC	ATGGGCACTG	60
AAGTATGCCA	CTGAATTTTT	GGGAAGTACC	ATTTTGATCA	TTCTTGGGAA	TGGTGCAGTT	120
GCCAACGTTG	AACTTAAAGG	TACGAAAGGT	CACCAAAGTG	GCTGGATCGT	CATCGCTGTT	180
GGTTATGGTA	TGGGGGTTAT	GATCCCAGCC	TTGATGTTTG	GTAACGTATC	TGGGAATCAC	240
ATCAACCCTG	CTTTCACCTT	AGGGCTTGCA	GTTAGCGGTC	TTTTCCCTTG	GGCACAAGTG	300
GTACCTTACA	TTATCGCGCA	AGTCTTGGGG	GCTATCTTTG	GCCAAGCCTT	AGTTGTGGCA	360
ACATACCGTC	CATTCTACTT	GAAAAGTGAA	AACCCAAATA	ACATCTTGGG	AACTTTCTCA	420
ACTATTTCAA	GTATTGACCA	TGGTACAAAA	GAAAGTCGCT	ATGCAGCAAC	TGTCAATGGT	480
TTGATTAATG	AGTTTGTTGG	TTCATTTGTT	TTGTTCTTTG	CAGCTCTTGG	TTTGACTAAA	540
AACTTCTTTG	GTGCTGAAGT	GCTTCAATTC	ATGAAACAAA	AGGCAACAGA	AGCAGGACAA	600
ACAGTTGATT	TTTCTGACTT	GGCTATTAAA	GCACAGGTGG	CTCCACACAC	TGCTTCAGGA	660
CTTTCTGTGG	CTCACTTGGC	ACTTGGATTC	CTCGTTATGG	CTTTGGTAAC	ATCACTTGGA	720
GGACCTACAG	GACCTGCCTT	GAACCCAGCC	CGTGACTTGG	GACCACGTCT	CCTTCATGCT	780

1247

TTCCTTCCCA AATCAGTTCT TGGTGAGCAT AAAGGCGATT CAAAATGGTG GTATTCTTGG	840
GTACCAGTAG TAGCACCTAT CGCAGCAGCA ATTGCGGCAG TAGCTGTATT CAAATTCCTT	900
TATCTCTAAG AAATAGCTCC TTTAACATTT GAGTGAGCAC CATCTATAAG TAAGAGAGGA	960
TCAGACTGGk TCTCTCTTTT kGATTTTtAG GGAAATGAAA GAAcTCTAAA CAAACTCCTC	1020
TCCAGCAGTG GTTTAGAAGT CTCAGTGGGC TATTCCAGCT TCAATGGACT ATAGTAGGTT	1080
GCAGTTGAAA TAATAGACCC TTGTTTCTAA AACATTGTGA GAAATTGGTT TGAATTCTCC	1140
AATCAAATTG TGCAGTTTTC ATTCTACTAT ATATTATCGG AATATTATCG GAGATGGGTT	1200
CCCTATCTTG TAAGTCTGCT TTATAGTGGG TTGAAGTTGG AATAGTCCTC CCTTCTTTCT	1260
CAAACATTGT GAGGAATTGA TTTACCTTCC TCAACAAAAT GTTCAGTTTC TATTTCATTT	1320
TACTATAAAA TAAGCGATTA GGGGGGCTAT TCTTCGACCT ACATTGACTC TGCTGAGTCC	1380
TATGATTGTT ATCGTTTTAT CTGCAATTTT ATACTCAATG AAAATCAAAG GGCAAACATA	1440
GAAGCTAGCC GCAGGTTGTT CAAAACACAG TTTTGAGGTT GTATAGTAGA TTGAAACTAG	1500
AATAGTACAC ATCTACTTCT AAAACATTGT TAGAAATCGA TTTGACTGTC CTGAACGATT	1560
TGCCCTATTC TTGTTTCATT TTACTATATA AACCAGAGAC TGTTTACATT TTCAGCAAGT	1620
GAGTGGATGG ATAATGCTGA AAACTCCTTG AAGGATAAGT CTATTTAGTA CTTTCTATTA	1680
ATTAGTTAAA TTTTACCAA GAATAATTCA CAAAACGTT GTAAAACACT TGCAATTTAG	1740
CTGAAATTTG ATAAAATAGT AAGGAAAGTT AGACTGTATT GCCTACTGTC TATCTATAAA	1800
ATATATTTTA TTGGAGGCTT TTACTCAAAT GGCAAAGAA AAATACGATC GTAGTAAACC	1860
ACACGTTAAC ATTGGTACTA TCGGACACGT TGACCACGGT AAAACTACCC TAACTGCAGC	1920
TATCACAAC GTTTTGGCAC G	1941

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 755 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ATTTGAAGAA ATTGAAGAAA TCGTAGCCCC TACAGATGGT GAATTTTGG GGGAAGTTTT	60
ACTTGGAAC GGGGTAGTTC TCTTAATTGG AGTAGCCTGT TGTAAAAAG ATAGGGAGTG	120
ATAATCATGC AAGATAACTT TTTATTTGAG GAAATTGAAG AAATTTTCACT ACCAGTTAAT	180

1248

GATTTTTCAG CTGGACTTGC AACAGGTATC GGATTGTTGTT TAGCAATCCT TGCTCTTGCT	240
GGTTGTTGAA GTTTGTTCAT TTACTAACAT CAAGCTTTTT CAATTTTCATT TTAGACAGTC	300
ATTTAAATTT TCCGTATTAG TCTTGCAGCA AGAGATTAAT AGAATTAGTC ATTATTTTAT	360
TGATTGCGGA CTGAGGGACT AGAGTATGTT TTAAGATATT ACCTACTCCT TATGAGGGAC	420
TTAGGTTTGT TATGAGAATT GTTGATAAGA TTAAGATATT ACCTACTCCT TATGAGGGAC	480
ACTATCATTT ATATATACCA TCCAGTAAGA AACATGTATT AGTTGGGAAA CAGGAAAAAA	540
ATGGTTAGAG CAACTAATAG GTCAAGAATT TACCATATCG GACTTATTAG TGTTAGTAGG	600
GAAGAAATAT TTTTAAAATA TCTTGGGACT TTAATATAAC ATTATCTGAA AAATTAAACT	660
ATAAAAGATT TAATAAGAAT TTTGAAAAAA TCCTATCTTG TTGTCATTAT ATTTGCAACG	720
ATACATGAAA TTAGTCATGC AATAATTGCT AATAA	755

(2) INFORMATION FOR SEQ ID NO: 230:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CCAGAAAAAC CGTAGTGGAG CTCGTGGAAC AGTGGAATTG ATTTTCCAAA AAGAATACAA	60
TAAATTTTCA AGTATCTCAA AGAGGGAGGC ATAAGATGTC AGATGCATTT ACAGATGTAG	120
CCAAGATGAA AAAAATCAAA GAAGAAATCA AGGCACATGA GGGACAAGTC GTAGAAATGA	180
CTTTGGAGAA TGGTCGTAAG CGCCAAAAAA ATAGATTGGG TAAGCTAATT GAAGTTTATC	240
CATCTCTATT TATTGTGGAG TTTGGGGATG TGGAAGGAGA TAAACAAGTT AATGTTTACG	300
TTGAATCCTT TACTTACTCA GATATTCTTA CAGAAAAGAA TTTGATTCAT TATCTTGACT	360
AAAGTGAGAA ATTTTCTCAC TTTTCTTTT TTCTCCGAAT AATTTAGGTG AAGGCAATCA	420
TCGCTTTATA TTATTTTCA AGGAGGAAGA ATGAAAATTT TACCGTTTAT AGCAAGAGGA	480
ACAAGTTATT ACTTGAAGAT GTCAGTTAAA AAGCTTGTTT CTTTTTTAGT AGTAGGATTG	540
ATGCTAGCAG CTGGTGATAG TGTCTATGCC TATTCCAGAG GAAATGGATC GATTGCGCGT	600
GGGGATGATT ATCCTGCTTA TTATAAAAAT GGGAGCCAGG AGATTGATCA GTGGCGCATG	660
TATTCTCGTC AGTGTAATTC TTTTGTAGCC TTTCGTTTGA GTAATGTCAA TGGTTTTGAA	720
ATTCCGGCAG CTTATGGAAA TGCGAATGAA TGGGGACATC GTGCTCGTCG GGAAGGTTAT	780
CGTGTAGATA ATACACCGAC GATTGGTTCC ATTACTTGGT CTACTGCAGG AACTTATGGT	840

1249

CATGTTGCCT GGGTGTCAAA TGTAATGGGA GATCAGATTG AGATTGAGGA ATATAACTAT	900
GGTTATACAG AATCCTATAA TAAACGAGTT ATAAAAGCAA ACACGATGAC AGGATTTATT	960
CATTTTAAAG ATTTGGATGG TGGCAGTGTT GGGAATAGTC AATCCTCAAC TTCAACAGGC	1020
GGAACTCATT ATTTTAAGAC CAAGTCTGCT ATTAAAAGT AACCTCTAGC TAGCGGAACT	1080
GTGATTGATT ACTATTATCC TGGGGAGAAG GTTCATTATG ATCAGATACT TGAAAAAGAC	1140
GGCTATAAGT GGTGAGTTA TACTGCCTAT AATGGAAGCT ATCGTTATGT TCAATTGGAG	1200
GCTGTGAATA AAAATCCTCT AGGTAAtTCT GTTCTTTCTT CAACAGGTGG AACTCATTAT	1260
TTTAAGACCA AGTCTGCTAT CAAAAGTCAA CCCCTAGTTA GTGCAACTGT GATTGATTAC	1320
TATTATCCTG GAGAGAAGGT TCATTATGAT CAAATTCTCG AAAAAGACGG CTACAAGTGG	1380
TTGAGTTATA CGGCTTATAA CGGAAGTCGT CGCTATATAC AGCTAGAGGG AGTGACTTCT	1440
TCACAAAATT ATCAGAATCA ATCAGGAAAC ATCTCTAGCT ATG	1483

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1027 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

CCCGGAAAAC AAGTTAAAGT TGAAGTTGGT CAAGCAGTTT ACGTTGAAAA ATTGAACGTT	60
GAAGCTGGTC AAGAAGTTAC TTTTAACGAA TTGTTCTTGT TGGTGGTGAA AACACTGTTG	120
TCGGAACTCC ACTTGTGCT GGAGCTACTG TAGTTGGAAC TGTTGAAAAA CAAGGAAAAC	180
AAAAGAAAGT GGTTACTTAC AAGTACAAAC CTAAAAAAGG TAGCCACCGT AAACAAGGTC	240
ACCGTCAACC ATATACAAAA GTTGTCAATCA ACGCAATCAA CGCTTAATTT TAAGGAGAAC	300
ACATGATACA GGCAGTCTTT GAGAGAGCCG AAGATGGCGA GCTGAGGAGT GCGGAAATTA	360
CTGGACACGC CGAGAGTGGC GAATACGGCT TAGATGTCGT GTGTGCATCG GTTCTACGC	420
TTGCCATTAA CTTTATCAAT TCTATTGAGA AATTTGCAGG CTATGAACCA ATCCTAGAAT	480
TAAACGAAGA TGAAGGTGGC TATCTGATGG TTGAAATACC AAAAGATCTT CCTTCACACC	540
AGAGAGAAAT GACCCAGTTA TTCTTTGAAT CATTTTCTT AGGTATGGCA AACTTATCGG	600
AGAACTATTC TGAGTTCGTC CAAACCAGAG TTATCACAGA AACTAACAC GGAGGAAAAC	660
ATTATGTTAA AAATGACTCT TAACAACCTG CAACTTTTCG CCCACAAAAA AGGTGGAGGT	720

1250

TCTACATCAA	ACGGACGTGA	TTCACAAGCA	AAACGTCTTG	GAGCTAAAGC	AGCTGACGGA	780
CAAACGTGTA	CAGGTGGATC	AATCCTTTAC	CGTCAACGTG	GTACACACAT	CTATCCAGGT	840
GTAAACGTTG	GTCGTGGTGG	AGATGATACT	TTGTTGCTA	AAGTTGAAGG	CGTAGTACGC	900
TTTGAACGTA	AAGGACGCGA	TAAAAAACAA	GTGTCTGTTT	ACCCAATCGC	TAAATAAAAA	960
GGTCCATTGA	ACCTTTTATC	CCGAACCTTG	AAATGTAGAG	GTGAGGAAGC	TAGAAACAGC	1020
TTAAAAAT						1027

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1990 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

CGGTTCAAAT	GGTGCAGGTA	AATCTACGTT	AATTAATTCT	ATTGTAGGTT	TTCAAGAGAT	60
TTATTTAGGA	GAAATAGAGT	ATTGTGATAA	AGATTTGATA	GTTAGTTCTC	AACCTTTTGC	120
TCATTTAGGC	TTTACTCCTC	AAACCACAGT	AATTGATTTT	TATACTACTG	TGAAGGACAA	180
TGTAATATTG	GGGCTGAACC	TTGCTGGAAA	GTTTGGGAAA	AATGCTGAGA	AGTTGTGTCA	240
AATAGCCTTA	GAAATTGTTG	GGTTAGCTGA	TAAAAAAAAT	AATTTGGTAG	AAACATTGTC	300
AGGTGGACAA	CTGCAACGCG	TCCAGATTGC	TAGAGCAATA	GCTCATAATC	CAGATTTTTA	360
TATTTTAGAT	GAACCTACCG	TTGGTTTAGA	TACTGAATCT	GCCGAAAAAT	TTTAAATGTA	420
TTTAAAAGAT	AAGAGTTTGG	AAGGAAAAAC	TATTATCATA	TCTTCACATG	ACATAAATCT	480
ACTCGAAAAG	TTTTGTAAAA	AAATACTTTT	TTTACAAAAT	GGCTCCATAT	CATTTTTTGG	540
TGATATGCGT	GACTTTGTAG	ATAATTCAAC	TATCAAATTA	AATTTTTCAT	TGCAGAATAG	600
AATTTCTAGA	TATCAAATTG	AATTTTTAGA	AAATTTTAGA	TTTAAAGTTC	ACATCGAAGA	660
TAATGATAGT	TTTACAATAG	AAGTCCCTAT	AGAAGAAAAG	ATCTTAGATG	TTATCAATGA	720
GGTAGGAAAA	GCATGTGAAA	TTAAAAACTT	TTCAACAAGT	AAATTAACCT	TACAAGAAAG	780
TTATTTGCAA	AGAATAGGAG	GAGAAAAATG	AAGGCTGATC	AATTAAGGCA	CAAATCGGAC	840
TTAGGTTTAA	GAGGTCTAGC	GATTATTGCT	AAAAATGAGA	TTATTGCTTT	TTTTAGAAGT	900
AAAGGTTTAA	TTATTTCTCA	GTTTCTACAA	CCAATCTTAT	ATGTTGTTTT	TATAATAATA	960
GGATTAAATT	CTTCGATAAA	GAACATTCAG	TTTAATGATA	TAAAAACCTC	TTATGCAGAA	1020
TATACAATCA	TTGGTGTTAT	AGCTTTATTG	ATAATCGGGC	AGATGACTCA	AGTTATTTAT	1080

1251

AGGGTGACAA TAGATAAAAA ATATGGGCTA CTTGCTCTTA AGTTATGCAG TGGAGTTCGT	1140
CCTTTATATT ATATTTTAGG GATGAGTATC TATTCTATAT TAGGGTTGAT AGTTCAAGAA	1200
ATTATTATAT ATATAATTAC GTTAGCGTTT GAGATAAATA TCGCAATGGA TAGATTTTTT	1260
TATACAGTTT TGTATCTAT TGTGTTTTTA TTATTTTGGG ACTCCCTTGC AATTTTACTT	1320
ACAATGTTTA TCAATGATTA CAGAAGACGT GATATTGTAA TACGTTTTGT ACTAACACCG	1380
CTTGGTTTTA CAGCTCCTGT TTTCTACTTA ATAGATTCTG CTCCTAGTAT TGTGAGATGG	1440
ATTGGTCAGT TAAATCCCTT AACTTATCAA TTAATATTT TGAGAACTT TTATTTTAAA	1500
AATTCAACAA CTTTGGAATT AGTTTTCTTA TTGTTAACAT CATTACTTGT CCTTATATCT	1560
GTATCTTTTA TTATACCAA GATAAAATTG ATACTGATAG AAAGATAAAA GTTGGGTCAT	1620
CCAACTTTTT TGTGTCTCC CGAAAACCAC TAGCTATGCT AGTGGTTCCA TAGAGCTTTT	1680
AGCGTGGTAA CAAAAAGAAC CTCCTAAAAT GATAAGATAG AAGTGGTTTC TCCGCCACTA	1740
CAACATATCA TACAGGAGGT ACCTCATGAG AGAGGATAAT CAAAGTTTAT CACATACCAC	1800
ATGGAATTGT AAATATCATA TTGTTTTTGC ACCCAAATAT CGTCGTCAA TCATTTATGG	1860
CAGATACAAA GCTAGTATCG GAAGAATCAT ACGTGACTTA TGTGAGCGTA AGGGTGTAAT	1920
AATCCATGAA GCGAATGCTT GTTCAGACCA TATTCACATG CTTATCAGTA TTCCTCCGAA	1980
ACTTAGTGTT	1990

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GAACATATATT GCATATATTT CTAGCAATGA TCATGGCGAA TCTTGGTCTG CACCAACTTT	60
ATTACCTCCT ATAATGGGAC TTAATCGGAA TGCGCCATAT TTAGGTCCTG GACGTGGAAT	120
CATTGAAAGC TCAACTGGAC GTATTCTTAT TCCGTCTTAC ACTGGTAAAG AGTCTGCGTT	180
CATTTATAGT GACGATAATG GAGCATCTTG GAAAGTTAAA GTAGTGCCAC TTCCTTCTAG	240
TTGGTCAGCA GAAGCACAAT TTGTAGAATT GAGTCCAGGA GTAATTCAAG CATATATGCG	300
TACAAATAAT GGTAATAATG CATATTTAAC AAGTAAAGAC GCAGGTACTA CTTGGAGTGC	360
ACCGGAATAT TTGAAATTTG TTTCAAATCC AAGTTATGGA ACACAATTAT CAATCATCAA	420

1252

TTATAGCCAA	TTGATTGATG	GTAAAAAGGC	TGTCATTTTA	AGTACTCCAA	ACTCCACAAA	480
TGGTCGTAAA	CACGGACAAA	TTTGGATTGG	TCTAATTAAT	GATGATAATA	CAATTGATTG	540
GCGTTATCAT	CACGACGTTG	ATTATAGTAA	CTATGGATAC	TCATATTCAA	CATTGACAGA	600
GTTACCAAAT	CATGAAATTG	GATTGATGTT	TGAAAAATTT	GATTCATGGT	CTCGTAATGA	660
ACTTCATATG	AAAAATGTTG	TACCATATAT	AACATTTAAG	ATTGAAGATC	TGAAAAAGAA	720
TTAAAGCTGA	AATTTGAAAA	TATATAAAAA	GAGGATAAAA	ATTATGGTAA	ATTACGGTAT	780
TGTTGGAGCT	GGATATTTTG	GAGCTGATTT	AGCTCGCTCA	ATGAACAAAA	TTGAAGATGC	840
AAAAGTGGTT	GCGGTATTTG	ACCCAAATCA	TGGAGAAGAA	GTTGCTCAAG	AGTTGGGATC	900
AGATGTTTGT	GCAAGTTTAG	ATGAACTTGT	AGCACGTGAA	GATATTGATT	GTGTGATCGT	960
AGCTTCACCT	AGCTACCTTC	ACCGTGAACC	AGTTGTGAAA	GCTGCTCAAC	ATGGCAAACA	1020
CGTATTTTGT	GAAAAGCCAA	TTGCATTGTC	TTATGAAGAT	TGTAAAGCCA	TGGTTGACGC	1080
ATGTAAAGAA	AATAATGTCA	TCTTTATGGC	TGGTCACATC	ATGAACTTCT	TTAACGGTGT	1140
ACACCATGCT	AAAGAATTGA	TTACTCAAGG	TAAAATCGGT	AAAGTTCCTT	ATTGCCATGC	1200
TGCTCGTACA	GGTTGGGAAG	AACAACAACC	AACTGTATCA	TGGAAGAAAC	TTCGTTCTCA	1260
ATCTGGAGGA	CATTTGTACC	ACCATATTCA	TGAATTAGAT	TGCATTCAGT	TTATCATGGG	1320
AGGACTTCCT	GAAAAAGCGA	CAATGGTAGG	AGGCAATGTA	TATCATAAAG	GTGAAAACCT	1380
TGGTGATGAA	GATGATATGC	TCATTGTAAA	CTTAGAATAC	TCTGATGATC	GTTATGCTGT	1440
TTTGGAATAT	GGTAATGCTT	TCCGTTGGGG	TGAACACTAC	GTCTTGATTG	AAGGAACTGA	1500
AGGAGCTATC	AACTTGACT	TGTTCAATAC	TGGCGGTACT	CTTCGTGTTA	AAGGTGAAGG	1560
AGAATCACAC	TTCTTAGTTC	ATGAAACTCA	AGAGGAAGAT	GATGATCGTA	CAGCTATCTA	1620
TACCGGTCGT	GGTATGGATG	GAGCAATTGC	GTACGGTAAA	CCAGGAGTAC	GTGCCCCATT	1680
ATGGTTGCAA	ACATGTATTG	ATAAAGAAAT	GGAATATCTA	CATGACATCA	TTAAAGGTGG	1740
AGAAATTACA	GAAGAATTTG	AAAAACTTCT	CAATGGTGTA	GCTGCTTTAG	AATCAATCGC	1800
TACCGCTGAT	GCATGTACTT	TATCAGTTAA	AGAAGATCGA	AAAGTAAGTC	TTTCAGAAAT	1860
CACAAATGCT	TAACTTTTGT	AAAACAGAAT	AGTAAATTCT	TGTCATTATA	TAATTTCTAA	1920
AGTTCTGTGA	TACAACTCAT	TGAATAAAGA	AATAGAGATG	GGACTGGGAT	AATGCCCAGT	1980
CCCATTTTTT	ATCAAAAAGT	AATGAGATCA	AAAATGTGGG	AGTGTTGAAA	TGAAGATTAT	2040
AGGTATCGAT	ATTGGCGGAA	CAACAATTAA	GGCAGATTTA	TACGATGAGT	TTGGAACGAG	2100
TTTGAATCAT	TTCAAAGAGA	TAGAAACAAT	TATTGACTAT	GATTTGGGAA	CGAATCAGAT	2160
ATTAAATCAG	GTCTGTGATT	TAATTGGTGA	GTATACTTTA	AATCATTCAA	TTGATGGTGT	2220

1253

TGGGATTTCC	ACTGCTGGAG	TTGTTAATGC	TAATACTGGA	GAAATCATCT	ATGCAGGCTA	2280
TACAATACCA	GGGTATATCG	GAGTAAACTT	TACTGCCGAA	ATAGAAAAAC	GTTTTGGGTT	2340
GTATACTTTT	GTTGAAAATG	ATGTTAATTG	TGCTGCATTA	GGTGAATTGT	GGAAGGGACA	2400
AGCCAAAGAT	AAGAAAAATG	TAGTAATGGT	TACTATTGGA	ACAGGTATAG	GAGGCAGTAT	2460
TATTGTCAAC	GGACAAATTG	TTAACGGATT	TAACTATACT	GCTGGTGAAG	TAGGTTATAT	2520
TCCTGTAGGT	AATTCGGATT	GGCAAAGTAA	AGCCTCAACA	ACCGCATTGA	TTCATTTATA	2580
TCAAAAAAAG	AGCTTGAAAA	CTAATCAAAC	TGGACGTACT	TTCTTCACTG	ATTTAAGATC	2640
TGGAGATAAA	GTTGCTGAAG	AAACTTTTGA	AATTTTGTGA	GAAAATCTAA	CAAAAGGTTT	2700
ATTAACGATT	TCTTATCTAC	TTAATCCAGA	AATTCTCATA	TTAGGAGGTG	GGATTCTGGA	2760
TAGTAAGGAT	ATTTTGTTAC	CTGAAATTCA	AAGTTCTTTA	GCTAAAAATG	CAATGGATAA	2820
TAGGTTTTTA	CCTAAAAATC	TTGTGGCAGC	TACATTAGGA	AATGAAGCTG	GTCGTATAGG	2880
AGCTGTAAAA	AATTTCTTAG	ATAGAAT TTC	TAATAAATAG	TATGTAAGAT	AAGGAGGTGT	2940
CACAATGACT	AACTCTGTAT	TTTCGACAAT	GCAAGATATT	GAGAATGTTG	CAACCGATAT	3000
TATAAAATCA	TATGATAATG	AGATTTATAC	TTATAAAGCT	GTTTCCCAAG	AAGAATTGGA	3060
AAACTAGAA	AAAAGTTATG	ATGAAAAAAG	TCACGAAGAA	TTAGTTTCAA	TAGAAAGCAA	3120
TTTAGAAATG	AAACAACAGA	ACCTTATTGA	TGAGGTTAAT	AAAACAATCA	AGGAAAATGA	3180
TGCAAAATAT	CAGTATATTT	CATCAAGTAG	GAGAGGAGAA	TTTGTAGAAA	AAATTATTGG	3240
TAGGGTGGTA	GAAAAATATG	GCCATTAGTC	AGATGAAAAG	AATCTCTCTA	CTATTTTCTA	3300
AAAGTAGTCT	TGATGATGTT	TTAAAACTA	TTCAAGAACT	AGAGTCAGTG	CAGTTCCGTG	3360
ATTTAAAGGT	TCAGGATAAC	TGGTCAGAAG	CTCTAGAAAA	AGATGAAGTT	GTATTTCCAA	3420
CTATTCAAAT	TTTTCATACT	TCTAATTCCA	ATCATGGGGT	TATTGAGGGA	AATGATGCCT	3480
TGACTTATTT	GATGAATCAA	CAACAACATT	TAGAAGCAAC	TGTAGAGAAA	TTACAAGAAT	3540
ACCTACCGAA	AGAAAACACG	TTTAAATTAT	TGCAGCAACC	TCCGATAACT	ACCTCTTATG	3600
AAGAATTAGA	GAAATTTGGT	AAAGCTAATG	TTGCTGAGGG	TGTTCTTAAA	AAAGTGAATC	3660
ATCAAATTAA	CAGAGTTCAT	GAATTAGAAA	GACACATTCA	AAGTAATAAT	GAGGAAATAG	3720
AGCGATTAAT	AAAGTGGGAA	AAATTAGAAA	TTGTTCCCTGC	GAATTTAGAA	CAATTTTCTT	3780
TCTGTAAAGG	AAAAGTCGGA	ACAATTCCAA	GGACTGAAGA	TAATCGCTTA	TACAATAGTC	3840
TTTTAGAAAA	CAATATTGAA	GTTCAAGAAA	TATTTTCTAA	TGATAGAGAG	TACGGTGT TG	3900
TTGTTTTCTA	TCAGTCTAGT	TACTCTATAG	ATTTTGATGA	ATACTTATTT	GAACCATTTG	3960

1254

ATTATTCTAG AAAGGAATTA CCGAAGCAGC GAGTAGTAGA TTTAGATCAA GAAAACATGC	4020
AGTTAATAAC TGAAAAAGAG AATATTATCG CATCGTTGCA AGATTCAAAG AAATATTTGA	4080
TAGATTTACA ATGGCAAATA GACTATATTT TATCTATCTA TGCTCGTCAA ATCTCTAAGA	4140
ATAACTTTTT GTGCACTCCG CATCTAGTTG CATTAGAAGG ATGGATAGAA GAAACTCGTA	4200
TTTTATATTT TATAAAAGTT ATGGATGAGC ATTTTGGACA TTCTATTTAT ATTTATGAAT	4260
CGGAAACATT GACGGATAAT CAAGATGAAA TACCTATCAA ATTAACGAAT CATTCTTTAA	4320
TTGAACCATT TGAATTATTG ACAGAAATGT ATGCTCTGCC CAAATATTAT GAGAAAGATC	4380
CTACACCTGT ATTAGCACCA TTTTACTTTA CATTTTTTGG AATGATGGTT GCTGATTTAG	4440
GCTATGGTTT ACTATTGTTT TTAGGAACAA TGTTAGCATT AAAAATTTTT CATCTACCTT	4500
CAGCAACTAA GAGATTTTTA AAATTCTTTA ATATATTAGG GGTAGCCGTT GCAATTTGGG	4560
GTGGAATCTA TGGCTCATTT TTTGGATATG AGTTGCCATT TCATCTGATA TCTACAACCT	4620
CTGATGTCAT GACTATATTA GTAGTGTGAG TTGTGTTTGG GTTTATTACA GTATTTGCAG	4680
GTTTGTTAGC TTCAGGACTA CAAAAAGTAA GAATGAATAA ATATGCAGAA GCATATAATT	4740
CAGGATTTGC GTGGTGTGTT ATTCTG	4766

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

CCTTTTAGAA AAAATTAAAG AATACGACAC CATTATCATT CATCGTCATA TGAAACCAGA	60
CCCTGATGCC TTGGGAAGTC AGGTGGGATT GAAAGCCTTG CTGGAACATC ATTTCCCAGA	120
AAAAACCATC AAAGCCGTCG GTTTTGATGA ACCAACTCTT ACTTGGATGG CTGAGATGGA	180
TCTTGTTGAA GATAGAGCCT ACCAAGGCGC ACTTGTCATC GTCTGTGATA CAGCTAATAC	240
TGCTCGTATC GATGATAAGC GCTATAGTCA AGGTGATTTT CTCATTAAGA TTGACCACCA	300
TCCAAATGAT GATGTATACG GTGACCTGTC TTGGGTCGAT ACTAGTTCAA GTAGCGCTAg	360
aGaTGATTAC CCTATTTGCC CAAACAACCC AACTAGCCTT GGCAGATCGC GATGCTGAGT	420
TGCTCTTTGC AGGAATTGTC GGTGATACAG GTCGCTTCCT CTACCCCTTCT ACCACTGCAC	480
GGACTCTTCG CCTGGCTGCT TATTTGAGAG AACATAACTT TGACTTTGCG GCTCTCACTC	540
GCAAAATGGA CACTATGAGC TACAAAATTG CTAAACTGCA AGGCTACATC TACGACCATC	600

1255

TGGAAGTGA	TGAAAATGGT	GCTGCTCGCG	TTATCCTGAG	TCAGAAAATC	TTGAAACAAT	660
ACAATATAAC	CGATGCTGAA	ACTGCGGCCA	TTGTAGGTGC	ACCTGGACGC	ATTGACAGAG	720
TGAGTCTCTG	GGGAATTTTT	GTCGAACAGG	CTGATGGCCA	CTACCGAGTT	CGCTTACGCA	780
GTAAAGTCCA	TCCTATCAAT	GAAATTGCCA	AGGAGCATGA	TGGTGGAGGC	CACCCTCTAG	840
CAAGTGGTGC	TAATTCCTAT	AGCCTAGAAG	AAAACGAAAT	CATCTACCAA	AAGTTAGAAG	900
ACTTGCTTAA	AAACTGATAA	AATACTTGCC	AAACTTTTCA	GAATCTGATA	GACTAGTATA	960
GTAACAATCT	ATGGCTCGCA	AAGAGACCAT	GGCAGAAAGG	AAATATTGCA	AAATGAAAAT	1020
AGATATCCAT	CCAGAATATC	GCCCAGTTGT	CTTCATGGAC	ACAACACTG	GTTACCAATT	1080
CCTTAGCGGT	TCAACAAAAC	GCTCTAACGA	AACAGTTGAG	TTCGAAGGCG	AAACTTACCC	1140
ATTGATCCGT	GTGGAAATTT	CATCAGACTC	ACACCCATTC	TACACTGGAC	GTCAAAAGTT	1200
CACTCAAGCA	GATGGACGCG	TGGATCGTTT	CAACAAAAAA	TACGGTCTCA	AATAATGATA	1260
AGAGAACAGT	TTTGGCTGTT	CTTTTTTGTT	TCTTGAAATC	AACTGCTGTT	TTCATGTTCC	1320
AGACTCATCT	GTAGGTTCGA	TTCCATGCT	ACTAGGCAGG	AAGGAAATAG	CTGTTTCAAC	1380
ACGTCCATAA	TGAGCTATAC	TATTGTCACG	AACCACACTT	TCATTGATGG	TCCAAGTGGA	1440
ATTCATTTTC	TTAAAAGCTT	CTCGGACTTT	TTCCAAATCT	TTGGAGGCAA	TGGCCTGCTC	1500
TAAGGTTTCA	AAACGAGGAC	TTATACTCAT	CTGCTTTCAA	AAAGCATTCT	AGTCCATCTC	1560
CGATTACCGA	TGGACTTTAT	CACCTCCTTC	TCCAGTCCTT	GTATGACATC	TTGAAGTTGA	1620
TTCATGACAT	CTTCCAAAGT	TCGAAAGGCT	TTATTCTTAA	ATCCACGTTT	ACGAATCTCT	1680
TTCCACACTT	GTTCAATGGG	TTCATCTCTG	GTGTGTATGG	AGGAATAAAG	GTAAAATCAA	1740
TATTAGTCGG	AATATTTAAG	GTACTTGATT	TATGCCATAT	AGCATTGTCC	ATAACGAGTA	1800
AAAGGATAAG	CTTGTGAAAG	CTCTTCTAAA	AAGGCGTTCA	TCCACACTCC	TTTTTATAAA	1860
CCTGAAATAA	GGCATCAATT	GTAACAAATT	CTCCTGCCTC	TGTAGCCTTC	AAATGACGGG	1920
CAAGAAAGGC	TTTCTCTTCC	TCAACTGTCA	TATATGCATG	GTTACGACCA	CCACGTGTTT	1980
CTTGAAGGAG	AGAGTCGAGT	CCGAACTCCT	CATATTTTTT	TACGTTTCGC	CAAATCGTTG	2040
TTTGATTACA	GTCTAAAAGC	TCTATAATCT	CTTTATAAGA	TTTGCCCATC	AGACGAAATA	2100
TAGTAGATTG	AAACTAGAAT	AGTACACCTC	TACTTCTAAA	ACATTGTTAG	AAATCGATTT	2160
GTCCTGTTCT	TGTTTCATTT	TACTATAGAA	CGATTTGAAG	GCGTTTATAA	TATTTAGCTG	2220
TACGAGAGTC	TTTTAAAAGT	GTTTTGATGG	TTTGGATTTC	TTCTTTAGTT	GATTTCATAT	2280
TACTATTATA	TAATGCTTTT	TGATTTTAGT	CTGGTATAAA	TATTGCTTTC	CTCCAAAATG	2340

1256

GTCATAGTTT TACTGGCAAA TCTAACATAT CACGGATAAA TTAACAAGTG ATTTCTGAAT	2400
TGCTAAACAT TTTCTTTTCT TATAGCATAC TTTAAGATTT TGTCTTTGAG AAAGATATTT	2460
CCAAGAAAAA CGTTCGTTTT TTGG	2484

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

CTAGATATAG CTATAATTTT ATTTATAACA AGAGGATAGA AATGACCGAA TTAGAAAGAA	60
AAAATCGAAA AATTAGCTAA GAAATATTCT GATAACTTAA ACATCAAAGT TCAAGAGAGA	120
GTTCGTGAAA TGGCAAATGA TAATAAGAGC CATTATTTGA TATACAGAGT TTTAGGTATT	180
TCATTTGAAG AAGGAGAAAA TATCGATTTG TATCAAAATA AAGGTCGTTT TTTATACAAA	240
TATGCTGGTT CATTTTGTAGA AGAAGCTGCA GTACTATGCT TTAACGAAAA ATTTGGTACA	300
GAAAATACTT AAAAAGTTAA CATTCCTAAT TCTGAAAGTA CAAAACCTAA GACTTTTGAA	360
ATTGATTGTT TAGTCGGAGA AAAACACGCA TACGAAATAA AATGGTGGGA TGCAACTACA	420
GATGGAGACC ATATAACTAA AGAACACACT AGAATAAAAG TTATTCATAA CAAAGGATAT	480
ATACCAATTC GGTTAATGTT CTACTATCCA AATAGAACTC AAGCTATAAA AATTCAGCAA	540
ACTTTAGAAA CATTGTATAA CGGTATTGGA GGGAAATATT ATTATGGAGA TTCTGCCTGG	600
GAACATTTAA GAGCAGTGAC CGGTATTGAT TTACTTAGTA TTCTAACAGA TATTGCAAAT	660
AAAAAAACAG GGGTAAAATC AAAATGACAG TATTTAAAGG AGATAACTTA GAAATATTAA	720
AAACTATTGA ATCCTCAAGT ATTGATTAA TCTATATGGA CCCTCCTTTC TTTACACAGA	780
AAACCCAAAA ATTATCTAAT AACAAAAATA TTATGTATTC ATTGGAAGAT ACGTGGACTT	840
CGATTGAGGA TTACAAAGAA TTTTGTCTG TAAGATTAGA AGAATGCAA AGAGTGCTAA	900
AAAATAGTGG CAGTATTTTC GTTCATTGTG ATAAAATTGC AAATCATCAT ATTAGATTAA	960
TTTTAGATAA TATCTTTGGA GTAGATATGT TTCAAAGCGA AATTATATGG AACTATAAAC	1020
GGTGGTCTAA TTCAAAAAAG GGATTATTGA ACAATCATCA AAACATTTAC TTTTATTCAA	1080
AGTCAAAAGA TTTTAAATTT AATACAATTT TTACAGAGTA TTCTTCTACT ACAAATATCG	1140
ACCAAATACT AGTGGAACGA AAACGAGATG GAAACTCTAA AACTATATAT AAGGTTGATA	1200
ATAATGGTAA CTATATTCTA GCAAAAGAGA AAAATGGAGT TCCCCTTTCA GATGTTTGGA	1260

1257

ATATACCATT TCTTAATCCA AAAGCTAAAG AAAGAGTAGG TTATCCTACA CAAAAACCTA	1320
TTCTGTTATT AGAACAAATT ATAAAGATTG CTAAGTATAA AAATGATATA GTTTTAGACC	1380
CGTTCTGTGG AAGTGGAAC TCTTTAGTAG CCTCCAAGAT TTTGAATAGA AATTATATGG	1440
GGATTGATTT ATCTGAGGAA GCTATCAATA TAACTCAGCA ACGTCTGGAA AATGTTATAA	1500
AAACAAGTTC AAATTTATTG AATAAAGGAA TCGAAGCATA TAGAACCAAA ACTGAGGAAG	1560
AGGAAAACAT TCTTAAATTA TTACAGGCAA AAATTGTTCA AAGAAATAAA GGAATTGATG	1620
GTTTTTTACC TAAACATTTT CAAAAAAAC CGATACCTAT AAAAATTCAA AAAAATAATG	1680
AATGTCTGAA TGAGAGTATC TCTTTATTAC AGAATGCTAT AAACCTCAA AAACCTGATT	1740
TTGGAGTAGT TATAAAAACT CATTCG	1766

(2) INFORMATION FOR SEQ ID NO: 236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 748 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

CCGAAAATCA AATTCAAACC ACGTCAACGT CGCCTTGCCG TACTCAAGTA CAGCCTGCGG	60
CTAGTTTCCT AGTTTGCTCT TTGATTTTCA TTGAGTATTA AACTAAATTA AATAATATTA	120
GCGCGGAGAA TTTCTAATTC TTCCTTGGTC AAGCGACGCC ATTCCCCTCG TTCTAGGTTC	180
TCATCTAATA CTAAAGTTCC CATAGTCAAT CGTTGCAAGT CCACCACTTC CTTGCCACAG	240
TAGCCACCA TACGCTTGAT CTGATGAAAC TTCCCTTCTG CAATGGTCAC ACGGATTG	300
CTTTGATTCT TTTCTGTATC TATGGATACA AGCTCCAGTA TAGCGGGTTG ACAGGTAAAG	360
TCTTTGAGAG GAATACCCTC AGCAAATGTC TCCACATCTT CTTGGGTCAT GATTCCCTTG	420
ACTTGTGCCA GATAAGTCTT GTCCACATGA CGCTTGGGCG AAAGAAGAAC ATGAGCCAGC	480
TGACCATCAT TGGTCAAGAG CAAAAGACCA TCGGTGTCAA TATCCAAGCG TCCTACTGGG	540
AAACTTCCT TACTCCGCGC CAAGTCATCC AACAAGTCCA GAACGGTCT GTGCTTGGGA	600
TCCTCAGTCG CTGAGATAAC TCCTTTGGGC TTGTTTCATCA TGTAAGTAGAC AACTCTTCA	660
TACTCCAACA CTTGCCCATC AAAGCGAATC TCATCTATTT TTTCATCAAT CTGCAATTTA	720
GCTGATTTTT CTTTTTGACC ATTTACAG	748

(2) INFORMATION FOR SEQ ID NO: 237:

1258

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1449 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

AAAAGATTAC ATTGCAACAA TTGAAAATTA TCCAAAGGAA GGCATTACCT TCCGTGATAT	60
TAGTCCTTTG ATGGCTGATG GAAATGCTTA TAGCTACGCT GTTCGTGAAA TCGTTCAGTA	120
TGCTACTGAC AAGAAAGTCG ACATGATCGT GGGACCTGAA GCTCGTGGAT TTATCGTGGG	180
TTGTCCAGTT GCCTTTGAGT TGGGAATTGG TTTTGCGCCT GTTCGTAAGC CAGGTAAATT	240
GCCACGCGAA GTTATTTCTG CTGACTATGA AAAAGAGTAC GGTGTCGATA CCTTGACTAT	300
GCACGCGGAT GCCATTAAGC CAGGTCAACG TGTTCCTTATT GTAGATGACC TTTTGGCGAC	360
AGGTGGAAC TTTAAGGCAA CTATCGAGAT GATTGAAAAA CTTGGTGGTG TTATGGCAGG	420
TTGTGCCTTC CTTGTTGAAT TGGATGAATT GAACGGCCGT GAAAAAATTG GTGACTACGA	480
CTACAAAGTT CTTATGCATT ATTAATGAAA ACAGTCCCTA GGGCTGTTTT CTCTACACTA	540
GGATATAAAA ATAGACTATA ACTAGTTAGA GAAAACTAT AATTGAAAAC TATATCTTCT	600
TGCAGTATAA TAAAAGGACT AAGTGTTTGA GATTTGTCTT CAAACATATG CAATTATTCC	660
TGAAAGAGTA CAGTTAGGAG AGGGTTATGC CGATTCTGAAT TGATAAAAAA TTGCCAGCTG	720
TTGAGATTTT ACGGACAGAG AATATCTTTG TCATGGATGA TCAACGTGCT GCCCACCAG	780
ATATCCGTCC TTTGAAGATT TTAATTTTAA ATCTCATGCC ACAGAAAATG GTCACAGAGA	840
CCCAGTTGTT GCGCCACTTG GCTAATACAC CCCTACAACT GGATATTGAT TTTCTCTATA	900
TGGAGAGCCA CCGTTCTAAA ACAACTCGTT CAGAGCACAT GGAGACCTTC TATAAACTT	960
TTCCTGAAGT CAAGGATGAG TATTTTGATG GGATGATCAT CACGGGTGCT CCAGTTGAGC	1020
ATTTACCATT TGAGGAAGTG GACTATTGGG AGGAATTTAG ACAGATGCTT GAGTGGTCTA	1080
AGACTCATGT CTATTCGACC CTTCATATCT GTTGGGGGGC TCAGGCTGGG CTTTATCTGC	1140
GCTATGGTGT AGAAAAATAC CAGATGGACA GTAAGCTATC AGGTATTTAT CCTCAGGACA	1200
CCCTAAAAGA GGGTCACCTT CTATTTAGAG GCTTTGATGA TAGCTATGTA TCCCCTCATT	1260
CACGGCACAC GGAGATTTCT AAGGAAGAGG TCTTAAACAA GACCAATCTC GAGATTTTAT	1320
CAGAAGGACC TCAGGTTGGG GTTTCTATTw TGGCCAGTCG TGATTTACGA GAAATTTATA	1380
GTTTTGGTCA TTTGGAGTAT GACCGTGATA CTTTGGCAAA AGAGTATTTT CGAGATCGTG	1440
ATGCAGGTT	1449

1259

(2) INFORMATION FOR SEQ ID NO: 238:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 904 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

TACCCGCTTC TTTCAAGAGT TGGAGCAGGG CTTGTTTGCG ATCTTTTGTC ATAGTTCTTC	60
CTTTTAACGG CGTTTTTCGAA GCACTTTATA GACAGCTAGT GCTAATGTAT AGTCTACCAT	120
ACTATGGATA ATTGTACCAA ATCCAAC TAG TACAAATAGA ACATAAAACA TATTTTCTAC	180
ATTGGTACCA GAAGTTGCGT AAAAAACGAC ACAGGCCAAT ACTTCAGCAA GGGCATGAAC	240
AACAGCCAAA ACAAAGTTGA AAATCCAGGA AGATTTTGGT TTATCTAGGG TATCGGGGAA	300
TTTTTG TAGG TAAAGAGCTC CTAAAGCACC AAAAGATATA TGGGAAAAAG CCCGAAAAAC	360
GATAACCATG GGATAGCCAG CCATCAAAAA TCCAAAACTA GAGGCTAGGA TGACAAAAAC	420
TGCCATCAAG GGCGACAAGA ACATGGCTAT AAAAATAGCG ATGTGGCTCC CCAAAGTATA	480
GGAAGCAGGT GGAATGACAA TCTTGAAAGG CATAACAATT GGAATCAAAA TCGCAATAGC	540
CGTTAAAAGG GCTGTCATTG TCATAAATTG TGTCTTTTTC CGTGTATTCA CAAGAATCTC	600
CTTTTAACT GCATATACAC TAGTATGGTA CAATAAACCA GACAATAAAG CAAGAATTTA	660
CTTGGGTTTA TAGATCATTT TTTAGTTAAA AGTTATAGTA GATTGAACT AGAATAGTCC	720
ACCTCTACTT CTAAACATT GTTAGAAATC GATTTGGCTG TCCTGATCGA TTTGTCCTGT	780
TCTTATTTTCG TTTTACTATA GTAAAGATTT CATTAAAAAG AACTGTATA GAGCAAAATC	840
TCCACCTTCA GGT TTGGAAA GCGGAGATTG TTTnTTATTT TTTCCAGGGT TTGTAGTCGT	900
GGGA	904

(2) INFORMATION FOR SEQ ID NO: 239:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 946 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

CACTCAAACA TGACTTATAT CAAGACGGAT GGA CTTC AAG ACGATGCCAA TCGCTTGAAT	60
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1260

CGTAACATTC AGTTTGGTGT TCGTGAATTT GCAATGGGAA CAATCTTGAA CGGGATGGCC	120
CTTCATGGTG GACtTCGTGT ATACGGTGGA ACTTTCTTCG TCTTCTCTGA CTATGTGAAG	180
GCAGCTGTCC GCTTGTCAAG CTTACAAGGA CTTCTGTGA CTTATGTCTT TACCCATGAT	240
TCAATCGCAG TTGGGGAAGA TGGTCCGACT CATGAACCAG TTGAGCATTT AGCAGGTCTT	300
CGTGCTATGC CAAATCTAAA TGTTTTCCGT CCAGCAGATG CGCGTGAAAC GCAAGCAGCT	360
TGGTACCTTG CAGTGACAAG TGAGAAAACA CCAACTGCCC TTGTCTTGAC ACGTCAAAAT	420
TTGACTGTTG AAGATGGAAC AGACTTCGAC AAGGTTGCTA AAGGTGCTTA TGTGTATAT	480
GAAAATGCAG CCGACTTTGA TACCATCTTG ATTGCGACAG GTTCAGAGGT TAATCTTGCT	540
GTCTCAGCTG CTAAAGAATT GGCTAGTCAA GGCGAAAAAA TCCGCGTAGT CAGCATGCCA	600
TCTACAGATG TCTTTGATAA ACAAGATGCA GCTTACAAGG AAGAAATTCT TCCAAATGCA	660
GTCCGCCGTC GTGTTGCAGT CGAAATGGGT GCAAGTCAAA ACTGGTACAA ATATGTTGGT	720
CTCGATGGTG CCGTTCTAGG TATTGATACT TCGGAGCCTC TGCCCCAGCA CCAAAAGTAT	780
TGGCAGAATA TGGCTTTACT GTAGAAAATC TTGTAAAAGT TGTTCGAAAC TTGAAATAAT	840
CCTAAAAATC AGGGCGTAAG CTCTGGTTTT TCTTACCAGA AAAGTAAGGT ACAATCTTGT	900
AAAAGTAGCT GAAATTTGAT ATAGTAGTCC TATGTAAAAG ACAAAG	946

(2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2764 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

CGGGGCTCCc TAGTTCTTAG GGAGCTATTT TTGTTTTTTC AAGAAGTTAT CTTCTTGAT	60
TTTATACTCA ATGAAAATCA AAGAGCAAGC TAGGAACTA GCCGTAsstG CTCAAAACAC	120
TGTTTTGAGG TTGTAGATAA GACTGACAAA GTCAGGAACA CATATCTACG GCAAGGCGAC	180
GTTGACGCGG TTTGAAGAGA TTTTCGAAGA GTATTAGTTG TGAATCTGGT GCAGTCGTCC	240
CAGATTATTC TTATTAGTAG GGTCTTGTTT TCTATATCCC CTCGTAGTTA ACAAGACCTT	300
GAGCATTTTA GAAAGAGGAA TCTATGTCTA CGAAATATAT TTTTGTAAC TGGTGGTGTGG	360
TATCGTCCAT TGGGAAAGGG ATTGTGGCAG CGAGTCTAGG CCGTCTCTTG AAAAATCGTG	420
GTCTCAAAGT AACCATTCAA AAGTTTGACC CTTATATCAA TATTGATCCG GGAACCATGA	480
GTCCTTACCA GCACGGGGAA GTTTTTGTGA CAGATGACGG AGCTGAGACA GATTTGGACT	540

1261

TGGGTCACTA TGAACGTTTC ATCGATATCA ATCTCAACAA ATATTCCAAC GTGACAACTG	600
GGAAAATTTA CAGTGAAGTT CTTCGTAAAG AACGCCGTGG AGAATACCTT GGGGCAACTG	660
TTCAAGTCAT TCCTCATATC ACAGATGCTT TGAAAGAAAA AATCAAGCGT GCCGCTCTAA	720
CGACCGACTC TGATGTCATT ATCACAGAGG TTGGTGGAAC AGTAGGAGAT ATCGAGTCCT	780
TGCCATTCCCT AGAGGCTCTT CGTCAGATGA AGGCAGATGT GGGTGCGGAT AATGTCATGT	840
ATATCCATAC AACCTTGCTT CCTTACCTCA AGGCTGCTGG TGAAATGAAA ACCAAACCAA	900
CCCAACACTC TGTCAAAGAA TTGCGTGGCT TGGGAATCCA ACCAAATATG TTGGTTATTC	960
GTACAGAAGA GCCAGCTGGT CAAGGAATTA AAAATAAACT GGCCCAGTTC TGTGATGTGG	1020
CACCAGAAGC CGTTATCGAA TCGTTGGATG TTGAACACCT TTACCAAATT CCACTGAACT	1080
TGCAGGCACA AGGGATGGAC CAAATTGTTT GTGATCATTT GAAATTAGAC GCACCAGCAG	1140
CGGATATGAC AGAATGGTCA GCCATGGTGG ACAAGGTCAT GAACCTCAAG AAACAAGTTA	1200
AGATTTCCCT TGTGGAAG TATGTGGAGT TGCAAGATGC CTATATCTCA GTGGTCGAAG	1260
CCTTGAAACA CTCTGGCTAT GTCAATGATG CAGAAGTTAA AATCAATTGG GTCAATGCCA	1320
ATGATGTGAC AGCAGAGAAT GTAGCAGAAC TCTTGTCTGA TGCGGACGGG ATCATCGTAC	1380
CAGGTGGTTT TGGTCAACGT GGTACAGAAG GGAAAATCCA AGCCATCCGC TATGCGCGTG	1440
AAAATGATGT TCCAATGTTG GGAGTCTGCT TGGGAATGCA GTTGACATGT ATCGAGTTTG	1500
CTCGTCACGT TTTAGGTCTT GAAGGTGCCA ATTCTGCAGA GCTTGACCA GAAACAAAAT	1560
ACCCTATCAT TGATATCATG CGTGATCAGA TTGATATTGA GGATATGGGT GGAACCCcTTC	1620
GTTTGGGACT TTATCCGTCT AAGTTGAAAC GTGGCTCTAA GGCTGCTGCT GCTTATCACA	1680
ATCAAGAAGT GGTGCAACGC CGTCACCGTC ACCGTTATGA GTTTAATAAT GCCTTCCGTG	1740
AGCAGTTTGA GGCAGCAGGT TTTGTCTTTT CAGGAGTTTC TCCAGACAAT CGTTTGGTAG	1800
AAATCGTGGA AATTCCTGAA AATAAATTCT TTGTAGCTTG TCAGTATCAC CCTGAACTGT	1860
CAAGCCGTCC AAACCGACCA GAAGAACTCT ACACTGCCTT TGTTACTGCA GCAGTTGAGA	1920
ACAGCAATTA GCAAAATCAG AACCTTTGAG AAAAATCTCA GAGGTTTTTT GCATACGATG	1980
ATATTGCAGT ATATCTGAGG TAGGGGTCCT CTGTATGTAC CTGCTACCGT TGAAATCAAT	2040
AGCGACTCCC TCTTGCCCTG TGCTAGTGAA TGGATTTATC AGTATATTGA AATGAAATAA	2100
AATTTGAACA AATTAATTCG GAAAGCCAAA TCAATTTCTA GCAAAGTTTT AGGAACTGGA	2160
TTGTATAGTG AATTGAAATA AGATGTGAAC ATCTCTATCA GGAAAGTCAA ATTAATTTAT	2220
AGAAATATTT TAGCAGTCAA GATGTACTGT TATAGATTCA ATACATTATA CTTTTTTAAT	2280

1262

TTAATCCACT ATAGTAAAAT GAAATAATAA CAGGACAAAT CGATCAGGAC AGTCAAATCG	2340
ATTTCTAACA ATGTTTTAGA AATAGAGGTG TACTATTCTA GTTTC AATAT ACTATCCCAA	2400
ATCATTCATA CCTCTCTCAA CTAGATGTAA CTTACAAAAC CCCTGACCTC ATGAGCCACT	2460
TTCTTCCTCC TCATGAGGTC AGTTTTACTT TCTGCTGTTC CAGTATCGTT TTCCTCGCT	2520
AGATTTCCCTC AAAAGGGCAG ACTCCTCCCT TGGTGCGTCA CACGATTTTT TCATCTCGAC	2580
TGTTCTTTAA TGCATCATTA ACGACGCTTT TCTTCTAGGT GGTTCATAAG GAACAGGAAG	2640
ATTCAGGTTG ACTTTTCTAA TCCTAGAATA AAGTGCTGAA AACAATTCGG AATAGGCATA	2700
GAGACTAGAC AATTGAGGA GCTGCTTGCG TCCTGTTCGA ACACATTTTC CCACCACGTG	2760
AAGA	2764

(2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1682 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

CCGTTTTTTT CATTGTT CAG TACTACA ACT TACGTTGTAG CGCCCTGCAC ATTGGTTCGT	60
CTTGTT CAGT TTTCAAAGGT CTTTGTC ACT TGCTTCTCTC AAGCGACAAC TATATTAGTA	120
TATCACA ACT GCTTTCGCTT GTCAACACTT TTTTGAAGAT TTTTAAGTTT TTTTAAACTT	180
TTTTTTCATCA AGTGGTCCTG ACGCAACATA CCATAGTCCG TACGGGATTC GAACCCGTGT	240
TACCGCCGTG AAAAGGCGGT GTCTTAACCC CTTGACCAAC GGACCTGAGT TGTTATTTTC	300
AACTCTTACT ATTATACAGT CTTTTCAAAC TTTGTCAACT ACTTTTTTAA ACTTTTTTTA	360
TTAATTTTAC AACAGCTTCA GTTCGAGCTG TATGTGGGAA CATATCGACC GACTGGATAT	420
AATGAAGATC ATAGACTTCT ACTAAGCGTA CCAAATCACG AGCCAAGGTC GAAACATTAC	480
AAGAAATATA AACCATTTTT TCTGGTACAT AAGTAAGAAT AGTATCTAAT AACTTATCAT	540
CCAGACCTGT ACGTGGTGGG TCAACAATCA AAGCATCTGC TCGGTAGCCT TCCTTGTAAC	600
AACGAGGAAT AATCTCTTCT GCCGTTCAG CTTCATAATG AGTATTGTCA AATCCCATT	660
TTTTAGCATT TCGCTTGCA TCTTCAATAG CTTCTGGAAT AATATCCATA CCTCTGAGTG	720
TTTTTACTTT CTTTGCAAAG GCAAATCCAA TCGTTCCAAC TCCACAATAA GCGTCAATCA	780
AATGGTCTTC TTTATCAACA TCCAGCGCTT TTAGTGCTTC GCTATAGAGG ACTTCTGTTT	840
GCTCAGGATT TAGTTGATAA AAAGCTCGAG GGGATAGTGA AAATTCATAA TTGAGTACAC	900

1263

CTTCTTGAAT ACTCTCTTGC CCCCAGATAA TCTCTGTCTT TTCACCATAT ATCTCACTGG	960
TTTGTAGCTGT ATTTGTATTA ACAGCTACTG TCACAACCTC TGGGAAATCT TTAACCAACT	1020
CTTTTACCAA TTGAGTTAAA TTAAGCTGGC GGTTCGTAAAC AATAATAATC TGAACCTGTC	1080
CGGTCTTTCT CGCGCGTCGG ACCATAATAG TACGGACACC TAGAACTTTT CTCTCATCCG	1140
TGATTGGAAT CTGGTGATAA GTAAGTAATT CTGCTAAGCG ATTAGCAATC ACTTGGGTTT	1200
CCTTATCTTG TACCAGGCAG TCTTTCAACT CTACTAAATA GTGAGAGTTT TGTGCATATA	1260
AGCCCGCCTT GACCTGATTT TTAAATTTTC GAGTCTGAAA TTGTAACCTA GCTCTGTAAT	1320
ATTTTGGTTC CTGCATTCCA ATAGTTGGAC GAATTTTATA ATTTTCATAT CCTGCAGGAG	1380
CAAATTTTTT CAGCGCTTGA TGAAGTAAGT CCGTCTTGAA CTCCAGCTGC TTATCATAAT	1440
GCAGGTGCAT GATTTGGCAG CCTCCGCATT CATTATAAAT AGTACAAGAT GGCACAATTC	1500
GAAATTTAGA CTTCTTGTTG ACCTTCAGTA ATTTTGCTTC AACAAAGTTG CGTCTAATAG	1560
AAGTAATCTG ACAATAGATA TCTTCGCCTT TGAGAGCTCC TGGTACAAAG ACTAATGTTT	1620
TTTGGTAAAA GCCGATTCCC TCACCGTTAA TTCCCATGCG CTTGATTTTT AATGGTATTT	1680
TT	1682

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

TTAACTTTGG TCAATCTTTT AAAGTCATCC TCTGTAAGCA TGTCTAACCA TTGATGTTTC	60
CCTTTATTGC TAAAATCACC AATCCGACT ACAGCTATAT CTAAATCTTT CCAACTATTT	120
TTCAAATTTT CAAAATATCT TGATTGCAAA ATACCATCTG CTAACAATTT ATTTTCTTGC	180
ACAATCGTTG CATTCATAAA TGTACACTCT CCATGAAATT TTCTAGACAT TTCATAAATC	240
AGTGTATTCA CATGGTATTT AGCGTGTATG TGA CTAGGAC CACCTGCTAG AGGATAGAAG	300
TGAACATTTT GGACACTTTT ACTGTGAATT AAATCTACTA AATTACTTAA ACTTTTCCCC	360
CAAGAAAAGC CAATTTTCAT ATTATCATCA ATTAGATTCC TAAGGACGCC TGCTGCAACT	420
TGAGAAATTC TTTCAGATAA AATTGTTGGA GTATCATCAA ATTCATTTGG AATAATTTCT	480
AAACTTTCCA AACTGTATTT TTCTTTTACA TAATTTTCCA ACTTAAACAT ATTGGTATCA	540

1264

AAATTCTCTA	TTTCAATTTT	AACAATTCCT	ACATTCCTTG	CTTCTGTTAA	CATTCTACTA	600
ATAGAGGTC	TATAAATTCC	TAATTTTGCT	GCTATTTGTG	ACTGATTTAA	GTTTTCAATA	660
TAATACAGAT	AAGCAATTTT	AGAAAGCAGT	TTATTCCTAT	CTTGATTCAT	ACACTTAACC	720
TCTTACGAAA	CTACCTTAAC	CATTATCCCA	GCATTTTCTA	ATGTAGCTAT	ATTTTGTTTA	780
GAAAGTTTTT	CGTCTGTTAT	TACTTCATAG	ACTTGACTTA	AAGCAAATCT	TCTTACTGTA	840
CCTCTTTTAT	CAAATTTACT	TGAGTCAGTT	AGGACAATGA	CTTTATCCGA	CACTGCTGAA	900
ATATATTGAA	CTACCTCACT	GCGCATTAAG	TCTTTTCCGG	TAAAGCCCAT	CTCTTTATCG	960
TAACCATCTG	TCCCAACAAA	AGCTTGACAC	ACATGAAAAG	TCTGTATCAT	TTCTTTTAAT	1020
AAAGGTCCTA	CAGTCACCTG	TGAATCTTTC	TGAAACTCAC	CACCAAGAAC	AATAACACGA	1080
CATGAATCAT	AAGCTCTCAC	AAAATTTGCT	ATAAAAAACG	AATTTGTTAC	AATCGTAACA	1140
TTTCTTTTTT	GCTTGCAAAT	TTCTCAGCA	AGTAAAGCAC	AGGTCGATCC	AGATTCTATC	1200
ATTATTGTTT	CATTATCTGA	CACCAATTTT	ACTGCTTCCT	GAACAATTTT	TCTCTTAGTT	1260
TCATAATTAA	TTGACAAACG	TACATTTAAG	TCATCTCCAC	TATTTAATAC	AGCATATCCA	1320
TGCTCTCTGT	GTAATAAACC	TTTTGACTCT	AATTTATCTA	AATCTTTTCT	AATCGTTACT	1380
TTGATACAT	TTAATTTTTC	CGATAATGTA	TTAACGTCGA	TCTTTTCATA	TTCTGATACT	1440
AATTTAATAA	TTTGTTCCAA	TCTTTTCATT	TTACACCTCC	GTTTTATTCT	ACCAAAATAA	1500
AAAGCAAAAA	ACAACAAATT	AACCTTTCGT	TCGTAATTGT	TTTTCTTTCT	TTTTTGATGAT	1560
AGGATAGACT	TATGAAGAGG	AGGAATCTTT	ATGGAAATAT	CTAAAGGAAT	TATTTTTAAT	1620
ATTCAACACT	TTTCAATTCA	TGACGGTCCG	GGTATTCGTA	CAACTGTTTT	TTTAAAAGGA	1680
TGTCCTCTGC	GCTGTCCATG	GTGTTCTAAT	CCTGAATCTC	AAAGAATGAA	ACCTGAAAAA	1740
ATGAAAGATG	CTCAACGAGA	GAAATTCACC	TTAGTCGGTG	AAGAAAAGAC	TGTAGAAGAA	1800
ATTATTACAG	AGGTATTAAA	AGACAAAGAA	TTTTACGAAG	AATCCGGTGG	AGGTTTAACT	1860
TTATCAGGAG	GTGAAATATT	TGCTCAGTTT	GAATTTGCTA	AAGCCATCTT	AAAATCAGCT	1920
AAAGAACATC	ACATACACAC	TGCCATTGAA	ACTACTGCCT	TTGTTGATCA	TGAAAAATTT	1980
ATTGATTTAA	TTCAATATGT	GGATTTTATC	TACACAGACC	TAAAACATTA	TAATTCTATA	2040
AAACATAAAA	AAGTGACTGG	GGTTTTTAAT	CAAATGATTA	TTAAAAACAT	TCATTATGCT	2100
TTTTTCACAA	ATAAACTAT	CGTTTTAAGA	ATCCCAGTTA	TTCTTAATTT	TAACAATAGT	2160
TTAGAGGATG	CAGAAAAATT	CGCTACTCTA	TTTAACTCAT	TAAATATCGA	CCAAGTTCAA	2220
CTACTCCCTT	TTCATCAATT	TGGTGAAAAC	AAATATCGTT	TATTAAATCG	GAAATATGAA	2280
ATGGATGGAA	TCAACGCACT	TCATCCwGAA	GATCTTATTG	ATTATCAAAA	GGTATTTCTG	2340

1265

AACCACCATA TTAATTGTTA TTTCTAGTTT ATTTCTTGA AATGCTCTAG CTATTTGCAG	2400
ATAACAAGCA TCTATAATAC ATACTTAACT TTTCAAAAGG TTTAGCTAAA AAATTTTAGC	2460
CAAACCTTTT CTATTTTACC TTGCTCTAGA ATTTTAAAC TGCTATACTT ATCACAAAAA	2520
AACG	2524

(2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

CGTGCTTGGG GGCTTGTGGT CAAAAGGAAA GTCAGACAGG AAAGGGGATG AAAATTGTGA	60
CCAGTTTTTA TCCTATCTAC GCTATGGTTA AGGAAGTATC TGGTGACTTG AATGATGTTT	120
GGATGATTCA GTCAAGTAGT GGTATTCACCT CCTTTGAACC TTCGGCAAAT GATATCGCAG	180
CCATCTATGA TGCAGATGTC TTTGTTTACC ATTCTCATAC ACTCGAATCT TGGGCAGGAA	240
GTCTGGATCC AAATCTAAAA AAATCCAAAG TGAAGGTCTT AGAGGCTTCT GAGGGAATGA	300
CCTTGGAACG TGTCCCTGGA CTAGAGGATG TGGAAGCAGG GGATGGAGTT GATGAAAAAA	360
CGCTCTATGA CCCTCACACA TGGCTAGATC CTGAAAAAGC TGGAGAAGAA GCCCAAATTA	420
TCGCTGATAA ACTTTCAGAG GTGGATAGTG AGCATAAAGA GACTTATCAA AAAAATGCGC	480
AAGCCTTTAT CAAAAAAGCT CAGGAATTGA CTAAGAAATT CCAACCAAAA TTTGAAAAAG	540
CGACTCAGAA AACATTTGTA ACACAACATA CAGCCTTTTC TTATCTAGCG AAGAGATTTG	600
GGCTTAATCA ACTTGGTATT GCAGGTATCT CTCCTGAACA AGAACCAAGT CCACGACAAC	660
TAACAGAAAT TCAGGAATTT GTTAAGACCT ATAAGGTAA AACGATTTT ACAGAAAGTA	720
ACGCTTCTTC AAAAGTAGCT GAAACTCTTG TCAAATCAAC AGGTGTGGGT CTTAAAACTC	780
TGAATCCTTT AGAGTCAGAC CCACAAAATG ACAAGACCTA TTTAGAAAAT CTTGAAGAAA	840
ATATGAGTAT TCTAGCAGAA GAATTAAAGT GAGGAAAGAA TGAAAATTAA TAAAAATAT	900
CTAGCAGGTT CAGTGGCAGT CCTTGCCCTA AGTGTTTGTT CCTATGAGCT TGGACGTTAC	960
CAAGCTGGTC AGGATAAGAA AGAGTCTAAT CGAGTTGCTT ATATAGATGG TGATCAGGCT	1020
GGTCAAAAGG CAGAAAACCT GACACCAGAT GAAGTCAGTA AGAGGGAGGG GATCAACGCC	1080
GAACAAATTG TTATCAAGAT TACGGATCAA GGTATGTGA CCTCTCATGG AGACCATTAT	1140

1266

CATTACTATA ATGGCAAGGT TCCTTATGAT GCCATCATCA GTGAAGAGCT CCTCATGAAA	1200
GATCCGAATT ATCAGTTGAA GGATTCAGAC ATTGTCAATG AAATCAAGGG TGGTTATGTC	1260
ATTAAGGTAA ACGGTAAATA CTATGTTTAC CTTAAGGATG CAGCTCATGC GGATAATATT	1320
CGGACAAAAG AAGAGATTAA ACGTCAGAAG CAGGAACGCA GTCATAATCA TAACTCAAGA	1380
GCAGATAATG CTGTTGCTGC AGCCAGAGCC CAAGGACGTT ATACAACGGA TGATGGGTAT	1440
ATCTTCAATG CATCTGATAT CATTGAGGAC ACGGGTGATG CTTATATCGT TCCTCACGGC	1500
GACCATTACC ATTACATTCC TAAGAATGAG TTATCAGCTA GCGAGTTAGC TGCTGCAGAA	1560
GCCTATTGGA ATGGGAAGCA GGGATCTCGT CCTTCTTCAA GTTCTAGTTA TAATGCAAAT	1620
CCAGCTCAAC CAAGATTGTC AGAGAACCAC AATCTGACTG TCACTCCAAC TTATCATCAA	1680
AATCAAGGGG AAAACATTTT AAGCCTTTTA CGTGAATTGT ATGCTAAACC CTTATCAGAA	1740
CGCCATGTGG AATCTGATGG CTTATTTTTC GACCCAGCGC AAATCACAAG TCGAACCGCC	1800
AGAGGTGTAG CTGTCCCTCA TGGTAACCAT TACCACTTTA TCCCTTATGA ACAAATGTCT	1860
GAATTGGAAA AACGAATTGC TCGTATTATT CCCCTTCGTT ATCGTTCAAA CCATTGGGTA	1920
CCAGATTCAA GACCAGAAGA ACCAAGTCCA CAACCGACTC CAGAACCTAG TCCAAGTCCG	1980
CAACCAGCTC CAAGCAATCC AATTGATGAG AAATTGGTCA AAGAAGCTGT TCGAAAAGTA	2040
GGCGATGGTT ATGTCTTTGA GGAGAATGGA GTTTCTCGTT ATATCCCAGC CAAGGATCTT	2100
TCAGCAGAAA CAGCAGCAGG CATTGATAGC AAAGTGGCCA AGCAGGAAAAG TTTATCTCAT	2160
AAGCTAGGAA CTAAGAAAAC TGACCTCCCA TCTAGTGATC GAGAATTTTA CAATAAGGCT	2220
TATGACTTAC TAGCAAGAAT TCACCAAGAT TTAAGTGATA ATAAAGGTCG ACAAGTTGAT	2280
TTTGAGGCTT TGGATAACCT GTTGGAACGA CTCAAGGATG TCTCAAGTGA TAAAGTCAAG	2340
TTAGTGGAAG ATATTCTTG	2359

(2) INFORMATION FOR SEQ ID NO: 244:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1052 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

TTCTTTCTGC TATAATCGTA TAAAATACTT ACTTTAGGAG TTCTTATGAA AGTTGTTAAA	60
TTTGAGGTA GTTCTCTTGC CTCTGCTAGT CAATTAGAAA AAGTTTTTAAA CATCGTCAAA	120
AGCGATTCAG AGCGTCGTTT TGTAGTCGTT TCTGCGCCTG GTAAACGCAA TGCTGAAGAT	180

1267

ACTAAGGTTA CGGATGCCCT GATTAAATAC TACCGCGACT ATGTTGCGGG TAACGATATT	240
AGCAAGAACC AAAGCTGGAT TATCGACCGC TATGCTGCTA TGGTTAGTGA ATTGGGACTA	300
AAACCAGCTG TGCTAGAAAA AATTTCTAAA AGCATTCACG CCTTGGCCAC TCTTCCTATT	360
GAAGAAAATG AATTTCTCTA CGATACTTTC CTAGCAGCCG GTGAAAATAA CAATGCCAAA	420
TTGATTGCTG CCTACTTTAA CCAAAATGGT ATCGATGCAC GCTATATGCA CCCTAGAGAA	480
GCTGGGATTG TGGTCACAAG TGAACCTGGT CACGCTCGCA TCATTCCATC AAGTTATGAC	540
AAGATTGAAG AATTGACAAA CACCAATGAA GTCCTTGTC A TTCTGGTTT CTTTGGTGTC	600
ACTAAGGAAA ATCAAATCTG TACTTTCTCA CGTGGAGGTT CTGATATTAC AGGTTCTATC	660
ATTGCTGCTG GTGTCAAAGC TGACCTCTAT GAAAACTTTA CGGACGTTGA TGGTATCTTT	720
GCAGCCCACC CTGGTATTAT CCACCAACCA CACTCGATTC CTGAGTTGAC CTACCGTGAA	780
ATGCGCGAGT TGGCCTATGC AGGCTTCTCA GTCCTTCATG ACGAGGCTCT TCTTCCTGCC	840
TACCGTGGAA AAATTCCTCT GGTATCAAG AATACCAACA ACCCTGACCA TCCAGGTACT	900
CGTATCGTTC TAAAACACAG TAATGATGAA TTTCCAGTTG TGGGAATTGC TGGTGACTCA	960
GGCTTTGTCA GCATTAACAT GTCGAAATAC CTCATGAACC GTGAGGTTGG ATTTGGCCGC	1020
AAGGTTCTGC AAATCCTGGA AGAACTTAAC AT	1052

(2) INFORMATION FOR SEQ ID NO: 245:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 855 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

CCCTCGAAAA CTAAGCCGAT GAAGTCAGAA CACTTCAATC CTGTTCTGTA CTGGTGGGAA	60
AATCGTGAAG AGATTCTGGA AGGTAAGTTC TACAAATCTA AATCATTTAC ACCTAGTGAA	120
TTGGCTGAGT TGAATTATAA TTTAGACCAG TGTGACTTTC CAAAAGAGGA AGAGGAAATC	180
TTAAATCCCT TTGAGTTGAT TCAGAATTAT CAAGCGGAAA GAGCAACTTT AAATCATAAG	240
ATTGATAATG TATTAGCTGA TATTTTGCAG TTGTTGGAGG ACAAATAATG ACACCAGAAC	300
AACTTAAAGC AAGTATTCTC CAAAGAGCGA TGGAAGGGAA ATTAGTGCCG CAAAATCCCA	360
ATGACGAACC TGCAAGTGAA TTATTAAAGA GAATTAAAGC TGAAAAAGAA AACTTATCA	420
GTGAAGGAAA AATCAAACGA GATAAAAAGG AACTGAGAT ATTTCTGTGGT GATGATGGGA	480

1268

AACATTATGG GAAGTTTGCT GATGGAAGCA CTCAAGAAAT TGATGTTTCCT TATGATATTC	540
CTGATACTTG GGAGTGGGTG AGGATAAAAT CAATTTATTG GAATTTTGGG CAAAATAAGC	600
CAGAGAAATC CTTTAGGTAT ATAGATACGT CTAGTATTGA TAGAAAAAAG AACATAATCA	660
ACTACAAAAA TCTACAATAT CTTTCACCTG AACAGCGCC TTCCCGTGCT AGAAAATTAG	720
TTTCGCAGAA TAGTGTCTTA TTTTCAACAG TTAGACCATA TCTAAAAAAT ATTGCTGTAG	780
TTAGAGAACT TAAAGAGTAT TTGATAGCTA GTACAGCATT TAATGTTTTG GGATACTTTA	840
CTTAACGAAA CATAT	855

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

TTTAGGAAGG CTATCCGTAA TTTTACAAAG GATTTAGATA TTACAGAGGA ACATTTAGAT	60
ATTATCAAAA GAGAGATGTT TGGCGAATTT TTCAGTAGCA TGAAGTCTCT TGAATTTATT	120
GCAACGCAAT ATGATGCTTT TGAAAATGGT GAGATAATTT TTGATTTGCC GAAAATTTTA	180
CAGGAAATTA CTTTAGAGGA TGTCCTTGAT GCTGGACATC ATTTAATAGA TGATGGTGAC	240
ATAGTTGATT TTACAATATT CCCATCGTAG TAACCTATTA TAATAGACAC TAGAAAGAAG	300
GGATGACAAG TATGAGAAAA AAAACAATTG GAGAGGTTTT ACGATTAGCT AGAATCAATC	360
AGGGATTGAG TTTAGATGAA TTGCAGAAAA AGACAGAAAT CCAGTTAGAT ATGTTGGAAG	420
CAATGGAAGC AGACGATTTT GATCAACTTC CAAGTCCTTT TTACACGCGT TCTTTCTTGA	480
AAAAATATGC ATGGGCTGTT GAGTTAGATG ACCAAATTGT TTTGGATGCT TATGATTCTG	540
GGAGTATGAT TACTTATGAG GAAGTAGATG TTGATGAAGA TGAGTTGACA GGTCGTAGAC	600
GTTCAAGTAA GAAAAAGAAG AAAAAACAT CATTTTTACC TTTATTTTAT TTTATCCTGG	660

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1805 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

1269

CCGGTTGCAC	AGGATCGTGC	ATAGTCAACT	CTTCAAGTAT	AGCATATCTC	CTATTTTCTT	60
ACAAGTAATA	ACACCTAAAA	TGAAGCTTTT	TCTTTTACTT	TTTTCTGCCA	AGAGGCAAAA	120
AGCATGCTGA	GGTAAAAAAC	GCTCATCATA	ATAGGAACAC	CAAGAATGGT	CTTTTCATGA	180
TAGAAAATCG	TCAAATAGGC	TGAAAAGACA	ACGCCAAGGA	CAAACTACT	AAGCAGGCTA	240
ACAAATATGA	ATCCTTCACG	CAAAAAAGGA	GTGTGCTTGG	TTCGGAAATA	ATCTCCAAAA	300
GCCAGCATGG	TCCGTTTGAT	ATTCCCTGTC	ATAAAAGCGT	TATTATAGGC	AATACCCGAC	360
ACTTCTCCAA	AAGCAGTTGT	CACCAGTCCC	ATACAGAAGG	CCAAGGGCGG	CACTAGATAG	420
ATATTATCCA	CAGTTTGCGG	CACAAAAGCA	ATAATGATTG	ATAAGATTGC	CAAGGGAATC	480
AAGGACAGAA	TAGGTTTTTT	CACAATTCTC	AATTTTTCCT	TATAAATCGT	TAATAAAAAG	540
ACTCCCATCA	TAAACGCTAG	CAAGGTGAGA	ACCTTGTCCT	TAACATCCGA	AACATTATTT	600
TTAATTAATT	CTACTGAAAG	AAAGACAACA	TTTCCAGTTT	GTCCAGCTAC	AAGGGTATTC	660
CCGCGAACAA	TAAAAGTGTA	AGCATCCACA	TATCCAGCAC	AAAACGTCAA	AAAAAGTGCT	720
AACCTTTTAG	ACTGACGTGA	TATTTTCTCT	ATAGGTAATA	ACCTCATTTT	ACCTCCCATT	780
GTATTTTCTC	TTAGAAATAT	TGTACCATTT	TCTTTCTAAA	AAATCGTAGG	CTACCATTTA	840
GATTTTACTA	TTAGCATAAA	AATAATAATA	GACAACTATT	TATCCAAAAA	TAGATAGATG	900
TAACATGTTT	GCAAACAAAG	CATACGAACC	TTTAGTAAAA	TCATTTCCAT	GAAACTAGAA	960
TAGAGCCCTC	TTAGCAAAAA	TCATTATTTT	AATTTATTTT	TAATCACTCC	TTGACATAAA	1020
TAACCTCTAC	CAATAAAAGA	CTATGTCTTA	AAAAAATGGT	ATAATAAAAT	CAATACTTGG	1080
GCTTGATGGC	TATGCTACTA	ATAACAATTA	GGAGAGAAAA	TCAGGCACTT	GTTAACAACA	1140
AGGATTATCC	CCTTGAGATG	AAAGGAACTT	TAGAAATCTT	ATGATGAACA	TGCAAAACAT	1200
GATGCGTCAA	GCACAAAAAC	TTCAAAAAACA	AATGGAACAA	AGCCAAGCTG	AACTTGCTGC	1260
TATGCAATTT	GTTGGCAAAT	CTGCTCAAGA	TCTTGTCCTA	GCGACCTTAA	CTGGCGATAA	1320
GAAAGTTGTC	AGCATTGATT	TCAATCCAGC	TGTCGTTGAC	CCAGAGGACC	TTGAGACTCT	1380
TTCTGATATG	ACCGTTCAAG	CCATCAACTC	TGCTCTTGAA	CAAATCGATG	AAACTACCAA	1440
GAAAAAACTG	GGTGCTTTTC	CTGGGAAATT	ACCTTTCTAA	AAACAAGGAG	CTAGAACAAT	1500
GCTTGTCGAT	AACAAAGGCT	AAGAAAGGTG	CAAAAATGAC	TCTATAATAT	TTGTAGTGGG	1560
TAAATCCCCCT	ATGGATATTA	TGGAGCCTAT	TTTTGTGTAG	AAAAAAGTCC	CATATGACCT	1620
ATAATGAAAA	GCGACAAAAAC	AACTCATTAG	AAAGAATCAT	ATGGAACAAT	TACATTTTAT	1680
CACAAAATTA	CTAGACATTA	AAGACCCTAA	TATCCAGATT	TTAGACATCG	TCAATAAGGA	1740

1270

TACACACAAG GWAATCATCG CCAAAC TGGr CTATGAAGCT CCATCTTGTC CTGAGTGCGG	1800
AAGTC	1805

(2) INFORMATION FOR SEQ ID NO: 248:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

CTGCATCTAG TTTGTTTCTC CCTACAGTTT TAGCTAGACA GATTGGAGAT TATGATTAA	60
CGTCGCCGCG TTGGGGTTCG GATACAACTA GTGAGCTTGA GAAAGAAAAC TCCTCTGCTG	120
GAATTAATAA TAATGACAGC ACTGGTGGCG GTAAAAGGTT AAATACCTCT ATTCGTAGCG	180
CCTATAGTGG GTCAGATATT ACCCCGGTAT ATTCATTGGG GTCTGGCTCT AGGATTGTCA	240
TGTACTATAA TGGAGGTGGT GACAATTATA TTGGTTCTGG TACTAGATTA GCTATGGCGC	300
CACAATTTGG AAATCATGTA AGAATTCATA CTTCAGGTTT TTGGAATCCA GATTCTTATT	360
AACTTACTTG TCAGAGTAAG CCTTAAAGAT GGTTGATTGT GGGTGTAGCA TGAAAAAGA	420
ATGCTACACC CTATTTTAT TATAAGGAGG AGTAAGGATG GAATTTTCA TTTGTAATCT	480
TGTACGAGTC GTTCAATCAC CTCGATTTTA TATGTCTTTA TTTTGGACCC TTCTTTGCAT	540
GAGTTTAGGA AATTCCTTG CTTTCAATGG TATTTATAAA ATTGAAGGTT TATCGATTTT	600
TTTTGCCGCT TCTTCTATTC GAGGATTTTC ACCGATTAGC CTAGTAGCTG CACTTATCTG	660
TACACTGCCC TATTCTAGTC AGATAATAGA GGATGCTGAG AGTCATTTTC TAACAGCACA	720
ATTGTGTCGA ATTTCTAAAA AGAAGTATCT GGCTATTGTG GGTAGTACTG TAATTATTTT	780
TTCTTTTCTA GTCTTTTTC TCCCCTATTT ATTATTATTA GGAATTAATC TTTTAGTGAC	840
TCCTTATCAG GAAATTTATA TTGGAGATTA TAGTGGTGCC TTAAAAGAAT TATTTGATTC	900
CAATCAGTTT CTCTATAGTC TTGTAACGAC TCTCTGGTAT GGAGTTTGGG GCGCTGTGTT	960
CTCTATTTTT GGACTAGCTA GTGCTTTGCT AGTGAAGAAA AAAATAGGAG CTATTTTCAT	1020
CCCAGTTGCC TATATGATGG TTGGTGGTAT TTTTGGGCT ATTTTAGGGC TATCTTACTT	1080
AGAACCTGTG ACAACGCTAG CTTTGGGATA TCAGAAAGAT ATCAGTCTTT CCTTAGTTAG	1140
TGCTCATCTT GCTTTTATTT TATTTGTTAG TTGTTTGGTT GTTTATGGTA CATTTTTTCT	1200
ACATTCAGAG GACTATGTAT AATGAAACAA TTTGTTCAAT TTTATAAAAA AGATTTCTTA	1260
GCAGTATTGG TTTATTTTAT ATTACTGCTA TCCTGTGTTT TATCTAGTAC AGTATATTTA	1320

1271

TTGCGCtGTC	GCCAATATTC	AATCCATCCA	AATGTATTAG	AATGGATCTT	AGTTTTACTT	1380
CAAGATATGA	CGACTGGAGT	ATATTGCTTT	CCGTTACACAT	ATATATTGTT	CTTTTTTTAT	1440
TTGATGAATA	ACTATTTTAA	TAGGTTGGAG	TGTCGCATTC	GTCTGAAATC	AATTAAGCAC	1500
TTTACCAGTT	TTAGTTTCAA	ATTAGCAGCT	CTTAGTACGG	GGATTGAC	GGCGACTTTA	1560
TTTTTATTGA	TTTTTCTAAT	TGCATTTAGT	AATGGTTTTA	GCTTCTCTTT	GGAGATAAAG	1620
GAGGTTGATT	TTTTAAGAGA	ATTTTATGGT	ATAAGTATTG	CAAACAATGC	TAGTTTCTTT	1680
ATAGGATTTT	TTTTCTCTTA	TATAGCATAC	TATTTCTTTT	TATCCTTACT	TACTATTAGC	1740
AGTTTTTCTT	GGTTTAAAAA	ATCAAACATG	AGCTTAGTAT	TTCTGTTTAC	TTTTTTATTT	1800
GTAGAATCCT	TATTCTGGAT	TTATCAGTTG	GACAATGGGA	TAATTGGATT	ATTGCCAATT	1860
TTTCAGTATA	TGGTAAATTC	CAATCCGTAT	GCATTGATTT	ATTGGCTTAC	ATTACTATCT	1920
ATCATAATTC	CATTGACTGT	ATTTTCTGTT	CATAGAACT	GGAGGAGAGT	GTAAAAGTTG	1980
GAAATGGGAA	AGTTAAGTAG	TCACATGTGG	AGGTTGAATC	AGATAATCTA	TACCAAGTAC	2040
TTTTGGGGTT	ATGTTCTTTT	TTGGATATTG	ATTTGTTTAG	GATTATGGTA	TTGGTTAGAA	2100
GGAAATGATA	GACTTGTTAT	AGAAATTTTA	AAAGGGCCTA	ATCTGAGTCA	AAACTCTTTT	2160
TTAGTCTTAT	CTATATGGTT	GCTTCATTGG	TTTATTATTC	ATACATTTT	TCTAGCAGTT	2220
GTATATCGTA	GAAGAGCATC	CGATTTCTTT	ATGGAAGTGA	TTCGATTTTC	TTCTATTAAG	2280
CTCTGGATTA	GGTATCAGAT	TTGGACCTGT	TTTCTTTATG	GACTCATTTT	AATCATGGTA	2340
AAAGTTCTAG	TGATTCAATT	TATGTTACAG	TTACCAAAT	GGGATATAGG	AGTTTTGTTT	2400
ATAGTTGATT	CTTTGAATGC	TTGTGTGTTA	GTCTTGTTTT	GCTTTATGTT	ATACGCACTA	2460
GGAGCGAATG	TACAAATGAA	CTTTGCTTGC	GTTAGTTTCT	TTTTACTCAT	GATTGG	2516

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1364 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

CGGTGTTTTT	TTGTAAATTT	TCTAGCACTT	GTATGGTAAA	ATAGATACAG	GTGTTTCATTA	60
AACTAGACTA	AAAACCTATT	TAAGCAGGCA	AAATGAAGAA	ATACCAACAA	TTATTTAAGC	120
AAATCCAAGA	AACCATTCAA	AACGAGACTT	ACGCTGTCGG	AGATTTCCCTT	CCTAGCGAGC	180

1272

ACGACCTTAT GGAGCAATAT CAAGTGAGTC GTGATACCGT CCGAAAGcCC TGTCTCTCCT	240
CCAAGAGGAA GGATTGATCA AAAAGATAAG AGGGCAAGGT TCTCAAGTCG TCAAAGAAGA	300
AACCGTCAAT TTCCCTGTAT CCAACCTAAC CAGCTACCAA GAACTAGTTA AAGAACTTGG	360
ACTGCGCTCT AAAACCAACG TGGTCAGTCT GGACAAGATT ATTATTGATA AAAAATCCTC	420
ACTGATAACC GGTTCCTCCAG AGTTTCGGAT GGTTCGGAAG GTGGTCCGCC AGCGTGTTGGT	480
GGATGATCTG GTATCCGTTT TGGATACGGA CTATCTGGAT ATGGAACTCA TCCCAAATCT	540
CACTCGCCAA ATTGCTGAGC AGTCTATCTA TTCTTATATA GAAAATGGCC TCAAACCTCCT	600
TATTGATTAT GCTCAGAAGG AAATCACCAT TGACCACTCA AGCGACCGAG ACAAGATTCT	660
CATGGACATT GGCAAAGACC CTTATGTCGT TTCGATTAAA TCAAAAGTCT ATCTCCAAGA	720
CGGACGCCAA TTTCAGTTTA CCGAAAGTCG CCATAAGTTA GAGAAATTTA GATTTGTAGA	780
TTTTTGCAAAA CGCAAGAAAT AAAAGACTGA GACACCAGAT CTCAGCCTTT TTCGGCTCTA	840
TAATATTTGT AGTGGGTAAC CCCCCTATGG ATATTATGGA GCCTATTTTG TGTAAGAAAA	900
AAGTCCCATA TGACCTATAA TGAAAAGCGA CAAAACAACT CATTAGAAAG ATTCATATGG	960
AACAATTACA TTTTATCACA AAACTGCTCG ATATTAAAGA CCCAAACATC AAGATTCTAG	1020
ACATCATCAA TATGGATACC CACAAAGAAA TTATCGCTAA GCTGGATTAT GAGGCTCCAT	1080
CTTGCCCTGA TTGTGGAAGT CTAATGAAGA AATATGACTT TCAAAAACCG TCTAAGATCC	1140
CTTACCTCGA AACAACCTGGT ATGCCTACTA GAATTCTCCT TAGAAAGCGT CGTTTCAAGT	1200
GCTATCATTG TTCTAAAATG ATGGTCGCTG AAACTTCTAT CGTCAAGAAG AATCATCAAA	1260
TTCCTCGTAT TATCAACCAA AAAATTGCGC AAAAGTTGAT TGAGAAGATT TCTATGACCG	1320
ATATTGCTCA TCAGCTGGCC ATTTCAACTT CAACTGTCAT TCGG	1364

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

CCATGAAGAC CGCTTGGAAT TGGAATGGCA CAAGTCTTTG TTGAATGGTC TATTCCCATT	60
GACAATCGGT GGAGGAATTG GACAATCTCG TATGGCCATG TTCCTACTTC GCAAGAGACA	120
CATCGGAGAA GTGCAAACAA GTGTTTGGCC TCAAGAAGTC CGCGATACTT ACGAAAATAT	180
TTTGTAGAGA ATCGAACCGC AAGGTTGCGT TTTCTTTCTC TTTTGTCTA TAATTTGGTA	240

1273

TAATAAACAG TATGAAAATC GTATCAGGAA TCTATGGGGG ACGTCCCCTC AAGACACTAG	300
AAGGCAAGAC GACAAGACCT ACTTCGGATA AGGTAGGGG AGCCATTTTT AACATGATTG	360
GTCCCTACTT TGAAGTGGGA CGAGTCTTGG ACCTTTATGC AGGTAGTGGT GGTTTATCTA	420
TCGAAGCAGT ATCGCGTGGC ATGTCCAGTG CTGTTTTGGT GGAGCGAGAC CGTAAGcTCA	480
GACCATCGTG GCTGAAAATA TCCAGATGAC CAAGGAAGTT GGAAAATTTT AACTCCTCAA	540
GATGGATGCA GAAAGGGCAT TGGAACAGGT ATCTGGGGAA TTTGACCTCG TTTTCTTAGA	600
CCCTCCCTAT GCCAAGGAAC AAATCGTAGC AGATATTGAA AAAATGGCTG AGAGAGAGCT	660
TTTTTCTGAA GATGTTATGG TTGTGTGCGA GACGGATAAA GCCGTGGAAC TTCCAGAAGA	720
AATTGCCTGT CTGGGTATCT GGAAGGAAAA GATTTATGGA ATTAGTAAGG TGACAGTCTA	780
TGTCAGATAA GATTGGCTTA TTCACAGGCT CATTTGATCC GATGACAAAT GGGCATCTGG	840
ATATCATTTGA ACGGGCGAGC AGACTTTTTG ATAAGCTTTA TGTGGGTATT TTTTTAATC	900
CCCACAAACA AGGATTTCTC CCTCTTGAAA ATCGTAAACG GGGGTTAGAA AAGGCTGTGA	960
AACATTTGGG AAATGTTAAA GTCGTGTCTT CTCATGATAA ATTGGTGGTC GATGTCGCAA	1020
AAAGACTGGG GGCTACTTGC CTAGTGCGAG GTTTGAGAAA TGCGTCGGAT TTGCAATATG	1080
AAGCCAGTTT TGATTACTAC AATCATCAGC TGTCTTCTGA TATAGAGACT ATTTATTTAC	1140
ATAGTCGACC TGAACATCTC TATATCAGTT CATCAGGCGT TAGAGAGCTT TTGAAGTTTG	1200
GTCAGGATAT TGCCTGCTAT GTTCCCG	1227

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3652 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

CCGGTCAAGT TAAAAACGCT ATTTCTTCCC ATTTTATTTA TTTTTTAGGA GTGGTAACGT	60
ATCAAAATAG CCCAAGCGTT CTCACCCGTG TGAGTTTGAA TAATGGAACC CGTTTCCAAA	120
ACAGAAATTG GCTTTTCAAC ATAAGCTTGT AAGCTTTCTT TCATCTCTTT TGCCCAATCA	180
TCACTACCAG AATATGAAAT TCCAATCTCT GCTACAGCAC GTTCAGAAAG CGATGTTATC	240
AACTCATCTA ACCATTTTTT AAATGTTTGA GTTCCACGAC CTTTAACCAT TGGCTGCAAT	300
TCATGGTCTT TCATTTGCAT GACAGCACGG ATATTGAGAA GAGAGCTCAA CAAGCCAGTT	360

1274

ACACGGCTAA	TTCGTCCACC	TTTGACAAGA	TTTTCCAAAG	TTGAAACACC	AATATAAAGC	420
TCTGTATGGT	TTTTAACCTC	TTCTACATGA	GATAAAATTG	CCTCCATATC	TTTACCTTCT	480
TGAGCTAACT	TCGCAGCCTC	AACAACCTGG	AATTTTCAGGG	CTTGGTCAGT	GAAGGAACTA	540
TCAACAACAG	TCACATCTGC	AGTAGATAGG	CTAGCACCTT	GGCGTGCTGC	TTCTACCGTA	600
CCCGAAAGAG	CATGGGACAT	ATGAATAGCA	AGAATCTGGC	CACCATCTTT	GCATAGGTCT	660
TCAAAAATCT	CAGCAAAGAC	ACCTACAGGT	GGCTGACTTG	TTTTCGGAAG	ATTCTTACTT	720
TCTTGCATCA	ACTGAAGAAA	TTTACCTTCT	TCTTTCAAAT	CCGCATCAGA	ATAACAACA	780
TTATCAATCA	TTACAGATAA	TGGAACAATT	GTAATATCTA	ATTGCTTTAC	TAGTTCAGGT	840
TCAATAGTAA	CAGATGAATC	GGTTACAATC	TTAATTTTTG	TCATAGTATC	AATCTTTCTA	900
TTTTAGGATT	CAGATTGGTT	TCCTTACTTC	TAATTATATC	AAAAAAAAGA	TTAAAAATCC	960
TAATGGAGTC	AATCAAATTT	TCCGTAAAAT	TTGATATAAT	CAACTTATAA	GAAAAGAGGT	1020
GTCCTATGAT	TAAAAAAATT	TACCCCATTT	TTACCATTTT	ACTAGGTGCT	GCTATTTATG	1080
CTTTTGGACT	GACTTATTTT	GTAGTTCCCC	ATCATCTCTT	TGAAGGAGGG	GCGACAGGCA	1140
TTACCCTCAT	CACCTTTTAT	CTTTTTTAAA	TCCCTGTTTC	CCTCATGAAC	CTGCTGATTA	1200
ATATTCCCCT	TTTCATCCTA	GCTTGGAAGA	TTTTTGGAGC	CAAATCCCTC	TATTCTAGTT	1260
TACTAGGAAC	CTTAGCTTTG	TCCGGCTGGT	TAGCTTTTTT	TGAGCATATT	CCCCTTCATA	1320
TTGATCTTCA	AGGTGATTTA	CTAATCACAG	CCCTTATAGC	GGGAATCCTA	TTGGGAATTG	1380
GCCTTGGAAT	TATTTTAAAT	GCTGGAGGTA	CAACTGGCGG	AACTGATATT	CTAGCTCGTA	1440
TTCTCAACAA	ATACACTCAT	ATATCCATAG	GAAAACGCT	CTTTATCTTA	GATTTTGTGA	1500
TTCTCATGTT	GATTCTCCTA	ATCTTCAAGG	ATTTGAGATT	GGTTTCCTAC	ACGCTTTTGT	1560
TTGATTTTAT	TGTTTCTCGT	GTTATTGATT	TGATTGGTGA	AGGAGGATAT	GCCGGCAAAG	1620
GCTTTATGAT	TATCACAAAA	CGTCCTGACC	AACTTGCTAA	GGCGATTAAT	GATGACCTCG	1680
GAAGAGGTGT	TACTTTTATT	TCTGGTCAAG	GCTACTATAG	TAAAGAAAAT	TTGAAAATCA	1740
TCTACTGTAT	TGTCGGAAGA	AATGAAATTG	TGAAAACGAA	GGAAATGATT	CATCGAATCG	1800
ATCCTCAAGC	CTTTATAACT	ATTACAGAAG	CCCATGAAAT	CCTAGGAGAA	GGCTTCACCT	1860
TTGAAAAAGA	ATAAAAAGAG	GTAATGTCGT	GACCTCAAAA	GTTAGACTAA	ATCATCTATC	1920
TTTTGGGTTA	CAGACAACCT	CTTTTTTATT	TTATTTACTC	AAGCTCTTAA	GACCAATTCC	1980
GAGTTACTTC	TTCATCAGCC	TTTAACTGAT	CCACTAATTG	GTCAACTGAG	TCAAATTTGG	2040
TCATATCTCG	AATGCGATCA	AGCCAATAAA	CCATGACGGT	TTCCCCATAA	ATATCTTGAT	2100
TAAAATCAAA	AATATTGACT	TCAAAACGTG	CTTCTTCTCC	ATCAAAGGTC	ACATTTTTC	2160

1275

CGACACTAGC CATAGCACGA TACTTCTGTC TTTGAATCTC AACATCAACA ACATAAACGC	2220
CATCTGCTGG CATATAAGTA CGGTCTAAAA GCACTAAATT CGCTGTCGGA TAACCAATTG	2280
TACGACCACG AGCATTACCA TGAACCACCA TACCTCTTGA TGGAAGCGGT GCCCCCAAAA	2340
GTTTTCTGCTG TTCTTTCACA TTTCCATCTA AAATAGCTTG ACGGATACGA GTTGAACATA	2400
TCTTTCCTTT CTCATCTTCT ACAGGTGGAA CAATGATAAC TTCTCCATCA AAGTAATTCT	2460
TTAAATCTTC TGCTGTTTTT TTGTCAGAAC CAAATGTATA ATCAAAACCT GCAACAATAA	2520
TTTTGGCATT CATAGCCTTG ATATAAGTTG CAAAGAATTC TTGTGCAGTG AGACTAGCGA	2580
ATTGACTACT AAAATCAAGG AGATATAATT CTTCTACACC TTCGCGCTTT AATTTCTTTT	2640
CACGTTACAG AGGGTTCAAA ATATGCAAAA ACAAATCTGG ATGATAAGGC TCTAAAGCGA	2700
TCTTTGGAGA TTCATTAAAG GTCATAACGA CGATAGGCAA CAAATCCTTT CTCGCAGCCT	2760
TGTTGGCAAC ACGAAATAAT TCTTGATGCC CTTTATGTAT GCCATCAAAA TAGCCGAGAA	2820
CAACGACTGA ATCAGATGGT GTGCCAATAT CTTTTTGGTT TTTTATAGGA ATAGTAATAA	2880
TCATAAAATA ATTATATCAT AGCGATAGCT ATTTCTGGAA CAGAAAATCT GAAATGTTGT	2940
TTTTTTCACA TGAAGTGTAC CTGTTTTCAA AAAGCACTTT ATTCTATCGT TGCTTAACTA	3000
TGAACCTTGC AATATTCTTC TCAAAAACCT GTAGGACATC TTCAAAATTT TGCAAGGAGT	3060
GATTAGACTT GTTCGGTAAC CATAAAGTGT CATACTATGC TTATGTATGA AAAAGCAATG	3120
CAACTAACTC CTGAGAACTT TAAATTACTA ATTGGTGCCG AAAAGGTAGA ATTTAGAATC	3180
GAGGTACACC TATGGCTGTA AAATTTACAA AATGAGACAA CTTGGGCAAG ATGTTTGAAG	3240
AATTTCTTAA ACTCCCTGAT TTGAAGCAAG TCACTTTCCC TAATGACAAA GAAAAAGCC	3300
AAAACAGCAA AGAAAACTA GATGACTGCT TTCCAACAAC TCCCATCTAG TGTGCTTCAG	3360
ACTGGGCTAT TTTTCTCTCC ATCTGTTAGC TTGGATTCTC AGACCGTTTC AGCTAAAGAA	3420
TATCTTTTCC CTTATCAGAA GGAACGGCTC AAGCCATTCA GACAAGTGAA GGGACGACAA	3480
GCCAATATTT GAAACCAGAT AGCAGTTCTT ATAGTCAATT GAAATAAAAT CTGAAGAAAT	3540
CGAGTAGGAA ACTCATATCA ATGTTTAAACA GTGTTCTATT CCAGATTCAT ACTCAATGAA	3600
AATTAAAGTG CAAACTAGGA AGTTAGCCGC AGGTGATACT TTGGGTACGG CA	3652

(2) INFORMATION FOR SEQ ID NO: 252:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 743 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

GTACCGTGGT GCCAAAGTAC AGCAAGGTTG GCTTTTGTGAC AAACAATACC AATCTTGGTT	60
TTACATCAAA GAAAATGGAA ACTATGCTGA TAAAGAATGG ATTTTCGAGA ATGGTCACTA	120
TTATTATCTA AAATCCGGTG GCTACATGGC AGCCAATGAA TGGATTGGG ATAAGGAATC	180
TTGGTTTAT CTCAAATTTG ATGGGAAAAT GGCTGAAAAA GAATGGGTCT ACGATTCTCA	240
TAGTCAAGCT TGGTACTACT TCAAATCCGG TGGTTACATG ACAGCCAATG AATGGATTG	300
GGATAAGGAA TCTTGGTTTT ATCTCAAATC TGATGGGAAA ATAGCTGAAA AAGAATGGGT	360
CTACGATTCT CATAGTCAAG CTTGGTACTA CTTCAAATCC GGTGGTTACA TGACAGCCAA	420
TGAATGGATT TGGGATAAGG AATCTTGGTT TTACCTCAAA TCTGATGGGA AAATAGCTGA	480
AAAAGAATGG GTCTACGATT CTCATAGTCA AGCTTGGTAC TACTTCAAAT CTGGTGGCTA	540
CATGGCGAAA AATGAGACAG TAGATGGTTA TCAGCTTGA AGCGATGGTA AATGGCTTGG	600
AGGAAAAACT ACAAATGAAA ATGCTGCTTA CTATCAAGTA GTGCCTGTTA CAGCCAATGT	660
TTATGATTCA GATGGTGAAA AGCTTTCCTA TATATCGCAA AGTAGTGTCT TATGGCTAGA	720
TAAGGATAGA AAAAGTGATG ACA	743

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

TTTTGGTTGA TGATACGAGG GATTTGGTGA TTCTTCTTGA CGATAGAAGT TTCAGCGACC	60
ATCATTTTTG AACAGTGATA GCACTTGAAT CGACGCTTTC TAAGGAGAAT TCTAGTAGGC	120
ATACCAGTCG TTTCAAGATA AGGAATTTTA GAAGGTTTTT GAAAGTCATA TTTCTTCAAT	180
TGGTTTCCGC ACTCAGGGCA AGATGGGGCG TCGTAGTCCA GTTTGGCGAT GATTTCCCTG	240
TGTGTATCCT TATTGATGAT GTCTAAAATC TGGATATTAG GGTCTTTAAT GTCTAGTAAT	300
TTTGTGATAA AATGTAATTG TTCCATATGA TTCTTTCTAA TGAGTTGTTT TGTCGCTTTT	360
CATTATAGGT CATATGGGAC TTTTTTCTA CAATAAAATA GGCTCCATAA TATCTATAGT	420
GGATTTACCC ACTACAAATA TTATAGAACC GAATTAATTT AATTAGAGAG CCAACTTTCT	480
AATATAGTAA TCGCGTCATA ACAAGGTATC TATCATTCAT GGAGTTCCTC CTGTATACTA	540

1277

TTAGTAAAGT	AAAAC TATTG	GAGGATATTT	TAATGCCACA	ACCTATTGTT	CCTGTAGAGA	600
TTCCACAATC	TCGTCGTTTT	GATTCTAAAA	AGAGAAATGA	TATTCTGCTT	AAAATTCGTA	660
TTGGCAAGCT	TGAAGTAAGT	TTTTTTCAAT	CTCTCAATCT	CGAAATGGTA	GAACAGCTTT	720
TGGATAAAGT	GTTGCTCTAT	GACAATTCAT	CTATCTAGCC	TAGGGCAGGT	CTATCTCGTA	780
TGTGGGAAAA	CGGATATGAG	GCAAGGCATT	GATTCATTGG	CTTATCTGGT	TAAAACCCAC	840
TTTGAATTAG	ATCCTTTCTC	CGGTCAAGTT	TTTCTCTTTT	GTGGTGGACG	TAAAGACCGC	900
TTTAAAGCCC	TTTACTGGGA	TGGTCAAGGA	TTTTGGCTAC	TATATAAACG	CTTTGAGAAC	960
GGAAACTGA	CTTGGCCCAG	TACAGAAAAG	GATGTCAAAG	CTCTCACACC	TGAACAAGTA	1020
GATTGGCTTA	TGAAGGGCTT	TTCTATCACT	CCAAAAATAA	ATTTATCAGA	AAGTCGTGAT	1080
TTCTATTGAA	ATGAGGACTT	TCTTTT TAGT	TATAATAAAG	TTAGGAAATA	AGGAGAGGAA	1140
GCCCATGGAA	GAAGATTGAA	AATCATTCAA	CAACAGAGTG	CTACAATTGA	TAGTCTCACC	1200
AATGAAC TTG	CCCTTCTTCG	TGAACAAGTG	GCTTATCTAA	CGCAAAAGCT	CTATGGAAAA	1260
TCCTCTGAGA	AAAGTGTTTG	CCCATCTGGA	CAACTCAGTC	TTTTTTGAAGA	GGAACAAAAT	1320
ATGGAAGAAG	ACTCTGACTT	ACCCAGTTGA	AAGAGAAGAA	ATCACCTATA	AACGTAAGAA	1380
AGCTAAAGGG	AAACGTCAAG	CTCTTCTTGC	CCAATTTGAT	TCAGAAGAAG	TTCATCATCA	1440
AGTAGAAGAG	AGCATTTGCC	CTGATTGTCA	GGGAGATCTA	AAAGAGATTG	GAGCAACCCT	1500
TCAACGACAA	GAATTAGTCT	TTATTCCTGC	GCAATTAAAA	CGAATAGATC	ATATCCAACA	1560
CGCTTATAAG	TGCCAAGCAT	GCAGTGATAA	AAATCCGAGT	GATAAAATCG	TGAAAGCTCC	1620
TATTCCTAAA	GCCCC TTTGG	CGCATAGCCT	TGGCTCAGCT	TCTATTATCG	CTCACACCAT	1680
CCATCAGAAG	TTTAATCTGA	AGGTACCCAA	TTATCGCCAA	GAAGAAGATT	GGGCTAAGAT	1740
GGGTTTACCA	ATCACACGTA	AGGAAATTGC	TAATTGGCAT	ATCAAGGCGA	GTCAATACTA	1800
TTTGGAGCCC	CTTTATAATC	TTTTACGAGA	AAAGTTGTTA	GAACAAGCTC	TTCTTCATGC	1860
GGATGAAACC	TCTTATCGGG	TTCTAGAGAG	TGATAGTCAG	TTGCCTTACT	ATTGGACTTT	1920
TTTGTCTGGG	AAAGCTGAGA	ATCAAGCAAT	CACGCTGTAC	CACCATGATC	AGCGTCGGAG	1980
TGGTTTAGTA	GTACAAGAAT	TCCTAGGAGA	TTATTCTGGC	TATGTTTATT	GTGACATGTT	2040
GCGGCAGTAA	CTTAGGACTT	TAGTCCTCTA	GTTCTGCCTA	TGCGATAGCA	GTCCAAGGTT	2100
TAGGAGTAAG	GCGACGCTAA	GCTTGGTAAA	CTGCGAACAG	CTAGAAGCTT	ATCGTCAACT	2160
GGAAGAAGCT	GCACTTGTTG	GATGTTGGGC	GCATGTGAGA	AGGAAGTTTT	TTGAAGTGCC	2220
CCCCAAGCAA	GCAGATAAAT	CATCCTTAGG	AGCTAAAGGT	TTAGCTTATT	GTGATCAGTT	2280

1278

ATTTTCCTTG	GAAAGAGACT	GGGAGGCTTT	GCCAGCTGAT	GAACGACTAC	AGAAACGTCA	2340
AGAACATCTC	CAGCCCCTAA	TGGAAGACTT	CTTTGCTTGG	TGCCGCCGTC	AGTCAGTTTT	2400
AGCAGGTTC	AAACTAGGAA	GGGCAATTGA	ATACAGCCTC	AAGTATGAAG	AAACCTTTAA	2460
GACTATTTTG	AAAGACGGAC	ATCTGGTCCT	TTCCAATAAT	CTAGCTGAAC	GCGCCATTAA	2520
ATCATTGGTT	ATGGGACGGA	GTAAAAGAGT	CCAGTGGACT	CTTTTAGCCT	GAGCTCAGTT	2580
TAAAAAAGCG	AGGGTGGTTA	TTTTCTCAAA	GTTTTGAAGG	AGCTAAAGCA	AGAGCTATTG	2640
TTATGAGCTT	GTTGGAAACA	GCTAAACGTC	ATCAATTATA	GTGCGTTGAA	TCTATAACAG	2700
TACGCATCGA	CTGCTAAAAC	ATTTCTATAA	ATCAATTTTC	CTTTCCTAAT	CGATTTGTTC	2760
ATATCTTATT	TCAATCCATT	ATAAATAGCG	AGAAATATCT	ATCCTATCTT	CTAGAATGTC	2820
TTCCAAACGA	GGAAACTCTC	GTAAACAAAG	AGGTTTTAGA	GGCCTATTTA	CCGTGGACTA	2880
AAGTTGTACA	AGAAAAGTGC	AAATAAGAAA	TCTCCAGATT	AGGAACTATC	CGTGAGTTCT	2940
CTAGTCTGGA	GATTTTTCAA	TAGACTTCGT	TATTGGACGG	TTACAATTTA	TTATATGAAA	3000
ATCCCATATT	ATTCTCCAAT	TCTATATTTT	ACCTTTCTAA	ATGTATAGAT	TAACCTACCTA	3060
ATTATAGCAT	ATAACGCAGA	TTCCTTTCAA	TCGTATGATT	TACTGCATTA	AATTAAGTAA	3120
AAAAATAAAG	GCAGTCCGAA	GACTGCCGAT	ATTTATCTCT	CATCTCTTTA	ATTATGGTAA	3180
GTAAATAAAT	AATTTCCCTA	AAGATATGGA	AATTATTAAT	ACTATAAATA	CATATTATAA	3240
AGTTTATAAA	TACTGTAAAA	ATCCTGAAGT	TAATTTTCTA	ATAAATATCA	ATATGTGTTA	3300
GTATCTTTTA	AATTTTTAGA	CAATTTACTA	GTTCTATAGA	CATGTTTAAC	AGACTCTATT	3360
TTACAATTCA	AAAATTTTCA	CTGCCACTTC	ATTTAAAAAT	TCTATATCAT	GGGAAACAAT	3420
AAAAATTATT	TTATCCATGG	TTTTTATACT	ATTAATCAGT	TCAGATATTT	TTATCATATT	3480
GGAATAATCC	ATACCACTTG	AAGGTTTCGT	AAAAAAGACA	AATGGAGAAT	TCTTGCACAT	3540
AACAGATGCT	ATTGCAAGCC	TTTGCTTTTG	CCCTCCTGAT	AAACTCATCG	GATGCCTTTC	3600
AATAAATTCG	TCCAGGCATA	AATCTTTTAA	CCCAAATCAT	TCATACCTCT	CTCAACTAGA	3660
TGTAACCTAC	AAAACCCCTG	ACCTCATGAG	CCACTTTCTT	CCTCCTCATG	AGGTCAGTTT	3720
TACTTTCTGC	TGTTCCAGTA	TCGTTTTTCC	TCGCTAGATT	TCCTCAAAAG	GGCAGACTCC	3780
TCCCTTGATT	CGTCACACGA	TTTTTTTCATC	TCGACTGTTT	TTTAATGCAT	CATTAACGAC	3840
GCTTTTCTTC	TAGGTGGTTC	ATAAGGAACA	GGAAGATTCA	GGTTGACTTT	TCTAATCCTA	3900
GAATAAAGTG	CTGAAAACAA	TTCGGAATAG	GCATAGAGAC	TAGACAATTT	GAGGAGCTGC	3960
TTGCGTCCTG	TTCGAACACA	TTTTCCCACC	ACGTGAAGAA	AAAGATGGCG		4010

(2) INFORMATION FOR SEQ ID NO: 254:

1279

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

ATGCATCCGT TTGTCAAGCC TAAATTGTAA TTTTTTTTCAA TTAAAACAG AAAAACCCAG	60
GAAAATGACA TAAAAATATC ATTCCTAGGC CTATTTATGC TATTTCTCTC TGAAAAATAT	120
GAGTATTCAG TCGGTCAAAT GAAGCTGAAC GAACTCATTT TCCCTCGCCT AATTCAATGA	180
TTCGATGACA TTGTTGGGCT ACATAAGCAT CGTGGGTCAC GATAATGACT GTTTTCCCCT	240
CTCGATTCAT CTCTAAGAGA AACTTCAAGA CCAAATCTCT ATTTTCAGGA TCCAGAGAAC	300
CTGTCGGTTC ATCGGCTAAA ATCAGCTGGC TGGGTTTTAA GATGGCTCTA GCAACTGCAA	360
TTCGTTGTTG TTCGCCCCCA GACAACTCGG AGACCCTTTG ATGCAAAGTA GCTGATAAAC	420
CTACTCTCTC TAAAATCTCT TCCACCTTTT TGAGCTTGTC TTTCTTAGGC AATTTACAT	480
ATTTACAGCGC CACATGAGAT TGTACTCGAC CGTTTCATCA TCAATCAGGG CAAAATTTTG	540
AAACAGATAA GAGATATGTT CACGGATTAT TGTGTGCGAC TTAGCAGAAT TAACCGCTAG	600
ATTTGTCTGA CCAAAAATCT CATACCGTCC GCTATAATCA CCATCTATCA AACCCAATAA	660
ATTTAACAAG GTCGACTTCC CACTACCACT CTTACCAACA ATAGCTACCA AATCCCCCTG	720
ATCAATCCTG AGAGATAAGT TATCCAAAAT CACTTTTCCC CCAATGGTTT TGGTAATATT	780
TTTCAACTCA ATCATAAGAT GCCCCCTTTC AATAACTCTA CTAGACTTCT TTTCTCCATC	840
CTAGAAGCTA AGCCTAGCAC AAATAGTATA TCCAGACATG TAAAACCTGC AAACAGTAGA	900
AGTGGTAAGA ACGCATGGGC AAAGAAAATC AAGACTAGAA GAGGGAAACT ATAGCCCAGC	960
AAGAGCAGAA CGAGGAGAGG ACGGTAGCGA TCGACCAGTT TCCACCCCAT AAACCTTCTTG	1020
GTAATGATAT CCCTGCGCTT CAATAAGAAA GTTGTTACTA GTAAGAAGTA GGAAATCATC	1080
ATGCTAAGGA GACCAAACAA AGCAAAGAGT AGGTTAAAAT TCCGAACAGC ATCTCGATAA	1140
GAATCCACTT TCTCTTGTTG AATGGCTTGA ATAGATGAAA ATTTTAAATA ATTTCCATCT	1200
GACAATTTCT CAACTAACTC TGTAATCTCT TTTTGATGTT GAACCGTATT TTCAATTTTA	1260
ATCGGATTAT TTAAGCCAGT TGTGACAGG GAGGCTTTCT CATCCCACAT CATATCAGAA	1320
TCATTGACCA AGCTAATAAT TGGATTGGAG AGATTTTCCT TTCGCTTATC ACTATATGGG	1380
AAAAATGACC AATCTCCTTC ATAATAGGCA ATCTCGACAT CCATCTCCTC TATCGTTCGT	1440

1280

TTTTGCTGCT	CTTCATACTT	CATCGAATGA	AAGGCAATTA	ACTTCCCCAA	GAGCTGATTT	1500
TTATCTTCTT	CACCTTTCGT	ACTTGCTGGC	ATCAAAATAA	CTTTTTTAAAT	ACCGGTATTT	1560
GGTAGCTTGA	ATCCCTTGCT	CTTTAGAAAA	TTGCGATTGG	CATAGTAAAC	ATCCACCGTA	1620
TCTGTAACT	GATATTGCTG	AATCTGTTCT	GATTGGACAA	AATTTTTTAC	AGGAAGACTG	1680
CTACTCTGCA	CATAGCCCCG	CTGCGTTTTT	TCTACCAAAT	CCTGATAAAA	TCGATAGAAA	1740
TAATCTGTAG	ATTTCCCTGA	CCCTGCTAGC	TCTTCTTGCC	ACAGATTATC	ATTGAGTTTG	1800
AAGGTTTCTA	AGGTCAGGTA	ATTACCTTGA	CTTACCCACT	GTTGCTGATA	AGCAAGTTCT	1860
TTGTTTTCTT	GTTCTAACT	TCTGCCCACC	CCAATCAGTA	AGGCCGTCAG	TAAAATAGTT	1920
GTCCCTATTT	TCATCACATA	ATTGAAGATA	AGACCAAATT	TGAAAGATGA	AAAACCTTTC	1980
AGCAGAGAGC	TGATTGTCAT	TTTTTGGATT	AAGAGGTAAG	TCAACCAACT	GATAAAGAGA	2040
TAAAGCTGCA	ACAGCAAAAA	ATGAGACAAC	CACAGCATAG	GAAACAAATC	TTTTGGCTTA	2100
TAATCAAGCA	AGAAAAACAC	GCCTAGATTG	ATCACAAGAG	CCCCACCTAG	GAGGAGGTAA	2160
AGGTTGCCTT	TTACAACATC	AGCTAAAACA	GCCCTATCTT	GAAAACCAAG	TAATTTTTGT	2220
ACCCCAACTC	TTTTCATCTC	CATCATCGGT	TGATACACTG	TCACTAACAC	AAGAAGCAAA	2280
ATAGCCAAGA	CAAAAACAAT	GGCAGATAAA	AGCAAATCTC	GATTTATGAC	TTCCACTGCA	2340
CTTTTGTAGG	TCGGCTCTAG	CAAGGTAGCC	TGGTCTATCT	TGAAAAAATC	GCTCCATTTT	2400
TGTACAATCC	TATCCTTGTC	CATCTCTTGT	GTAGAAGTTA	TCGTATAGCG	ACCATTTAAA	2460
CTACGAGATG	TATCCTTGAT	ATAGGTTTGA	AAAGTCATAA	GCTGAATAGG	TTTGGCTTTT	2520
AGAAAGGTCG	GAATCGTACC	AAGTTTATTG	GAAATTTCTT	TATTACTATA	GA CTCCTTCA	2580
CCATCTGTGG	TAAAATCAAG	AGAAGAAATC	CCAACTCTT	GGTAGGGGAA	GGTATCTTTA	2640
TCAAAAACAC	CAGACTTGAC	CACCTCATCA	CCACTGTCTG	TTTTGATGAT	GGAGACTTTA	2700
TACTCCTTTG	ATACATCCTC	AAAAAATCGA	AGAACAGACG	CTGCAGGTTC	GTAAATATCT	2760
TTCAAATACA	AATCCAAAGA	ATCTACAGG				2789

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

CTGCGAATTT	TATTAAAGAT	AATGTGTTAA	TTACAGCGGC	TCACAACACTAC	TACAGACATG	60
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1281

ACTATGGGAA	AGAAGCGGAT	GATATTTATG	TTCTTCCGGC	TGTTAGTCCA	AGTCAAGAAC	120
CATTTGGAAA	GATCAAAGTA	AAGGAAGTTC	GTTATTTGAA	GGAAATTTAGA	AATTTAAATT	180
CTAAGGATGC	AAGGGAATAT	GACTTGGCTT	TATTAATTCT	AGAAGAGCCC	ATTGGTGCAA	240
AATTAGGGAC	TTTGGGTCTT	CCTACTAGTC	AAAAAAATTT	GACAGGAATA	ACTGTGACTA	300
TCACAGGCTA	TCCATCATAT	AATTTTAAAA	TTCATCAAAT	GTATACAGAT	AAGAAACAAG	360
TTTTAAGTGA	TGATGGCATG	TTCTTGGATT	ACCAAGTTGA	TACTTTAGAG	GGGTCTAGTG	420
GATCTACAGT	TTATGATGCT	AGTCACCGTG	TAGTAGGAGT	GCATACTTTA	GGAGATGGAG	480
CTAATCAAAT	TAACAGTGCA	GTTAAATTAA	ATGAACGAAA	TTTGCCATTT	ATTTAwTCGG	540
TTCTTAAAGG	TTACTCTCTT	GAAGGATGGA	AGAAAATAAA	TGGTAGTTGG	TACCATTATA	600
GACAACATGA	TAAACAAACG	GGTTGGCAGG	AGATAAATGA	TACCTGGTAT	TATTTAGACA	660
GTTCCGGTAA	GATGCTTACA	GATTGGCAAA	AAGTCCATGG	AAAATGGTAT	TATCTCAATT	720
CAAATGGAGC	AATGGTTACA	GGTAGCCAAA	CTATCGATGG	TAAAGTTTAT	AACTTCGCTT	780
CATCTGGTGA	GTGGATTTAA	TGTTGGAGGA	TATATAAAAT	GAAGCTTTTG	AAAAAAATGA	840
TGCAAATCGC	ACTAGCCACA	TTTTTCTTCG	GTTTGTTAGC	GACAAATACA	GTATTTGCAG	900
ATGATTCTGA	AGGATGGCAG	TTTGTCCAAG	AAAATGGTAG	AACCTACTAC	AAAAAGGGGG	960
ATCTAAAAGA	AACCTACTGG	AGAGTGATAG	ATGGGAAGTA	CTATTATTTT	GATCCTTTAT	1020
CCGGAGAGAT	GGTTGTCGGC	TGGCAATATA	TACCTGCTCC	ACACAAGGGG	GTTACGATTG	1080
GTCCTTCTCC	AAGAATAGAG	ATTGCTCTTA	GACCAGATTG	GTTTTATTTT	GGTCAAGATG	1140
GTGTATTACA	AGAATTTGTT	GGCAAGCAAG	TTTTAGAAGC	AAAAACTGCT	ACGAATACCA	1200
ACAAACATCA	TGGGGAAGAA	TATGATAGCC	AAGCAGAGAA	ACGAGTCTAT	TATTTTGAAG	1260
ATCAGCGTAG	TTATCATACT	TTAAAACTG	GTTGGATTTA	TGAAGAGGGT	CATTGGTATT	1320
ATTTACAGAA	GGATGGTGGC	TTTGATTCGC	GCATCAACAG	ATTGACGGTT	GGAGAGCTAG	1380
CACGTGGTTG	GGTTAAGGAT	TACCCTCTTA	CGTATGATGA	AGAGAAGCTA	AAAGCAGCTC	1440
CATGGTACTA	TCTAAATCCA	GCAACTGGCA	TTATGCAAAC	AGGTTGGCAA	TATCTAGGTA	1500
ATAGATGGTA	CTACCTCCAT	TCGTCAGGAG	CTATGGCAAC	TGGCTGGTAT	AAGGAAGGCT	1560
CAACTTGGTA	CTATCTAGAT	GCTGAAAATG	GTGATATGAG	AACTGGCTGG	CAAAACCTTG	1620
GGAACAAATG	GTACTATCTC	CGTTCATCAG	GAGCTATGGC	AACTGGTTGG	TATCAGGAAA	1680
GTTCGACTTG	GTACTATCTA	AATGCAAGTA	ATGGAGATAT	GAAAACAGGC	TGGTTCCAAG	1740
TCAATGGTAA	CTGGTACTAT	GCCTATGATT	CAGGTGCTTT	AGCTGTTAAT	ACCACAGTAG	1800

1282

GTGGTTACTA CTTAAACTAT AATGGTGAAT GGGTTAAGTA ATGAAGGCTA ATTGTAAACT	1860
GTGATGGATA CTTAACTTTG TATAATAGGT GGATAAAAGT CTTCAACAATC AAAAAACGCA	1920
TAGTATCAAG GTTTTTCTGT ACTGCCCTCA AACAGTTAGA CAATTAATTT ATCCGAAGgA	1980
TTTAGTTCTG TATTGCACAG GGCTAAGTCC TTTTAGTTTT ACCTTAATTC GTTTATTGTT	2040
GTAGTAATCA ATATAGTCTA TAATGGCTTG TTCCAATTGC TTAAGCGACT GAAACGACTT	2100
CTCATAACCG TAAAACATTT CCGATTTTCAAG AATCCCAAAG AAGGACTCCA TCATACTATT	2160
GTCTGGGCTG TTTCCCTTAC GTGACATGGA TGCTTGAATT CCCTTACTCT CTAGGAACCG	2220
ATGATAAGAA TCGTGTTGGT ATTGCCAGCC TTGGTCACTA TGGAGAATCG TATTCTCGTA	2280
GTGCTTCTCT GTGAATGCCT GTTCCAACAT TGTTTGTACT TGTTCTAAGT TGGGTGAAGT	2340
TGAAAGATTA TAGGCGATAA TTTCGCTATT AAAGCCATCT AAAACTGGTG ATAAGTAAAG	2400
CTTTTGAGTA CTTGCTGGAA TGGCAAATTC TGTCACATCT GTGTAGCACT TTTCCATTGT	2460
TTTAGAGCCT TCAAATTGGC CTTGAATGAG ATTCG	2495

(2) INFORMATION FOR SEQ ID NO: 256:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 870 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

TACCACCGTA TTCATCCAGC AAGATTGCCA TTTGTCTTTG GGTATTTTCGC AGTTCTTTTA	60
GCAAGTCATC CACAAAATA GTTTCAGGTA CAAAAGTGG ATCTTGTAAG ATTCTCTTCC	120
AAACAATATT GTCAAAACCG TCCACAAAGC CTGCCTTAAG GAGACTCTTG GTGTGAATGA	180
TTCCAATTAC ATTGTCCTTA TCCCCATCAT AAACCGGGAT ACGAGAATAA TTTTGTTTTA	240
AAATACTTTG GATAATGGCT TGACTATCAT CCTGAATATC CACCATAAAG GCATCCGTTT	300
GAGGAACCAT AACCTCTCGT GCCATCAGTT CATCGAGCGA AAAGACACCT TGTAGCATCT	360
CAATCTCATC AGCATCCAAT GTTCTTTCAC TATTTGTCAG CATATAGGCA ATTTTCATCAC	420
GGGTCATCTT TTCATCCGCA TCATCGAATG ACATAGGAGT CAAATGGCTC AAGAAATTGG	480
TCGAAGCAGC TAAAAGCCAA ACAAAGGAC TGACTAGTTT TCCGATCCCA ATGATAATCG	540
GCGCTGTACG AATTGCCAAG GCATCCTTTA GATTAAGAGC GATTCTCTTA GGATATAATT	600
CCCCAAAAC GATGGAAATA TAGGTCAAAA ATGCCAAGGA TAGAAAAGTT GCCACGGCTT	660
GTGCTGTTTC GCCATTCCCA AGCCAAGAGG CAATCACACG TCCTAGAGTA TCAGTTAAAC	720

1283

TCGCCCCCTGA TAAGATTGTA ATCAGGGTGA TTCCTACCTG GATGGTTGAT AAAAAGTGGT	780
TAGGATTTTC TAGTACCTTC AGCAGGCGGA TGTAGCGTCT GTCTCCTTCT TCCGCCTTTT	840
GTTCAACTCG GGCACGATTA AGAGAAACGG	870

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

CGTTCCCAGA AGCCCGCATT CTCATCGCCA ATGTCGTGAT TGATTTGGCC CTTTCTCCAA	60
AATCCAAC TC AGCCTATGTA GCTATGGATA AGGCACTTGC TGACCTCAA ACATCAGGGC	120
ACTTGCCTAT TCCGCGACAC CTGCGTGATG GGCAC TACAG TGGAAGCAAG GAACTGGGGA	180
ATGCCCAAGA CTATCTCTAT CCACACA ACT ATCCTGGAAA TTGGGTCAAG CAAGACTATC	240
TGCCAGAAAA AATTCGTAAT CATCACTATT TCCAAGCAGA AGATACTGGT AAATATGAAC	300
GGGCTTTGGC TCAAAGAAAG GAAGCTATCG ACCGTTTGCG AAAAATCTGA AATCCTTTTC	360
AAAAAATTGC ACTTTCCTCT TGATTTTTTT TGAAAAAGTG GTATCATATA AATATAGAAA	420
CGCTGTGGTG TACGACTTCA CACTTAAGTG TTGACCGACT ATTTTTTGTA TTATTAGGGA	480
AACAAAAGTC TTCTAACAGC ATGTAGGCCG TCTCACACGG AAACAGCTTC AGTTAGAGCG	540
AGTTGCCCAC CTGCTTAATT GCGCGGGTTC AATACAAACC GTGAAGTTTC GGCACCAATA	600
CAGCTTTTTT CTTTGCCTCC TTAGCTCAGC TGGCAGAGCA GCGGACTCTT AATCCGTGGG	660
TCACAGGTC GATCCCTGTA GGGGGCATAT AAATACAACA GGAAAAGCCT TATAATATAG	720
GGCTTTTTTT GCTTTCCTTT TAAAAATTGT CGTGCAATTT GCCGTGTTTT TACAACAAAC	780
TTTTTCACAGC CATAAACTCC TCACTAATTT TTTCTCCAA GGTATGCCCA TAAACGTCAA	840
TCAACATGGA GATATCTTTA TGTCC TAAAA TTTGGCTCTT TG TCAACTGT AGTGGGTGA	900
AGTCAGCTAA GCTCGAGAAA GGACAAATTT TGTCTTTTCT TTTTGTATAT TCAGAGCGAT	960
AAAAATCCGT TTTTGAAGT TTTCAAAGTT CCGAAAACCA AAGGCATTGC GCTTGATAAG	1020
TTTGATGAGA TTATTGGTCG CTTCCAATTT GCGGTTAGAA TAGTGTAGTT GAAGGGCGTT	1080
GACGATTTTC TCTTTGTCCT TTAGAAAGGT TT TAAAGACA GTCTGAAAAA GAGGAGGAAC	1140
CTGCTTTAGA TTGTCCTCAA TGAGTCCGAA AAATTTCTCC GGTGCCTTAT TCTGAAAGTG	1200

1284

AAACAGCAAG AGTTGATAGA GCTGATAGTG ATGTTTCAAG TCTTG 1245

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1684 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

ATGCCTATGT AACTCCACAT ATGACCCATA GCCACTGGAT TAAAAAAGAT AGTTTGTCTG	60
AAGCTGAGAG AGCGGCAcCC AGGCTTATGC TAAAGAGAAA GGTTTGACCC CTCCTTCGAC	120
AGACCATCAG GATTCAGGAA ATACTGAGGC AAAAGGAGCA GAAGCTATCT ACAACCGCGT	180
GAAAGCAGCT AAGAAGGTGC CACTTGATCG TATGCCTTAC AATCTTCAAT ATACTGTAGA	240
AGTCAAAAAC GGTAGTTTAA TCATACCTCA TTATGACCAT TACCATAACA TCAAATTTGA	300
GTGGTTTGAC GAAGGCCTTT ATGAGGCACC TAAGGGGTAT ACTCTTGAGG ATCTTTTGGC	360
GACTGTCAAG TACTATGTCG AACATCCAAA CGAACGTCCG CATTCAGATA ATGGTTTGG	420
TAACGCTAGC GACCATGTTC AAAGAAACAA AAATGGTCAA GCTGATACCA ATCAAACGGA	480
AAAACCAAGC GAGGAGAAAC CTCAGACAGA AAAACCTGAG GAAGAAACCC CTCGAGAAGA	540
GAAACCGCAA AGCGAGAAAC CAGAGTCTCC AAAACCAACA GAGGAACCAG AAGAATCACC	600
AGAGGAATCA GAAGAACCTC AGGTGAGAC TGAAAAGGTT GAAGAAAAAC TGAGAGAGGC	660
TGAAGATTTA CTTGGAAAAA TCCAGGATCC AATTATCAAG TCCAATGCCA AAGAGACTCT	720
CACAGGATTA AAAAATAATT TACTATTTGG CACCCAGGAC AACAATACTA TTATGGCAGA	780
AGCTGAAAAA CTATTGGCTT TATTAAAGGA GAGTAAGTAA AGGTAGCAGC ATTTTCTAAC	840
TCCTAAAAAC AGGATAGGAG AACGGGAAAA CGAAAAATGA GAGCAGAATG TGAGTTCTAG	900
TTCTCATTTT TTTCATGAAA ATGTGCAAAA TATAGTAGAT TGAAACTAGA ATAGTATACC	960
TCTACTTCTA AAACATTGTT AGAAATCGAT TTGACTGTCC TGTTCCTATT TCATTTTACT	1020
ATATCTTAAC AGATAGTGTA AATAAAGATA AACTATTTAC TGGCTAATTA ATCAGTTAAA	1080
CACTAGTTAA GGAGTAATGA TGAAAAAAG AACAATACTA TTATTGATGG CCAGTCTGTT	1140
AGCTCTTGTC TTAGGAGCAT GTGGTTTCTT GGACATATTG ATCCTGGATC ATTCTCATCA	1200
GGATTACTCT TTAGTGCTAT TTTAGAAACT GGGGTGGTTT GATGGAAAGT ATTGGTCTTG	1260
TTATCGTTTC ACATTCCAAA CACATTGCAG AAGGTGTTGT TGAAGTATT AGTAAAGTAG	1320
CTAAAGATGT TCCGATTACT TATGTAAGAG GAACCGAGGG CGGAGGAATT GGAACGAGTT	1380

1285

TTGAACAAGT AGATAGGGTT GTTTCCGAAA ATCCAGCAGA TACTTTACTT GCCTTTTTTTG	1440
ACCTAGGTTC TGCTAAAATG AACTTAAAAA TGGTGACTGA TTTCAGTGAT AAAAGTATCA	1500
TCATCAACAG GGTTCCAATT GTAGAAGGTG CCTATAATGC AGCTGCTCTT CTTCAGGCTG	1560
GTGCAGAACT GTCAGTTATT CAAACACAGT TaGCGGAgCt TGAAATCAAT AAATAAGGAA	1620
TTTTACTATA ACTCTTTTTA TAGATAAGCT ATTGaTTATC TCAACTATAA TAATGTTAAG	1680
TnAA	1684

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 970 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

AGGAGTGGAG AnATATGAAG ACACAAATTT TCACATTATT GAAAATCGTT GCTGAGATTA	60
TTATTATTTT GCCATTTCTA ACTAATCTAT AAGTTCTTTA TATTGCTGAA AACGCAATTC	120
AAAAAGGGCT ATTAATTGTG GATTTTCTAA TACCTGCAGA GATTGGATAA AGCGTTCAAT	180
CTCTTTTGA TTGCTTCCCT TTGTTTGAAG AAAGACACTC ATCTTCTTTA AAAATTGCCA	240
CGATACTTTT TCAAAAACAT CACACGGTCG TAACATCCTC TCCAACTCGG CTTCGAAGAT	300
TGGGATGTAG GAGAAAAGTT TTCGCTCCAT GAGTTCTGAT AAGATATTTA AGAGTCCTTG	360
CTTCATATAC AATCGATTGT GTACTAACTC TTAAATTTCT TTGGATTTTT CGAGTAAGGA	420
GGTTGATAAA AAAATCAGAT CTTGATTGCT CAAGAAGGGC ATGGTATTGC AAAAGAGATA	480
GAGTTCAAAC CAGGTCCAAG ACTCGATAGC ATAGAGATAG GTGGTCAAAA ACTCGCTATC	540
CTCCTCTGCT AGTGGGTAGC TTTTATTTAG TGAATGGATG GCATCTTTAA TCACGATGGC	600
ATTCAAACGA CGATAGGTCT GCGCCATCTG TTCTTGATCG ACTTCCTCCA ATAGCTGCTC	660
TAAAGCAGCT ATATCCTGAT GGGCAAAGCG ATTCACAACC TTTCGACCGA TTCGCATATG	720
TGGAGATTCT TGATAGTTGT TGAGCTTGTG CCCAACTCA TCAAAGGTCA CATTTATACC	780
TTGGATAGCT AGAATCAACT TATCCGCAGA CAGCATAGAC TGCCCTAGTT CAAACTTGGA	840
CAACTGAGAA GCTGTTAGAC CCTCACAAGC CACATCTGAC TGCTTGAGCT TTCTCGCCAA	900
ACGTAATTCC TTGTAAAATT CCCCAGTTC CATTCTCTCA ATCATCTGAC CACCTCCTAG	960
CTTTTGCAGG	970

1286

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2996 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

GTTGACCACG GGTA AAACTA CCCTAACTGC AGCTATCACA ACTGTTTTGG CACGTCGCTT	60
GCCTTCATCA GTTAACCAAC CTAAAGACTA TGCGTCTATC GATGCTGCTC CAGAAGAACG	120
CGAACGCGGT ATCACTATCA AACTGCGCA CGTTGAGTAC GAAACTGAAA AACGTCAC TA	180
CGCTCACATC GACGCTCCAG GACACGCGGA CTACGTTAAA AACATGATCA CTGGTGCTGC	240
TCAAATGGAC GGAGCTATCC TTGTAGTAGC TTCAACTGAC GGACCAATGC CACAAACTCG	300
TGAGCACATC CTTCTTTCAC GTCAGGTTGG TGTTAAACAC CTTATCGTCT TCATGAACAA	360
AGTTGACTTG GTTGACGACG AAGAATTGCT TGAATTGGTT GAAATGGAAA TCCGTGACCT	420
ATTGTCAGAA TACGACTTCC CAGGTGACGA TCTTCCAGTT ATCCAAGGTT CAGCACTTAA	480
AGCTCTTGAA GGTGACTCTA AATACGAAGA CATCGTTATG GAATTGATGA ACACAGTTGA	540
TGAGTATATC CCAGAACCAG AACGTGACAC TGACAAACCA TTGCTTCTTC CAGTCGAGGA	600
CGTATTCTCA ATCACTGGAC GTGGTACAGT TGCTTCAGGA CGTATCGACC GTGGTATCGT	660
TAAAGTCAAC GACGAAATCG AAATCGTTGG TATCAAAGAA GAAACTCAA AAGCAGTTGT	720
TACTGGTGTT GAAATGTTCC GTAAACA AACT TGACGAAGGT CTTGCTGGAG ATAACGTAGG	780
TGTCCTTCTT CGTGGTGTTT AACGTGATGA AATCGAACGT GGACAAGTTA TCGCTAAACC	840
AGGTTCAATC AACCCACACA CTAAATTCAA AGGTGAAGTC TACATCCTTA CTAAAGAAGA	900
AGGTGGACGT CACTCTCCAT TCTTCAACAA CTACCGTCCA CAATTCTACT TCCGTACTAC	960
TGACGTTACA GGTTC AATCG AACCTTCCAGC AGGTACTGAA ATGGTAATGC CTGGTGATAA	1020
CGTGACAATC GACGTTGAGT TGATTACCCC AATCGCCGTA GAACAAGGTA CTACATTCTC	1080
TATCCGTGAG GGTGGACGTA CTGTTGGTTC AGGTATGGTT ACAGAAATCG AAGCTTAATT	1140
CGATTTAGTT CCCAGAAGAA CAATTATTTA AGTTAGACAC TAAAAGAATC TTGCTTGGCA	1200
AGGTTCTTTT TTTAGATATT GAACTAATAC TCAATGAAAA TCAAAGAGCA AACTATAATA	1260
TATTGAAACT AGAATAGTAC ACATCTACTT CTAAAACATT GTTAGAAATC GATTTGACTG	1320
TCCTGATCGA TTTGTCTTGT TCTTATTTCA TTTTACTATA GAAAGTTAGC TACAGACTGC	1380
TCAAAACATT GTTTTTAGGT TG TAGATAGA ACTGACGAAG TCAGTAACAT CTATACGACA	1440

1287

AGGCGAAGCT	GACGCGGTTT	GAAGAGATTT	TCGAAGAGTA	TAATACTAGA	CTAAAATCAA	1500
AAAGCATTAT	ACAATAGTAA	TATGAAATCA	ATTAAAGAAG	AAATCCAAAC	CATCAAAACA	1560
CTTTTAAAAG	ACTCTCGTAC	AGCTAAATAT	CATAAACGCC	TTCAAATCGT	TCTATTTCGT	1620
CTGATGGGCA	AATCTTATAA	AGAGATTATA	GAACTTTAT	AGTGGTTTGA	AATAAGATGT	1680
GAACAACTCT	ATCAGGAAAAG	TCAAACATAAT	TTATAGAAAT	ATTTTAGCAG	CCAAGGTGTA	1740
CTGTTATAGA	TTCAATACAC	TTTAGACTGT	AATCAAAACAA	CGATTTGGCG	AAATGTAAAA	1800
AATATGAGGA	GTTCGGACTC	GACTCTCTCC	TTCAAGAAAC	ACGTGGTGGT	CGTAACCATG	1860
CTTATATGAC	GGTTGAGCAA	GAGAAAGTCT	TTCTTGCCCCG	CCATTTGAAG	GCTACAGAGG	1920
CAGGAGAAAT	TGTTACAATT	GATGCCCTTAT	TTCAGGCTTA	TAAAAAGGAG	TTAGGTCGTT	1980
CCTACACACG	TGATGCCTTC	TATCAACTGT	TGAAGCGCCA	TGGTTGGCGA	AATATTACGC	2040
CACGTCCAGA	ACATCCTAAG	AAAGCAGATG	CTCAAACCAT	TGTCGCGTCT	AAAAATAAAG	2100
TCTCAATTCA	AGAAGACAAG	TGAACTGCAC	CCCAAAAGTT	AGACAGAAAA	AATCTAACTT	2160
TTGGGGTGTT	TTTATTATGA	AATTAACCTTA	TGATGATAAA	GTTTCAGATCT	ATGAACTTAG	2220
AAAACAAGGA	TATAGCTTAG	AGAAGCTTTC	AAATAAATTT	GGGATAAACA	ATTCTAATCT	2280
TAGGTACATG	ATTAAATTGA	TTGATCGTTA	CGGAATAGAG	TTCGTCAAAA	AAGGAAAAAA	2340
TCGTTACTAT	TCTCCTGATT	TAAAACAAGA	AATGATTCAT	AAAGTCTGAC	ATGAAGGCTG	2400
GACTAAAGAT	AGAGTTTCTC	TTGAATACTG	TCTCCCAAGT	CGTACGATAC	TTCTTAACTG	2460
GCTAGCACAA	TACAGGAAAA	ACGGGTATAC	TATTGTTGAG	AAAACAAGAG	GGAGAGTACC	2520
TGAGAGCGGA	GAATGCCATC	CTAAAAAAGT	TAAGAGAACT	CCGATTGAAG	GAGGAAAAAG	2580
AGAAAGAAGA	AAGACAGAAA	TTATTCAAGA	ATTAATGACT	GAGTTTTTCGT	TAGATATTCT	2640
TCTAAAAGCC	ATTAAACTAG	CTCGTTTGAC	CTACTACTAT	CACTTGAAAC	AGCTAGATAA	2700
ACCAGATAAG	GACCAAGAGC	TTAAAGCTGA	AATTCAATCC	ATTTTTATCG	AACACAAGGG	2760
AAATTATGCT	TATCGTCGGA	TTTATTTAGA	ACTAAGAAAT	CGTGGTTATC	TGGTAAATCA	2820
TAAAAGAGTT	CAAGGCTTGA	TAAAAGTACT	CAATTTACAA	GCTAAAATGC	GACAGAAACG	2880
AAAATATTCT	TCTCATAAAG	GAGACGTTGG	CAAGAAGGCA	GAGAATCTCA	TTCAAGGACA	2940
ATTTGAAGGC	TCTAAAACAA	TGGAAAAGTG	CTACACAGAT	GTGACAGAAT	TTGCCG	2996

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 837 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

1288

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

CTTATCAACT CCCGACATGG CTCTCAGACC AATCCAAATC CCTAAAAAAA TCAGAACAAG	60
GATGGTGGTC AAGATCAAAC TCTCGAAATA TAAAGAAAAT AGTTGCAGTA GCATGATTTC	120
TCTCATTTCT ATCTTTTTTA AAGAGTAAAC TCAGCTAGTC CAACTAACTG AGTTTTCCCTT	180
TATCTATTAT ATCAAATATA AGTCCGTTTG TAACTAGCGA AGAATTCTTT TGTCCGCTCT	240
TCTTTAGGGG TGTGGATAAT CTCATCCGGA GTTCCAGACT CGATGATTTT CCCCTTATCT	300
AAGAAGAGAA TTTTATCCGC AACTTGGGCT ACAAAGGACA TGTCATGACT GACCAAAATC	360
ATGGTCTGAC CTGACTTAGC AGCATCTGCA ATAGACTTTT CTACTTCACC GACCAATTCT	420
GGGTCAAGGG CTGAAGTTGG TTCGTCTAAG AGCAAAACAT CTGGTTTCAT AGCAAGCGCA	480
CGCGCTAGGG CAACCCGTTG CTTCTGTCCA CCTGATAAAT GCGGAGGATA ATGGTTTTCA	540
CGGTCCGAAA GCCCAACCTT AGCCAACCTCT TCCTTGCAA TCTTAGTCGC TTCTTGGTCA	600
GATAATTTCT TGACAACAAC CAAGCCTTCT TTCACATTAT CAAGTGCTGT TCGGCGTTCA	660
AACAAATTAA ACTGTTGGAA AACCATAGAC AACTTACGAC GTAGGGCAAG GATTTCTTCT	720
TGAGTGATTT TAGAAAAATC AACTGAAAAA CCATCAATCT GAATAGAGCC ACTGTCAGGT	780
GTTTCTAGAT AATTGAGACT GCGAGAAAGG TTGATTTTCA GCTCTGAAGA CCAATCA	837

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 868 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CCGAACAAAA TGGGCTAATT AGATTATAGT AAGAAAGGTA AGTTAAAAAT GAGAATTGCA	60
ATTGGATGTG ACCACATCGT AACTGATGAA AAAATGGCGG TTTCAGAATT TTTGAAATCA	120
AAAGGATATG AAGTCATTGA CTTTGGTACC TATGACCATA CACGGACTCA CTACCCAATC	180
TTTGGTAAAA AAGTAGGGGA AGCTGTAAC TACGGTCAAG CTGATCTTGG AGTATGTATC	240
TGTGGTACTG GTGTTGGTAT CAACAACGCT GTAAATAAAG TTCCAGGTGT TCGTTCTGCC	300
TTGGTTCGTG ATATGACAAC AGCCCTTTAT GCTAAAGAAC AATTGAACGC TAACGTTATT	360
GGTTTTGGTG GTAAATTAC TGGTGAATTG CTTATGTGTG ATATCATCGA AGCTTTCATC	420

1289

CATGCTGAAT	ACAAACCAAC	TGAAGAAAAC	AAAAAATTGA	TTGCGAAAAT	TGAACATGTT	480
GAAAGTCACA	ATGCTCAACA	AACAGACGCA	AAC TTCTTTA	CAGAATTCCT	TGAGAAATGG	540
GATCGTGGAG	AATACCACGA	CTAAGAGGTG	ACCTATGATT	TTAACAGTCA	CAATGAACCC	600
ATCCATCGAT	ATTTCTTATC	CCTTGGATGA	GTTGAAGATT	GATACTGTCA	ATCGTGTGGT	660
GGATGTAACC	AAAACGGCTG	GTGGTAAGGG	ACTCAATGTT	ACCCGAGTAC	TTTCAGAATT	720
TGGCGATTCT	GTTCTTGCTA	CTGGTTTAGT	GGGTGGCAAA	CTTGGTGAGT	TTTTGGTTGA	780
ACATATCGAT	AATCAAGTAA	AGAAAGATTT	CTTCTCAATT	AAGGGAGAAA	CTCGTAACTG	840
TATCGCTATT	CTCCACGGAG	ACAACCAA				868

(2) INFORMATION FOR SEQ ID NO: 263:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3744 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CCGTTCAAAG	TCTTCATAAG	ACTCGAAAGT	CACAGTTCTT	TCGTTCTTGC	TGGCATCTAT	60
ATAGGTAATT	TCAATCATGT	TTAAAACTCC	TTTGTTTAAT	GCTAACTTTA	TTTTACTCCT	120
TATAAAAGAG	AATGTCAAGA	AAAATGATTG	CGCACGCAAC	TTTTTTTAAA	ATCATCTTAA	180
ATCAAGAAAT	CCAAACCTGC	TTCCAAGCTT	TCTTCGACAG	TCTTTTGTAG	CGAGGCCAGT	240
GTCTTTTGCC	CATCATTTGT	CAGGCAGATA	AAACTAGAGC	GTCTATCTTG	ATGGCAACAC	300
ATGCGACTGA	GTAGACCGCA	ATTTTTAGCT	TCCAAGCGAG	CCACCATCCT	AGAAACTGCG	360
CTCGGGCTCA	GATGAAGCTT	ATCTGGCAGG	TCAATCTGGC	GTAGAGATTT	TTCTTCAGCC	420
AAGTCCAGAT	AGTAGAGCAG	GTAGAACTCT	TTCAAGGTCA	GACTTTGCTC	GCTCTGTTGG	480
GCAATGGTCT	CTTCCAAGAG	ACTTTCAATT	TCTTTCTGAC	GCCGATTGAA	GTCAAACCAT	540
TTTTCCAAAT	AGGTCATAGT	GTCTCCTTTC	TTTTTAGAGT	CATAAATAGA	AGAAAGTCCA	600
TTAACGGGCA	GTCTCTGCGT	CACAAGATGA	TTGCGCATGC	AATAATTATA	CTACTTTTCA	660
AGAATGCTGG	CAAGCTCTGT	TTTTTAGTGG	TTTTATTTTT	GTGTGAATAA	TGGGGGAATC	720
CTATTGTTTC	AATTTCTAAC	TCCTTATCAC	ATTCTGAATTC	AGATTTTATT	TCATTTCTCT	780
ATCTATAGTT	GCTTAGTTTA	AAATAAGCAT	GGTCTAATAA	AGCTATGCAT	ATAGTACTGA	840
TTTTAAACAA	GGAGCATTAG	ATTCCATTAA	AGGAGGGCAC	AGACATGTCG	AGGCGGCCAA	900

1290

AGTTTTTGAT	GTCGGCGTCA	GAAGTCTCTT	CACGTGGGAA	AAGAAAGACG	TAAACAAGGG	960
AACTTAGAGC	GGAAAAAGCG	AGTCGTCAAA	AAGCGTAAGA	TCCCTTTAGA	AGAATTGAAA	1020
GCCTTTGTAG	AGGCTCATCC	AGACGCTTTT	TTACGGGAAA	TTGCGGCCCG	TTTTGATTGT	1080
GCTTTGCCCT	CCGTATGGGC	AGTTTTAAAG	CAGATTAAGG	TCATTTTAAA	AAAGACGACC	1140
AGTTTTAGGG	AACAAAAGCC	TGAGAAAGTT	TCTGAGTTTC	TTGATATTTT	GGATAACCTA	1200
AAAGATTTAC	CAGTCCTATA	TATTGACGAA	ACGGGAATCG	ACCGCTACCT	CTATCGTCCT	1260
TATGCAGGGG	CTCCTAGAGG	GGAGAAAGTC	TATGGCAAGA	TTAGCGGACG	GCGTTTTGAG	1320
CGGACTAATG	AGGTGGAGCA	AAAAGTCAAT	GGTAGTTTTC	TAATCAGATA	TATTGATTCA	1380
CAAATTAGAG	AATGAAAGAA	TAATTATGCA	TAAAAATAGG	AATATAAACC	AAAAATTAGC	1440
TGATTTATAC	TCATTTGCGT	GTCTTTATAA	AAAAGTTATC	TTATAATATA	TATATATATA	1500
TATACAAAAT	AGTAAAATGC	TTTTTTTTTT	TAGCAAAAAT	ACCTCAAGTT	TCTTGCTATT	1560
TTGGGTCCC	TATTCTATAA	TTATAGTATG	GTAATTTATT	TATATCCATA	CATGAAAATA	1620
ATACTCGAAA	GGAAATTTCA	AAATATTTTT	TAGACGTCAG	AAGGGTGAAT	ATAGAGAAAC	1680
AGACCGAGTA	ACTCGGTTCA	AATTAATCAA	ATCAGGGAAG	CATTGGCTAC	GGGCCTCGAC	1740
TTCTCTTTTT	GGCTTGTTTA	AGGTCTTGCG	AGGTGGTGTT	GATACTACTC	AGGTCATGAC	1800
CGAAACGGTA	GAAGATAAAG	TAAGTCATTC	AATTACTGGG	CTTGATATCC	TCAAGGGGAT	1860
AGTTGCTGCG	GGAGCTGTCA	TAAGTGGAAC	CGTTGCAACT	CAAACGAAGG	TATTTACAAA	1920
TGAGTCAGCA	GTACTTGAAA	AAAGTGTAGA	GAAAACGGAT	GCTTTGGCAA	CAAATGATAC	1980
AGTAGTTCTA	GGTACGATAT	CTACAAGTAA	TTCAGCGAGT	TCAACTAGTT	TGTCAGCTTC	2040
AGAGTCGGCA	AGTACATCTG	CATCTGAGTC	AGCCTCAACC	AGCGCTTCGA	CCTCAGCAAG	2100
TACAAGTGCA	TCAGAATCAG	CAAGTACATC	GGCTTCGACA	AGTATTTCTG	CATCATCTAC	2160
TGTGGTAGGT	TCACAAACAG	CTGCCGCTAC	AGAAGCAACT	GCTAAGAAGG	TCGAAGAAGA	2220
TCGTAAGAAA	CCAGCTAGTG	ATTATGTAGC	ATCAGTTACA	AATGTCAATC	TCCAATCTTA	2280
TGCTAAGCGA	CGCAAGCGTT	CAGTGGATTC	CATCGAGCAA	TTGCTGGCTT	CTATAAAAAA	2340
TGCTGCTGTT	TTTTCTGGCA	ATACGATTGT	AAATGGCGCC	CCTGCAATTA	ATGCAAGTCT	2400
AAACATTGCT	AAAAGTGAGA	CAAAGTTTAA	TACAGGTGAA	GGTGTAGATT	CGGTATATCG	2460
TGTTCCAATT	TACTATAAAT	TGAAAGTGAC	AAATGATGGT	TCAAAATTGA	CCTTTACCTA	2520
TACGGTTACG	TATGTGAATC	CTAAAACAAA	TGATCTTGGT	AATATATCAA	GTATGCGTCC	2580
TGGATATTCT	ATCTATAATT	CAGGTACTTC	AACACAAACA	ATGTTAACCC	TTGGCAGTGA	2640
TCTTGGTAAA	CCTTCAGGTG	TAAAGAACTA	CATTACTGAC	AAAAATGGTA	GACAGGTCTT	2700

1291

ATCCTATAAT ACATCTACAA TGACGACGCA GGGTAGTGGG TATACTTGGG GAAATGGTGC	2760
CCAAATGAAT GGTTCCTTTG CTAAGAAAGG ATATGGATTA ACATCATCTT GGAAGTACC	2820
AATTACTGGA ACGGATACAT CCTTTACATT TACCCCTTAC GCTGCTAGAA CAGATAGAAT	2880
TGGAATTAAC TACTTCAATG GTGGAGGAAA GGTAGTTGAA TCTAGCACGA CCAGTCAGTC	2940
ACTTTCACAG TCTAAGTCAC TCTCAGTAAG TGCTAGTCAA AGCGCCTCAG CTTCAGCATC	3000
AACAAGTGCG TCGGCTTCAG CATCAACCAG TGCCTCGGCT TCAGCGTCAA CCAGTGCGTC	3060
AGCTTCAGCA AGTACCAGTG CTTCAGTCTC AGCATCAACA AGTGCTTCAG CCTCAGCATC	3120
GACAAGTGCC TCGGCTTCAG CAAGCACATC AGCATCTGAA TCAGCGTCAA CCAGTGCTTC	3180
GGCTTCAGCA AGTACCAGTG CTTCAGCTTC AGCATCAACC AGCGCCTCGG CCTCAGCAAG	3240
CACCTCAGCT TCTGAATCGG CCTCAACCAG CGCCTCGGCC TCAGCAAGCA CCTCAGCTTC	3300
TGAATCGGCC TCAACCAGCG CCTCAGCCTC AGCATCAACG AGTGCTTCGG CTTCAGCAAG	3360
CACAAGCGCC TCGGGTTCAG CATCAACGAG TACGTCAGCT TCAGCGTCAA CCAGTGCTTC	3420
AGCCTCAGCA TCAACAAGTG CGTCAGCTCA GCAAGTATCT CAGCGTCTGA ATCGGCATCA	3480
ACGAGTGCGT CTGAGTCAGC ATCAACGAGT ACGTCAGCCT CAGCAAGCAC CTCAGCTTCT	3540
GAATCGGCCT CAACCAGTGC GTCACCTCAG CATCGACAAG CGCCTCAGCT TCAGCAAGTA	3600
CCAGTGCTTC AGCCTCAGCG TCGACAAGTG CGTCGGCCTC AACCAGTGCA TCTGAATCGG	3660
CATCAACCAG TCGTCAGCC TCAGCAAGTA CTAGTGCATC GGCTTCAGCA TCAACCAGTG	3720
CCTCGGCTTC AGCGTCAAAC AGTG	3744

(2) INFORMATION FOR SEQ ID NO: 264:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 795 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

CGATAAAGAG GCCTTGAGTA ATCTCAATTT GCAGATTGAA AATGGAGAGA TTATGGGCTT	60
GATTGGTCAT AATGGGGCTG GAAAATCGAC CACTATAAAA TCCCTAGTCA GTATCATTTT	120
ACCCAGCAGT GGTCGTATTT TGGTAGACGG TCAGGAGTTA TCGGAAAATC GCTTGGCTAT	180
TAAACGAAAG ATTGGCTACG TAGCAGACTC GCCTGACTTA TTTTACGCT TAACGGCCAA	240
TGAATTTTGG GAATTGATCG CCTCATCCTA TGATCTGAGT AGATCTGACT TGGAGGCTAG	300

1292

TCTAGCTAGG CTATTGAACG TTTTGTGATTT TGCTGAAAAT CGCTATCAGG TTATTGAAAC	360
TCTTTCTCAC GGAATGCGTC AGAAAGTCTT TGTCATCGGA GCACTCTTGT CTGATCCCGA	420
TATTTGGGTC TTGGATGAAC CCTTGACTGG TTTGGATCCC CAGGCTGCCT TTGATTTGAA	480
ACAGATGATG AAGGAACATG CACAAAAAGG GAAGACAGTC TTGTTTTCAA CTCATGTCCT	540
AGAGGTGGCA GAGCAAGTCT GTGATCGGAT TGCCATTTTG AAAAAGGGGC ATTTGATTTA	600
TTGTGGTAGT GTAGAGGACT TGAGAAAAGA TTACCCAGAC CAGTCTTTGG AAAGTATCTA	660
CCTTAGTCTT GCTGGTAGAA AAGAGGAGGT TCGGATGCG TCTCAAGGTC ATTAAAAAAT	720
TAGTTGATAT CAATATCCTT TATTCATCTC AAGAAGCTAA TCTGGCTAAT CTACGAAAGA	780
AGCAGGCTAA GAATC	795

(2) INFORMATION FOR SEQ ID NO: 265:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

TGGTAATGTG CTTGGCAGCw TCCTTGACAC TGCTACTACC ATTTCCCATATA GCGACCGACA	60
TACCAACGCC AGCCAGCATT TCAAGATCAT TATCTGAGTC ACCAAAAGCC ATGACTTGGT	120
TGAGGTCAAA GCCATATTCT TTCCCAACTC GCGGAATGCC TTCTAATTTA GAATTTCCCT	180
GATTGATGAC ATCCGATGCA AAAGGATTGC TACGTGTCAA TTTCAAGTCT TCAAAATCAG	240
CTGCCGCCTT CTCAGATTCT TCTGGTGTCA TCAGCATCAA AACTTGGTAG ATAGGCTGAT	300
TCATCAGGTG AAGCAGGTCC TCTTCCTTTT GGGGAACAAC CTTGCTGACC ATGCGATTAA	360
AAGACTGACT CACCGTCCGA GTTAAAACAG AGGGAACGAA GCGACTAATT CGTTGGGAAA	420
AAGAACCCAG ACCAAAGGAC ATGATTTTAG AACCCAACAT GGCATCCTTG GTCCCTAGAG	480
CAATCTCCGT GCCCTCTTTT TTAGCATAGC TAATTAGATG GCGCAAATGT AACTTGGAAA	540
TAGGGCTCGT GAACAAGACT CTGTCTTTAC TAAAGATATA CTGGCCATTA TAGGTTACCG	600
CAAAATCCAG ATCCAAATCG TCCATCAATT CCTTAACAAA AAAAGGTCCT CGCCCTGTCTG	660
CTACGCCAAC TAGTACCCCT TGTTCTTTGA CAATCTTAAT CGCATCCTTA GTGGATTTCA	720
AAACACTCTT GCGATTGTTG ACCAAGGTTT CATCGATATC AAAAAAACA GCTTTGACTT	780
CCATCCTATC CCAATCTCCC CTTTGTGAT ACAATGATTA TACCACATTT CAGAAAGAGT	840
GAGTAAATCA TGCCTAAGAA AATCCTTGTT TTACATACGG GTGGAACATAT TTCCATGCAG	900

1293

GCCGATGCTT CTGGCGCTGT TGTGACGAGT TCAGATAATC CCATGAACCA TGTGTCCAAC	960
CCACTTGAAG GAATCCAAGT CCACGCCTTG GACTTTTTTA ACCTTCCAAG TCCCCATATC	1020
AAACCCAAAC ATATGCTGGT CCTCTACCAG AAAATTAAAG AGGAAGCAGA TAACTACGAT	1080
GGAGTGGTGA TCACACACGG AACCGATACT TTAGAGGAAA CAGCCTATTT CCTTGATACC	1140
ATGGAAGTTC CCCATATGCC TATCGTTCTA ACAGGAGCCA TGCCTACTCC AATGAGCTCG	1200
GTAGTGATGG TGTTTATAAT TACCTAAGTG CTTTACGAGT GGCCAGCGAT GACAGGGCTG	1260
CTGACAAAGG AGTTTTGGTC GTTATGAACG ATGAAATCCA CGCTGCCAAG TATGTCACCA	1320
AAACACATAC GACTAATGTC AGCACCTTCC AGACTCCAAC ACATGGCCCC CTTGGTCTCA	1380
TCATGAAACA GGAAATCCTC TACTTCAAAA CAGCTGAACC TCGTGTTCGC TTTGACCTTG	1440
ATCACATACA AGGTTTAGTC CCTATCATCT CGGCTTATGC TGGTATGACA GATGAGCTGA	1500
TTGATATGCT GGATTTAGAA CACTTGGACG GTTTGATTAT CCAAGCCTTC GGAGCTGGTA	1560
ATATTCCCAA AGAAACGGCT CAAAAATTAG AAAGCCTTCT GCAAAAAGGA ATTCCAGTCG	1620
CTCTGGTATC ACGATGCTTT AACGGTATTG CCGAGCCTGT TTATGCATAC CAGGGTGGGG	1680
GCGTACAGTT GCAAAAAGCA GCGTTTTCTT TTGTTAAAGA ACTCAACGCC CAAAAAGCTC	1740
GCTTGAAACT CCTCATCGCC CTCAATGCCG GACTAACAGG ACAGGCTTTG AAAGACTATA	1800
TGGAAGGCTA ATACTCTTCG AAAATCTCTG CAAACCACGT CACGTCGCCT TACCGTATGT	1860
ATGGtACTGA CTTGTCAGT TTCATCTACA ACCTCAAAAA CATGTTTGA GCTGACTTCG	1920
TCAGTTCTAT CTACAACCTC AAAAACATGT TTTGAGCTGA CTTGTCAGT TCTATCTACA	1980
ACCTCAAAAA CATGTTTGA GCTGACTTCG TCAGTTCTAT CTACAACCTC AAAAACATGT	2040
TTTGAGCTGA CTTGTCAGT TCTATCTACA ACCTCAAAAA CATGTTTGA GCTGACTTCG	2100
TCAGTTCTAT CTACAACCTC AAAAACATGT TTTGAGCTGA CTTGTCAGk TCTATCTACA	2160
ACCTCAAAAA CATGTTTGA GCTGACTTCG TTAGTTTCAT CTACAACCTC AAAAACATGT	2220
TTTGAGCTGA C	2231

(2) INFORMATION FOR SEQ ID NO: 266:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

1294

GAGTCAAAGG CTCCGAGGTT GACTTTTTTAC AAGGGGACAG GTGAATATTA TCTAGACCTG	60
TCAGAAATTC TCTTCTTTGA AACAGAAGGG AGCAAGATCT ACGCTCATAA CCAGAAGGAA	120
GCTTATGAGG TTCGCCCTCAA GCTCTATGAG TTGGAGTCTA TCTTGCCTCG CTATTTTAAT	180
CGAGTTTCCA AGTCAACGAT CGCAAACATC CGTCAGATTT ACTCAGTGGA CAAGTCCTTT	240
TCAGGAACGG GCACCATTTT CTTTTATCAG ACGCACAAGG AGGTTCATGT CTCACGGCAT	300
TACCAATCCC TCCTAAAAGA AAATCTAAGA AACATGAGGT AAAAAACATG AAAAAGAAAG	360
CATTTGGTAT TGTTTTATTG GTTTTAGCAG CTTGGATCTT GCTGCAAGGG AATTTTGGAA	420
TTCTTCTTT GGATGGTAAA ATATGGCCTT TACTAGGTAT TGTTTTTTTT GCTTATAAGT	480
CCATTGAGTC CATCCTTAGA CGTCATCTCA CTTCCGGCAGT TTTTACAGGT TTACTGGCGC	540
TCATCATTGC AAATTACGCT TATGACTTGT TACCAGTTAC CAATCATTCT CTTATTTGGG	600
CTAGCATCTT GGTGGTACTT GGTGTTGGTT ATCTGACGCA TTCAAGTAAG TTCTGGAATG	660
AAAAAAAATG GTGGTACAAT GGGAAAAAAA CAGTCGTCAC GGATAAGGAA GTCGCTTTTG	720
GTAGCGGGAC CTTCTATAAG CAAGATCAAG ATCTCGTAGA TGACCAAGTG GAAGTCGCTT	780
TTGGGGATGC TAAAATCTAC TATGATAATG CAGAGATGCT AGGTGATTTT GCAACTTTAA	840
ATATTGAAGT GGCCTTCGGG AATGCAACCG TCTATGTTCC ACAACACTGG CGTG TAGATT	900
TGAAAGTAGA AACCTCCTTT GGTGCAGCTA AGGCTGACGC TCCTGTAGCC CCAACCAGCA	960
AAACCTTGAT TATCCGTGGA GATGTGGCTT TTGGGAAGTT GGAAATTGTC TACGTTAAAT	1020
AAAAAAATCT TCACTTCAAC CATCAAAATA GACGTACTAA GAGTAGGAAA TTGATGCCTT	1080
GCTCTGATTT CAGTTCTATG GTTGTTAGAC TTTAAAAAAT GAAATGCTGC CTTTAAAAGT	1140
TGTATATTTT TCGATATTTT GGCTTTTACG TTTGATGTAT CTATGTACTA CAGCGTAGAT	1200
GATGTAGTGT CAAATGCTTT TAAAAAACGG ATGATATTGG ACAGTTTTTT TGCCTTTAAT	1260
TGCTCAGGAA CCATGAAAGT CAGTACCTGG GTTTATGACA AGGGAGAATG	1310

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5922 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

ACTCTGATTT GATTGGAACG ACAGTCGGTG CCATTGCAGT TACTTCAAAC GTAACGACTT	60
ATGTTGAGTC TGCTGCTGGT ATCGGTGCAG GTGGACGTAC TGGTTTGACA GCCTTG GTTG	120

1295

TAGCTATCTG	TTTTGCGATT	TCAAGCTTCT	TTAGCCCACT	TCTAGCGATC	GTACCAACAG	180
CGGCTACAGC	TCCAATCTTG	ATTATCGTTG	GGATTATGAT	GCTTGGTAGC	TTGAAAAATA	240
TCCATTGGGA	TGATATGTCT	GAAGCAGTTC	CTGCCTTCTT	CACATCTATC	TTTATGGGAT	300
TCAGCTACTC	TATCACTCAA	GGGATTGCAG	TTGGTTTCTT	GACTTACACT	TTGACTAAGC	360
TTGTTAAAGG	TCAAGTTAAA	GATGTTTCATG	TCATGATTTG	GATTTTGGAT	GCCTTGTTTA	420
TCCTTAACTA	CATCAGCATG	GCCTTATAAT	AGAATGACCC	AGGGGGATTT	CCCCCCTTTT	480
TTAATACAaG	GAGATAGGTG	ATGAAAGAGA	AAAATATGTG	GAAAGAATTG	TTGAATCGTG	540
CAGGCTGGAT	TTTGGTCTTT	TTACTTGCCG	TCCTTTTATA	TCAGGTTCCC	CTAGTGGTTA	600
CCTCTATTTT	GACTTTAAAA	GAAGTAGCCC	TGCTACAGTC	AGGGCTGATA	GTTGCTGGCC	660
TTTCAATTGT	GGTCTGGCT	CTATTTATTA	TGGGAGCTCG	TAAAACCAAG	TTAGCTAGTT	720
TTAATTTTTTC	TTTTTTTAGA	GCTAAAGATT	TGGCACGTTT	GGGCTTGAGT	TATCTAGTTA	780
TTGTCGGGTC	AAATATACTT	GGTTCCATTT	TATTGCAACT	GTCAAATGAG	ACGACAACAG	840
CTAACCAGTC	TCAGATTAAT	GATATGGTTC	AAAATAGTTC	GTTGATTTCC	AGTTTCTTCT	900
TGCTAGCCTT	GCTTGCTCCG	ATTTGTGAGG	AAATCTTGTG	TCGTGGGATT	GTCCTAAAA	960
AGATTTTCCG	AGGCAAGGAG	AACTTGGGAT	TTGTAGTCGG	TACGATTGTG	TTTGCTTTAT	1020
TGCATCAACC	AAGTAATTTA	CCTTCTTTAT	TGATTTATGG	AGGTATGTCG	ACAGTTCTAT	1080
CTTGACAGC	CTACAAGACC	CAACGTTTGG	AAATGTCGAT	CTTGCTTCAC	ATGATTGTTA	1140
ATGGGATTGC	TTTCTGTTTG	TTGGCTCTTG	TGGTGATTAT	GAGTCGGACA	TTAGGAATTT	1200
CTGTTTAAAA	GTTTTTATGT	AGGAACCGAC	CTCTTCTAC	CAGGGAAAGA	TGAATGCAAT	1260
CGTGTCCATC	TTTTTCTTTT	TATGGTAAAA	TAGAAAAATA	ATATGATGAA	AATCCTTGAG	1320
GGAGTGACCG	ATATGTCAAG	TAAAGCCAAT	CATGCAAAGA	CAGTTATTTG	CGGAATTATC	1380
AATGTAACCC	CAGACTCCTT	TTCGGACGGT	GGTCAATTTT	TTGCTCTTGA	GCAGGCGCTC	1440
CAGCAGGCTC	GTAAATTGAT	AGCAGAAGGA	GCCAGTATGC	TAGATATCGG	CGGAGAATCG	1500
ACTCGGCCGG	GAAGTAGCTA	TGTTGAGATA	GAAGAGGAAA	TCCAGCGTGT	TGTTCCAGTG	1560
ATCAAAGCGA	TTCGCAAGGA	AAGTGATGTC	CTCATCTCTA	TTGATACTTG	GAAGAGTCAA	1620
GTAGCAGAGG	CTGCTTTGGC	TGCTGGTGCC	GATCTAGTCA	ATGATATCAC	TGGTCTTATG	1680
GGTGATGAGA	AAATGGCTTA	TGTGGTAGCT	GAAGCGAGAg	CGAAAGTGGT	CATCATGTTT	1740
AACCCAGTTA	TGGCTCGACC	TCAGCATCCT	AGTTCGCTTA	TCTTCCCTCA	TTTTGGTTTT	1800
GGTCAAACCT	TTACAGAAAA	AGAGTTAGCT	GACTTTGAAA	CATTGCCAAT	CGAAGACTTG	1860

1296

ATGGTGGCTT	TCTTTGAACG	AGCACTAGCG	AGAGCGGCAG	AAGCTGGTAT	TGCACCAGAA	1920
AATATCCTGT	TGGATCCAGG	AATTGGCTTT	GGTCTGACCA	AGAAAGAAAA	TCTGCTTCTT	1980
TTACGGGACC	TGGATAAACT	ACATCAGAAG	GGCTATCCAA	TCTTTCCTCGG	AGTGTCGCGC	2040
AAGCgATTTG	TCATCAATAT	CCTAGAGGAG	AATGGTTTTG	AAGTCAATCC	TGAGACAGAG	2100
CTTGGTTTCC	GAAATCGGGA	CACGGCTTCG	GCTCATGTAA	CTAGTATCGC	TGCGAGACAG	2160
GGTGTAGAAG	TGGTGCGCGT	GCATGACGTA	GCTAGTCACA	GGATGGCAGT	TGAAATTGCC	2220
TCTGCCATTC	GTCTGGCTGA	TGAAGCGGAA	AATTTAGATT	TAAAACAATA	TAAATAAGAT	2280
GAAAGAAATT	GAAAACAATC	AGTGGATTGC	TAATAACCGG	ACGGATCAAC	CGCATTTTGG	2340
CTTGGAACGA	ATGGTGGAAC	TGTTAGCTTT	GCGTGGCAAT	CCCCATCTCA	AACTCAAGGT	2400
CCTCCATATC	GGAGGGACTA	ACGGCAAGGG	CTCGACTATT	GCTTTTTTTGA	AAAAGATGCT	2460
AGAAAAGCTA	GGGTTGAGAG	TTGGCGTGTT	TAGCTCGCCC	TATCTCATTC	ATTACACAGA	2520
CCAGATTAGC	ATCAATGGGG	AATCGATCTC	AGAAGCGAGG	CTAGAAGCTC	TCATGGCAGA	2580
CTATCAGTCT	TTGCTGGAGG	GAGAAGCGGT	CGCCAATTTA	CAGGGCACAA	CCGAGTTTGA	2640
GATTATCACA	GCCCTGGCCT	ATGACTACTT	TGCCTCAGAG	CAAGTAGATG	TGGCCATCAT	2700
GGAAGTTGGC	ATGGGTGGAC	TTTTGGATAG	TACCAATGTC	TGTCAGCCCA	TTTTGACAGG	2760
AATTACAAC	ATTGGCTTGG	ATCATGTGGC	TCTACTTGGT	GACACCTTGG	AGGTCATAGC	2820
AGAGCAGAAG	GCAGGTATTA	TCAAACAAGG	GATGCCCTTG	GTAACAGGGC	GTATTGCTCC	2880
AGAAGCCTTG	GCTGTGATTG	ACCGCATTGC	GGAAGGGAAA	GATGCGCCGA	GACTTGCCTA	2940
CGGGACAGAT	TATCAGGTTC	GTCATCAAGA	AAGTGTGGTG	ACAGGGGAAG	TCTTTGACTA	3000
TACAAGTGCT	GTCAGACAAG	GTCGCTTCCA	GACTAGCCTG	CTTGGTTTGT	ACCAAATAGA	3060
GAATGCTGGG	ATGGCCATAG	CTTTACTTGA	TACTTTTTGT	CAAGAAGATG	GTCGAGAGCT	3120
AGCAAGCAAT	GATTTTCTTG	GTCAAGCCTT	GGAAGAAACA	AGTTGGCCAG	GGCGTTTGA	3180
AATCGTGTCA	AGAGATCCCT	TGATGATTTT	GGATGGAGCC	CACAATCCCC	ATGCTATCAA	3240
GGCCTTGTTG	GTAACCTTGC	AAGAACGTTT	TGCGGATTAT	CATAAGGAAA	TCCTCTTCAC	3300
TTGTATCAAA	ACCAAGGCCT	TGGAGGATAT	GTTGGACTTG	CTGGGAGCCA	TGCCAGTTAC	3360
CGAGCTTACT	CTAACACATT	TTGCGGATAG	TCGGGCGACG	GATGAAAACG	TGCTGAAAGA	3420
GGCAGCTAAG	TCTAGAAATC	TCAGCTACCA	AGATTGGCAT	GATTTTCTAG	AGCAGAATTT	3480
GACAGATAAA	AAAGAAGAGA	AACAAACAGT	TAGGATTGTC	ACAGGTTCCCT	TGTATTTCTT	3540
GAGCCAAGTG	AGGGCCTATC	TGATGGAGAG	GAAGAACGAG	AATGGATACA	CAAAAGATTG	3600
AAGCGGCTGT	AAAAATGATT	ATCGAGGCTG	TAGGAGAGGA	CGCTAATCGC	GAGGGCTTGC	3660

1297

AGGAAACACC	TGCTCGTGTA	GCCCGTATGT	ATCAAGAGAT	TTTTTCAGGT	CTTGGTCAAA	3720
CAGCAGAGGA	ACATTTGTCA	AAATCCTTTG	AAATTATTGA	CGATAATATG	GTGGTAGAAA	3780
AGGATATCTT	TTTCCATACC	ATGTGTGAAC	ACCACTTCTT	GCCATTTTAT	GGTAGAGCGC	3840
ACATTGCCTA	CATTCCAGAT	GGTCGTGTGG	CAGGCTTGTC	TAAGCTAGCC	CGTACGGTTG	3900
AAGTTTATTC	GAAAAACCA	CAAATTCAAG	AACGTTTGAA	TATCGAAGTG	GCCGATGCCT	3960
TGATGGACTA	TCTAGGTGCT	AAAGGAGCCT	TTGTTGTCAT	TGAGGCGGAA	CATATGTGTA	4020
TGAGTATGCG	TGGTGTTAGA	AAACCAGGCA	CTGCAACCTT	GACGACAGTA	GCTCGTGGTC	4080
TATTTGAAAC	AGATAAGGAT	CTCCGTGACC	AAGCTTATCG	TTTAATGGGG	CTATAAAAAG	4140
AATCCGCTTC	AAGCGGATTT	TTCTAGAAAAG	GAATCATTAT	GGATCAACTG	CAGATTAAGG	4200
ATTTGGAAAT	GTTTGCCTAT	CATGGTCTTT	TTCCTAGTGA	GAAAGAATTG	GGGCAGAAAT	4260
TTGTCGTTTC	AGCCATCCTA	TCCTATGATA	TGACCAAGGC	AGCTACAGAC	TTGGATTTAA	4320
CAGCCTCTGT	CCATTACGGA	GAATTGTGTC	AGCAGTGGAC	GACTTGGTTT	CAGGAAACGA	4380
GTGAAGATTT	GATTGAAACG	GTAGCCTATA	AACTGGTGGA	ACGTACCTTT	GAGTTTTATC	4440
CTCTTGTC	CAAGAAATGAAG	TTGGAACCTGA	AAAAACCTTG	GGCACCGGTG	CATTTGTCAC	4500
TAGATACTTG	CTCGGTAACC	ATTCATCGCC	GCAAGCAACG	AGCCTTTATC	GCCCTAGGAA	4560
GCAATATGGG	AGATAAACAA	GCAAACCTGA	AGCAAGCCAT	TGACAAACTG	CGAGCTCGTG	4620
GCATCCATAT	TCTCAAAGAG	TCCAGTGTCT	TAGCGACGGA	GCCTTGGGGT	GGAGTGGAGC	4680
AGGATAGCTT	TGCCAATCAA	GTGGTTGAGG	TGGAACCTG	GCTACCAGCA	CAAGACTTGT	4740
TAGAAACCTT	GTTAGCCATT	GAGTCAGAGC	TGGGACGGGT	GAGAGAAGTG	CATTGGGGAC	4800
CTCGTTTGAT	TGATTTGGAC	TTGCTCTTTG	TGGAGGACCA	GATCCTTTAT	ACAGACGACC	4860
TCATATTGCC	TCATCCTTAC	ATAGCGGAAC	GCCTTTTTGT	CCTTGAGTCT	TACAGGAAAT	4920
TGCGCCTCAT	TTTATCCATC	CGATATTAAA	ACAACCGATC	CGCAACTTGT	ATGATGCTTT	4980
GAAAAAATAG	AAAAACTCTA	GTTTTTCAGTT	ACTTGCAACT	GAAGGCTAGA	GTTTTTATAC	5040
TCTTCGAAAA	TCTCTTCAAA	CCACGTCAGC	GTCGCCTTAC	CGTACTCAAG	TACAGCTTGC	5100
GGCTAGCTTC	CTAGTTTGCT	CTTTGATTTT	CATTGAGTAT	TAAAATAGGT	CATTTTCTTC	5160
TGGGAGGAGG	ATAGTTTCTC	TACCGTCCAT	GTCTAAAACC	AGTACTCTTG	GGGGATAACG	5220
AGGGTCGAAA	GGATGGTTAA	AGTCAAAATC	AATGGCTGTA	GGGAGGTGTT	GACTTGAAAA	5280
GTGGAAGGTA	ATCTTTCCTT	GGTTATTAAG	CAATTGAAAC	TCGAGTTCTT	CTTCCAATTC	5340
AAAGACATTT	TTTAAGAAAT	GGTCGATGAT	ATACCAAAAA	GAGTCAATGA	TGTCATCAGG	5400

1298

CAAGCTGGTA ACAATACCAA AACTAGCAGA TCGCATGTGG GTATTGGTAA AAGCCATATC	5460
TCTGTCCCCT TTCTTTTCCC TTATCATACA GCAAATAGGA TTAAAAATCA AGAAAAGGTG	5520
ATTTTTTGAA AAGGATTTTA GTTACAGGGA GAAATAGGGA AAAAATTCCT AAAAATCTAC	5580
CGAAGTTAAT AGGTAAATTC CCAAATTAAC TTGATTATAT AACTTTCAGT TACTTTGAGA	5640
AGTTACCGAA AAATATTTTT CATATCTATT GACTTTTAGG GGTAATAATT GGTATGATAG	5700
TAGGCGGTAT TGTTTACCCC ATTTGAAAGG CCCCAGAAC TTCCAAATAC TTTTCGATGG	5760
GAAGGAACAC CCATCACCGT AAACAAAAAT CGAACTATAT ATAGGAGAAA TCATGAACAA	5820
AACAACATTT ATGGCTAAAC CAGGCCAAGT TGAACGTAAA TGGTACGTAG TTGACGCAAC	5880
TGATGTACCA CTTGGACGTC TTTCTGCAGT AGTTGCTAGC GT	5922

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1988 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

TAACATCTA CGATGAGCTG TTGTGATTCT CATTAGTTCC CCTTTCCCAA GAGGCATAGG	60
GGTGCGCATA ATAGATGTGC TCCTCAGAAA ATATATCAAA CAAGCGATTG AATCCGTTTC	120
CATTATCTGC CGTGATGGAA AGAATCTTGT GTTGTTTTAA GATGAGTTT AGAGCCTGAT	180
TGACCACCTC AGCACTTTTA TTTGGAATCA ATCGGATGAT CTGATGTCTA CTCTTTCGAT	240
CCGTCAAGAC AATCAAGCAG TAGTTTTTCG ATCTCGTAAG TAGAACCGTA TCAATCTCAT	300
AATGCCCAT CTCCAAGCGA AGATTGATAG CTCAGGCCG CTGTTTCGATG GATTGACCAG	360
CAGGTTTAAA GTTGGTGCTA GCCTGTTTCT TAAGCGCTTT TCCTTTTCTA GGGTAAAGCA	420
AATCCTGCTT GCTTAACCCC AATTTTCCAT GATGAATCCA ATAGTAAATG GTTGAAATTC	480
CCACGTTAAC CCCTTTAGCC ATAACCATCA TTTCAGGCGA AAATTTTGG TTATGATAGT	540
GGAGAATCTT TTCCTTTAGT TCCTTGGTCA AGCTTGATTT CTGACCGAG CGCTTGCGAT	600
TGTTTTCATA AGACTGTTGA GCGTAGTCGG CAGAATAAAC CTCTTTGAAG CGCCCTTTTC	660
CAAGACATTG TCGGACTGTC CCACGCTTGA TTTCAGTGTG ATAGTTTGAG GAGCTTTTCC	720
AAGTAGAGAG GCAATTTCTC TATTTGATTT TCCTTCTTTT TTCCATCTTT CGATTAAGCG	780
ACGGCTATCG ATTGTCAAAT GTTTGGCTTT TGTAGTATAA TTGTCTTGCA TCTCTGTGCC	840
TTTCTTGTGT TTGTGGTTGA ACAACAAGTA TAACACAGAG GTGCTTTCTT ATGCCTACAA	900

1299

GAGCTTTCAT TATTTCCATT TTCTTTTGGA TTTCACCTCTA TTCTGAAAAA CTTGTGTATA	960
TTTACTGAAG CTAGCAAGTC TTACCTGTAA ATTTAATGAA AGCAACACAA AATCCGAGAG	1020
GGGAATCTCG GATTAATAGA TAGAGAGTTT TTAGTTTAAA TAAATTGTTT AAAATATCAA	1080
CAACATCACT TCTTTTCTTA ACCTGATAAG TCTTGATTCC TAATTTTGGG GCTACGATTA	1140
TATTGTCCTC AATATCGTCT AGAAAGACAC AATTTCTAGG TTATAACTGG TATTTATCGA	1200
TAGTTACTCA TATACATCAG TCCACCTCCA TACTTATGTG CGAGCCTCTC TTTGTATTAT	1260
ACCTCCATAC TCACCTTACA GATTCTTTTG GTAATAATAT CTTTGCCTAA TGTAGAGACA	1320
GTCTTGCAAA GAAAAAAGTT CCTTGTAGCC ATGTTTCTGA TAAAAGTCCG GTGCCTGGAA	1380
CTGGTAAGTA TTGACAAAGG CAAAACAACA ATTTGATTTC TTAGCTTCAC TTTCTGCCTG	1440
TTGCAATAGT TTTGAACCGA TTCCTTGCCC TCGCAGTTCC TCTTTTACAA ACAAATACTC	1500
GATTTCTAGC CAATTTCCAA AAGTCTCTGC TATCAAACCT GCCAGGAGAT TGCCCTTTTC	1560
ATCTTCGACA TAAAGATTAA GTGGCTCACT TTCAGCCTCT TCTCTTTTGT AACGGTTATA	1620
AACACGAATC AGATTCCCTA TTTCTTGCGA TTTATGTGAT TCCTTATTTT CCAATCTAAA	1680
GTATAGTGAA ATGAAATAAA ACATGCGCAA ATCGATTAAG GAATTTAATC TAATTTCTAA	1740
CAATGTCTTA GAAATCAAAG TGTACTATTT TAACTTCAAT GCACTATACA TCTAATACTC	1800
AATAAAAATC AAAGAGCAAA CTAGGAAACT AGCCGCAGGT TGCTCAAAAC ACTGTTTGTGA	1860
GGTTGTAGAT AGAACTGACG AAGTCAGCTC AAAACATAGT TTTGAGGTTG TAGATGAAAC	1920
TGACGAAGTC GGCTCAAAAC ATGGTTTGTGA GGTGTAGAT GAAACTGACG AAGTCAGCTC	1980
AAAACAGG	1988

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 709 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

CCGGATATTT GTTTTATGTA ATTTTCTTGC AAGTTTCTTC TTAGTAGCTT GTCAGTCAGG	60
TTCTAATGGT TCTCAGTCTG CTGTGGATGC TATCAAACAA AAAGGGAAAT TAGTTGTGGC	120
AACCAGTCCT GACTATGCAC CCTTTGAATT TCAATCATTG GTTGATGGAA AGAACCAGGT	180
AGTCGGTGCA GACATCGACA TGGCTCAGGC TATCGCTGAT GAACTTGGGG TTAAGTTGGA	240

1300

AATCTCAAGC ATGAGTTTTG ACAATGTTTT GACCAGTCTT CAAACTGGTA AGGCTGACCT	300
AGCAGTTGCA GGAATTAGTG CTA CTGACGA GAGAAAAGAA GTCTTTGATT TTTCAATCCC	360
ATACTATGAA AACAAGATTA GTTTCTTGGT TCGTAAGGCT GATGTGGAAA AATACAAGGA	420
TTTAACTAGC CTAGAAAGTG CTAATATTGC AGCCCCAAAA GGGACTGTTC CAGAATCAAT	480
GGTCAAGGAA CAATTGCCAA AAGTTCAATT AACTTCCCTA ACTAATATGG GTGAAGCAGT	540
CAATGAATTG CAGGCTGGAA AAATAGATGC TGTTCATATG GATGAGCCTG TTGCACTTAG	600
TTATGCTGCT AAAAACGCTG GCTTAGCTGT CGCAACTGTC AGCTTGAAGA TGAAGGACGG	660
CGACGCCAAT GCCGyTGCTC TTAGAAaATA GTGATGATTT GAAAGAAGT	709

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1680 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

TATAAAATGT TAAGTTAAAT GATTTCAAAA TTCAGAAAGG GATTGCTTTA TGCAGTTCCT	60
TTTTATTTTA ACAGGAGTGA AACTATAGTG TTTCTAAATT GTGAATCAAT CAAAAGTATG	120
TGTGATGGGG CTATTCTAGC TTTAGAAACC TTCAAAAATT AAAATTTAAG GCAATCAATT	180
ACTTGGAAGA GTATGAAAGC ATTTAGTTTA TAGGAATTCT AGGTCTAGAA TTACATATAT	240
ATATTTATGA AGACGGGGTG TTCGATAGTT AGTATTGTTC TATTCTGAAA GATTTGAGCT	300
GTCAGTTGTA TAGAAAGTGT TCGAATTTTT TTAAGTGATT AAATTAGTTA ATTGTATGAG	360
GTGCTTTATG ATATAATGTT CTTAATGAAT TTTCAGAAAG GAAAACCTCA AATTGTTCTA	420
CAAATTTCTA CTCTTCGACC TCGACCACAC TCTTCTTGAT TTTGATGCTG CTGAGGATGT	480
GGCTTTGACC CAACTTCTAA AAGAAGAAGG AGTTGCGGAT ATTCAGGCTT ATAAAGATTA	540
TTACGTTTCCT ATGAACAAGG CTCTCTGGAA AGACTTGGAG CTGAAGAAAA TCAGTAAACA	600
AGAGCTGGTT AACACGCGCT TTTCTCGTTT ATTTGCTCAT TTTGGACAGG AAAAAGACGG	660
TAGTTTTTCTT GCCCAGCGTT ACCAATTTTA CCTCGCCCAG CAGGGACAAA CACTATCGGG	720
CGCTCATGAT CTCTTGGACA GCCTCATTGA GCGTGATTAT AACTTGTATG CTGCGACAAA	780
TGGCATTACT GCCATTCAGA CAGGACGTTT GGCTCAATCT GGTCTAGCAC CTTATTTCAA	840
TCAAGTCTTT ATCTCAGAAC AGTTGCAAAC TCAAAAGCCG GATGCTCTTT TTTATGAAAA	900
GATTGGCCAG CAAATTGCTG GATTTAGTAA AGAAAAGACG CTGATGATTG GAGATTCTCT	960

1301

AACCGCCGAC ATTCAAGGTG GCAATAATGC GGGGATTGAC ACTATCTGGT ATAATCCTCA	1020
TCACCTCGAA AATCACACAC AAGCCCAGCC GACTTACGAA GTCTATTCTT ACCAAGACTT	1080
GCTGGATTGT TTAGATAAAA ATATTCTTGA AAAGATCACA TTTTAAAGGA GACGAGCTAA	1140
TGACTACAAA AAAGCTAATA TTACTATTGA AGAGTACATT GAAATGTCTG AAGTTGATTT	1200
TAATGAAGCT GTTAATTATG AATTTACATC TGACACTTGT CAATTAGCAA ATAGTATTTA	1260
TCAATCTCTT TTTAAGTTTT TTGATAAGAA AAATTTCTCT GGCGATTAA TTTTACTTG	1320
GAAATCTCCA TCATTAGTCA AAGAAGGGGA TTATATTGGG AGAAGGGATT CACAAGTAGA	1380
TAATCTTAGA GTAATAGGAA ATATATTTCC GAATTATCTT ACTAATCGAA AATATAGCCT	1440
CAATATGAAT CGTAATGGCT GTATGGGAGA TTTTCCTCAT GACTTTTTTG ATATATACCT	1500
AGATCATGTA GCAAAATATG CCTACGAACA AAAAGTTAAT AATATTAAAG AGTATTATCC	1560
TTTAAAAAGA GCGATTTTAC ACCAAGAGAA TGCAATGTAT TTTCGATTTT TTTCTAATTT	1620
TGACGACTTT TTAGAAAAAA ATTATTTAAA GACTATATGG CAAGTTTCTA AAGAACTCC	1680

(2) INFORMATION FOR SEQ ID NO: 271:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 598 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

AGCTCGGTAC GTAGTATnTG TGGTGCATAA ATGAGTGAAA AGAGGATAGA GAGGATGAGG	60
CCGATAAGAA CACCGGTAGC TGCATCGTGA AATACTTGTT TTTTCATAGT TCTAATTTCT	120
CCTTGATGGT TTTTAGATAA CGGCGTGAAG AGTAGGTGAA GCTTTCGTTT TTCAAGAAAA	180
TTTCTACCAG ACCGTTTGGC GTGA _g CTTGA GGTGAGAGAT GGAATCGATA TTGATGATTT	240
CTGATTGGGA AATTTGGATA AAATTGGTTG GCAAGAGTTT AAGAACCTGA TAGAGTCGCA	300
AATCAATGCT GTAGGTCTGA CTCGCGGTTT CTGCTAGAAC CTTCCGATTC TCGATATAGA	360
AGCGCTGAAT CTTGCCAATC TCAACTAGAT AGACCTGATC ATCGATTTTT CTTTGATTT	420
TTTCTCTTTG GTCCAGATTT TCTGCGAACT CGATGACTTT CTGGACTTTT TCGGTTTCTT	480
GAGGTGCTTG GACAATCAGC TTTTCCTCCT CGTAAGTCTC ACTAATCTGT AGTTCTACTT	540
TCATAGTTTT CTCTCCTTTT CAGTTATACA AGGTTGTGAT CACTTCCTGT ATATCCGG	598

(2) INFORMATION FOR SEQ ID NO: 272:

1302

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1099 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

CCAGCAAATC AATAACTGCA ATTGCTATAA AATGGATTCT ATAGAGTTTT TTCATGACAA	60
GACCTCCCTC TTTTATCTAA CTTCATTCTA CTCCAAAAGA ATGGGAGTTA CAACTAAAAT	120
GATAAAAATA GCAGAAGGGA GATTCTCTTA AGTTGGCTAG TATTCTTTAT TTGAGTTTCC	180
TTCTATTATC TAACTTCTTC ATCATTCAG ACAAATAAAG CTCCGATTGC ATTGAGGATA	240
TAAAAGATGT ATTTACCGAT ATTGGCGAAG TTTCTTGAA TACCAGCTTT TGTCAGCTGA	300
ACGAAATTGT AAATCAACCA AAAGCCCCAC TGAGTTGTGA GTTTTAATGC ATTCAAAGCA	360
TTGGCAATGA GGGACAGTGC AAAGGCAATA GTTGTTACGT AGGCAAGGAG ATTCATCTTG	420
CCCCCATATC CGATATAGTT GGTCACAAAG GCAAAGAGGA AGGCGATGAT GGAAATGATG	480
ATGGCCGCCA ATTTTACCTG TTTTGGCTC ATTTGGTTGG GTCTGCCTTC TTGCGAAGCT	540
TCCCACTTCT TTATAGCAAA GGTATAAATG AGGAAGGTGA CGGGATAGGT AATGATGGCC	600
GCCTTATTTC CAAGGATATA ATCAATAGCA CCGGACAAAA TGGTATTAAC AATACCAAAG	660
TAATTTCCCC ATTTGCTTAA TTTCCCCGTG AAACGAGTGG ACAACATGGA AATCCCAACG	720
TTGGTTACGG AAATCAATCC AAAGGGTACA AGAGCTGTCC ATGATCCCCA GTCTACAAAT	780
TTATCGAGGT GTGAGTTGAG GTAACCAGAT GCAATCGCAA TCCCAACGAC CAAAGCAACC	840
CCGAAGAGGT CAACTATTT AGATGTAGCA AAAATTTTTA GTGATTTTTT CATAGGTAA	900
ACTACCTTTC TTTTTTTCAA ATATTCTCCC ACCAAATGAA AGTAAAATAA AATGATAGAA	960
ATAAAACCCT GAAAATAAAG GTTCTATAAT ATTTGTAGTG GGTAATCCA CTATAGATAT	1020
TATGGAGCCT ATTTTATTGT AGAAAAAAG TCCCATATGA CCTATAATGA AAAGCGACAA	1080
AACAATCAT TAGAAAGAT	1099

(2) INFORMATION FOR SEQ ID NO: 273:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2723 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

1303

CTGGGATTCA	CGTGAAAAGG	AAGCCCAGAG	AGTAGCCAGG	TGTACTGCTA	GAACAGTGAG	60
TGAAATTGAA	TATTACCATA	GAGAGTCAAC	CCAGATAGCT	CAGGCTTTAG	TTGAAAATCA	120
AGCTCGTATC	GAGGGAATCT	ATAAATACTT	TAGCCTTAGC	ATGCCAGACT	ATTTTACTG	180
GCAATTAGAG	CGGAAAGCTT	CGCCTTATAT	ATCAGTCTCT	CTGTATGAAA	ATGTTGATGA	240
CCTCTATGTT	CGAAATGATT	TTGTAACTGG	GGTGGCCATT	GCTTTTCAAG	ATTACAAGGA	300
AGTCTATGTT	TCTACTAAAG	ACAAACGTAG	GkkAGAAAAA	ATCAGGGCTG	AGGATTTCAA	360
ACCAGCAGGA	AATAGTTTTG	CCATTCCAGT	GTCAGATCCA	GTGTCAGATC	AAGACTTAGG	420
AGTGATTTAC	ATCTCCTTGG	ATCCTGCTGT	TTTATACCAT	GCCATTGATA	ATACTAGAGG	480
TCATACTCCG	ATGGCAGTAA	CAGTGACCTC	ACCTTTTGAT	ACGGAGATTT	TTCATATGGG	540
TGAGACAGTT	GATAAGGAGA	GTGAAAATTG	GCTAGTTGGC	TTAACTTCTC	ATGGATATCA	600
GGTTCAGGTG	GCAGTTCCTA	AAAACTTTGT	TTTACAAGGA	ACAGTGACTA	GCTCTGCTTT	660
GATTGTGGGT	TTGAGCCTTC	TCTTTATTGT	CATTCTTTAT	CTGACTTTGA	GGCAGACTTT	720
TGCTAATTAC	CAAAGCAGG	TAGTGGATTT	AGTAGAATCC	ATTCAAGTCA	TTGCTCAAGG	780
CGAAGAGGGG	CGTCGGATTG	ACATTTCCGA	GAAAGATCAG	GAATTACTCC	TAATCGCGGA	840
GACGACCAAT	GATATGTTGG	ATCGATTGGA	AAAGAATATC	CATGATATTT	ACCAGTTAGA	900
GCTTAGTCAA	AAAGATGCCA	ATATGCGAGC	CTTGCAGGCG	CAAATCAATC	CTCATTTTAT	960
GTATAATACG	CTGGAGTTCT	TGCGCATGTA	TGCAGTTATG	CAGAGTCAAG	ATGAGTTGGC	1020
AGATATCATT	TATGAATTCA	GTAGTCTCTT	GCGTAACAAT	ATTTCCGACG	AAAGAGAGAC	1080
CCTCCTCAAA	CAGGAATTAG	AATTTTGCCG	TAAATACAGC	TATCTCTGCA	TGGTTCGCTA	1140
TCCCAAGTCC	ATTGCCTATG	GTTTCAAGAT	AGATCCAGAG	TTAGAGAATA	TGAAGATTCC	1200
CAAGTTTACC	TTGCAACCGC	TGGTAGAAAA	CTATTTGCGC	CATGGTGTTG	ACCACAGGCG	1260
GACAGATAAT	GTGATTAGCA	TCAAGGCTCT	TAAACAGGAT	GGTTTTGTGG	AAATTTTGGT	1320
GGTCGATAAT	GGTAGAGGAA	TGTCGGCTGA	AAAGTTGGCA	AATATCCGAG	AAAAATTAAG	1380
TCAGAGATAT	TTTGAACACC	AAGCCAGCTA	CAGTGATCAA	AGGCAGTCTA	TCGGGATTGT	1440
CAATGTACAC	GAGCGTTTTG	TGCTCTATTT	TGGAGACCGC	TATGCCATTA	CTATAGAGTC	1500
TGCAGAGCAA	GCCGGTGTTT	AGTATCGTAT	TACAATTCAA	GATGAGTAGA	AAGGGAGAAA	1560
ATGTATAAAG	TATTATTAGT	AGATGATGAG	TACATGGTGA	CAGAAGGTCT	GAAGCGTTTG	1620
ATTCCCTTTG	ATAAGTGGGA	TATGGAGGTC	GTCGCAACAG	CCAGTCATGC	CGATGAAGCT	1680
CTAGAATATG	TTCAGGAAAA	TCCTGTCGAT	GTCATCATTT	CCGATGTCAA	TATGCCAGAC	1740

1304

AAAACAGGGC TTGATATGAT TCGGGAGATG AAAGAGATCT TACCAGATGC TGCCTATATC	1800
CTGCTCTCAG GTTATCAGGA GTTTGATTAT GTAAAAAGAG CAATGAACCT TAGTGTGGTG	1860
GACTATTTGG TCAAGCCTGT TGATAAGGTA GAGCTGGGAA ATCTGCTGGA GAAGATTGCA	1920
GGTCAGCTCG GCGAGAGAGG GAAGAAAAGT CAGACTCTTA GTCAAGAATT AGACGAGGCT	1980
GGATTTGTTA GTTATTTAGG GGATAAGGAG AATTGGTGGA TAGGTCTATC CAAGGAAAAA	2040
CAAGGTTCCCT TCACCATTCC CTACTATGTC TTGGGTCAAG ACTGGCAGAT TTTCATTTCT	2100
GGCCACCCCC TAGATGGTTT AGTCGTTACA CCTTTTGAAG CTCCTTATCA AGAACACTTT	2160
GAACGCTGGA AGCTGAATGC TGAGAAAACC CTCTTTTACG GTTCTGTAAA TCTGCAGCAG	2220
TCTGAGAGTC TCTTTGCCTA TTACGAACCG ATTTATAGGG TTATCATTCA GGGAAATCTC	2280
AATCAAATCG TAGAAGAGTT AAATCTCTTG GAGAAGGTAG TTCTTGAAAA TACACCTCGT	2340
GTTCGATTA CTAAACAGCT TTTTATCCAG TTTGTCATGG ATGTTTTCCA TTTATTTGAA	2400
CATCTCAAAG CTGATGATAT GACGGACATT GTCAAAACCA TTCATGCTAT TCAATCCTTC	2460
GATGAATTGG TTTCTTATAT CAAGGAAACT CTGATCAGCT TTTTCGGTCA ATACCGTATG	2520
AATGAAAATG TGGTCAGTGT GCTGGAAGTC ATTGGTCGTG ATTACCAAAA AGAGCTTTCC	2580
CTCAAGGATA TCAGTAAGGC CCTCTTTATC AATCCTGTCT ATCTAGGGCA GTTGATTAAG	2640
CGTGAAACCG ATTCGACCTT TGCAGAGTTA CTAAACAAAC AACGTATTAA GGCTGCCCAG	2700
CAGCTCTTGC TTTCAACTAG TGA	2723

(2) INFORMATION FOR SEQ ID NO: 274:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 836 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

CCGCAGTTTT TTAAACCGT ATATAAGTAT AGCATAGTCA AAAAAAGAAT GCAAGATTTT	60
TGCAAACCTTT TTAAAATTT TTCGTAATTT TTCTTTTAAA GTTCTACTGT CAGGACTTGA	120
CCTTGCTTAA CAACCTGTTC TCCGGCGATA TAAACATCAT CTACATCACT AGATTTAACT	180
GCATAAACCA GGTGAGACAG CATATTTTCC TGAGGTTGGA GATGAATTTT CCCTTGTTGGT	240
TGAATGACCA GAAAATCTGC TTGCTTGCCG ACTTCCAGAC TTCCTATCTG ATTTTCCATT	300
CCAAGGACCT TAGCCCCTTC GATTGTCAGT ACCTTGAGAG CTGTTTCGAT TGGAAACTGG	360
CTGGCATCCC CACTTTTCAT CTTCTGAAGA AGAGCTGCAG TCCTTCCTTC CTCAAACATA	420

1305

TCTAGATTGT TATTGGAAGC AACCGAGTCA GTCGCAATTC CGACTGCTAC TCCCGCTTTT	480
TGGAGCTGGA TAATTGGAGC AATTCCTGAT GCCAGTTTGA GGTTACTGAT AGGATTGTGG	540
GCGATAGCnA CTTGAGAAGA TGCCAAGCGT TCAATTTCTC TCTCGTTTAA TTCGACCCCG	600
TGAGCAAATA CGGACGGATG ATCTAAATAA CCCAGTTCTT CAAGAAAAGC AAGGGGGCGT	660
TTGCCGTATC GTTTGAGGAT AATTCCTGAC TCCTCCTTGG TCTCCGCCAC ATGGACATGG	720
AGCGGAATAT TTAGCTCTTT TGCCATTTCC AACTCGCTT CCAGCAAGTC TCTACTGCAG	780
CTATACGGAG AATGAGGTGC TACCATAACC TTGAAATTG GATTTTATA TTTTAA	836

(2) INFORMATION FOR SEQ ID NO: 275:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

ATTTTATTTT ACTTTTTAGG TGGTCTGGGG CTATTCTTAT ATAGCnTCAA GACCATGGGA	60
GACGGTTTAC AACAAGCTGC TGGAGATCGC CTGGGTTTTT ACATTGACAA ATATACTAGT	120
AATCCTTTGT TTGGAGTTCT GGTGGGTATT GGGATGACTG CTCTAATTCA GTCTAGTTCT	180
GGTGTAACAG TTATCACAGT CGGCCTGGTC AGTGCCGGTC TCTTAACCTT ACGTCAGGCT	240
ATCGGGATTG TCATGGGTGC TAATATTGGG ACAACTGTCA CATCCTTTCT CATCGGTTTT	300
AAATTAGGTA ACTATGCCCT ACCTATGCTC TTTATCGGTG CCGTCTGTCT TTTTTTTACG	360
AAAAATCGGA CAGTCAATAA TATCGGACGC ATCCTCTTTG GTGTCGGTGG TATCTTTTTT	420
GCCCTCAATC TCATGAGCGG CGCAATGGCT CCACTCAAGG ATTTACAGGT CTTTAAGGAC	480
TATATGATTG AGCTAAGTAA GAATCCTGTT TTGGGTGTCT TTGTCGGTAC TGGCTTGACC	540
TTGCTAATTC AAGCTTCTTC GGCTACCATT GGGATTTTAC AAAACCTCTA CGCCGGCAAT	600
CTAATTGATC TACAGGGAGC TTTGCCAGTT CTATTTGGTG ACAATATCGG GACAACCATT	660
ACAGCCATCA TTGCCTCTTT AGGGGCTAAT ATTGCAGCTA AACGGGTAGC AGGAGCTCAT	720
GTTGCCTTCA ACGTTATCGG AACAGTTGTC TGC GTTATTTT TTCTAGTTCC TTTTACTGTC	780
CTGATTCATT GGT TTGAAGC TACGCTAAAT CTAGCACCGG AAATGACCAT CGCCTTTGCT	840
CACGGAACCT TTAATATTAC CAACACCATT GTCCAATTTT CATTTATCGG AGCTCTGGCT	900
TACTTTGTAA CCAAGATTAT TCCTGGAGAG GACGAGGTG TCAAATACGA ACCCTTATAT	960

1306

CTTGATGAAC	ATTTTCATCAA	ACAGGCCCCCA	TCTATCGCTC	TAGGAAATGC	TAAGAAAGAG	1020
CTCTTGCACT	TAGGAAACTA	CGCTGCTAAA	GCCTTTGACC	TTTCCTATAA	GTACATCATT	1080
GACTTGGATG	AAAAAGTTGC	TGAAAAAGGG	CATAAAACCG	AAGAAGCAAT	TAACACCATC	1140
GATGAGCAAT	TAACACGTTA	TCTCATTGCC	CTTTCAAGCG	AAGCTCTCAG	CCAAAAAGAA	1200
AGTGAAGTGC	TTACCAATAT	CCTTGATTCC	TCCCGTGATT	TGGAACGGAT	TGGAGACCAC	1260
ACGGAGGCTC	TACTCAATCT	GACTGACTAT	CTTCAACGGA	AAAATGTTGA	ATTTTCTGAT	1320
GCCGCCTTGA	AAGAATTAGA	GGAAGTTTAC	CGCCAAACTA	GTGACTTTAT	CAAAGATGCT	1380
CTGGATAGTG	TGAAAAACAA	TGATATTGAA	AAAGCACGCA	GTCTTGTAGA	ACGTCATGAA	1440
GCAATCAATA	AGATAGAACG	TGTTCTCAGA	AAAACCCACA	TCAAACGCCT	CAACAAAGGC	1500
GAATGTTCAA	CACAAGCTGG	GGTCAACTTT	ATCGACATCA	TCTCACACTA	CACTCGTGTA	1560
TCAGACCACG	CTATGAACCT	TGCTGAAAAG	GTTTTTGCAG	AACAAATCTA	AGAACCAAGA	1620
AGCTATCCAT	CATAATTGGA	TGGCTTTTTA	CTTTTTCCTA	AGCAAGACTA	GGATGAATGA	1680
AACTGAAAGA	GTATTCTGCA	GATATATAGT	CCCCAATTAT	TCACCCCAAA	TCTAAAAACC	1740
ATCCAGAATC	CTTGCCCTAG	CTTAGATCCT	GGATGGTTTC	TTTTTTCACC	CAATGGGTGT	1800
TTTTTACTAG	ACAAAAAAGA	GTTTCCCCTT	TATGGTATAA	GTGTAGAAAA	AAACACAAAA	1860
AGAAAGGAAA	CTCACATGAA	CAGTTTACCA	AATCATCACT	TCCAAAACAA	GTCTTTTAC	1920
CAACTATCTT	TCGATGGAGG	TCATTTAACC	CAGTATGGTG	GTCTTATCTT	TTTTTCAGGAA	1980
CTTTTTTCCC	AGTTGAAACT	AAAAGAGCGG	ATTTCTAAGT	ATTTAGTAAC	GAATGACCAA	2040
CGCCGCTACT	GTCGTTATTC	GGATTCAGAT	ATCCTTGTC	AGTTCCTCTT	TCAACTGTTA	2100
ACAGGTTATG	GAACGGACTA	TGCTTGTA	GAATTGTCAG	CTGATGCCTA	CTTTCCAAAA	2160
TTGTTGGAAG	GAGGGCAGCT	TGCTTCACAG	CCAACCTTAT	CCCGTTTTCT	TTCCAGAACT	2220
GACGAGGAAA	CAGTCCATAG	TTTGCGATGC	CTCAACCTTG	AATgGkCGAA	TTCTTTTAc	2280
AGTTTCACCA	GCTAAACCAA	CTCATTGTAG	ATATCGATTC	TACCCATTTC	ACAAC	2335

(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 752 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CGGATTCACT	GTTGTTGACT	AATCAATAAC	ACAGTAGAAA	ATCTCACAGC	AGTCTATTAG	60
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1307

TTGCTTTTCA TACTAGGCAA GTGACTGAGG CTTGTACTTG GGTACAGCAA GGGAGCTTAA	120
GGCCGTAGAA GAGAAAAATA GTAGACTGAA AACCCGCAAG ACTTCATCAT TTCGAGAAGT	180
GACGTGGGAG ATGAAAATCG ATTGAACCAC TTACAAGGAG AATAGAAAAT GGCTAAAAAA	240
AGCAAACAAC TTCGTGCTGC TCTTGAGAAA ATCGACAGCA CAAAAGCATA CAGTGTAGAA	300
GAAGCTGTAG CACTTGCAAA AGAAACTAAC TTTGCAAAAT TTGATGCAAC TGTAGAAGTT	360
GCTTACAACT TGAACATCGA CGTTAAAAAA GCTGACCAAC AAATCCGTGG AGCAATGGTA	420
TTGCCAAACG GTACTGGTAA AACTTCACGT GTTCTTGTTT TCGCACGTGG TGCAAAAGCT	480
GAAGAAGCAA AAGCTGCTGG TGCAGACTTT GTTGGTGAAG ATGACCTTGT TGCTAAAATC	540
AACGACGGTT GGTGACTT CGACGTAGtT ATCGCTACAC CTGATATGAT GGCTCTTGTT	600
GGACGTCTTG GACGTGTCCT TGGACCACGT AACTTGATGC CAAACCCTAA AACTGGTACT	660
GTAACAATGG ATGTTGGCAA AGCGGTTGAA GAGTCTAAAG GTGGTAAAAT CACTTACCGT	720
GCTGACCGTG CAGGTAACGT TCAAGCAATC AT	752

(2) INFORMATION FOR SEQ ID NO: 277:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2643 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

GTCAACATTG ATTTCAAGGC TGTGCTTT CTATCTCCCC TTTTTCATAA TGTATAATAA	60
AATGAAATAA TAACAGGACG AATTGATCGG GACAGTCAAA TCGATTTCTA ACAATGTTTT	120
AGAAGTAGAG GTGTACTATT CTAGTTTCAA TCTACTATAT TTTCGTACAG GTGCTTCAAC	180
CATTTGAACG ATTTCAAATC CTTCTTTTTG GTAAAGATTC TGAGCTCTTT GATTGCTTC	240
GAAGACATTT AGAGAAATAC TGTCTATATC TCTATTTTCA AATGCTAAAC TAACAAATTT	300
CCTTAAAGCC TTGCTACCTA AGCCTTGCTC CTGTTTCTGG GGGTTGATAA AAAATCTCCC	360
GATATGAAGA TTGCTGTCTT CTAGCCTGAT TTTCTGGATA AATCCCACAA ACTCTGTTC	420
ATCAAAGATT GAAAAGACTC CTTCCAAGGC TTGAAGTGTC AGTAGAAAAG GAATCCTTGG	480
TCCCATCCAT TGTCTTGAA AGGATTTGCC TAGGGAGTTG GACCACTGGC ATACAAATTG	540
AGCGTTTTCT GTGCTCACCT TTTCTTCAA ACGAATTGTC ATCTTTTCCT CACCACCTTA	600
TCTATGTTTC TCCATTATAC TATTTCTCCC ATTTTTTACG AATAGATAAG TATGATTGAT	660

1308						
TTTTATTTTT	TTCTCGTCGG	GAGCATTCTA	GCTTCCTTTC	TTGGTTTGGT	CATTGACCGT	720
TTTCCAGAGC	AATCCATTAT	CAGTTCAGCC	AGTCACTGCG	ATTCCCTGTCA	GACTCCCTTG	780
CGTCCCTTAG	ATTTGATTCC	GATTCTCTCA	CAGGTCTTCA	ATCGCTTTCG	CTGTCGCTAC	840
TGCAAAGTTC	GCTATCCTGT	CTGGTATGCC	CTCTTTGAAT	TAAGCTTAGG	ACTCCTCTTT	900
CTGCTTTACT	CTTGGGGATG	GCTCTCCTTG	GGGCAAGTCG	TCCTAATCAC	CGCTGGTTTG	960
ACCTTGGGTA	TCTACGACTT	TCACCATCAG	GAATATCCCT	TACTGGTCTG	GATGACTTTC	1020
CAGCTAATCC	TAATAGCTTC	CTCTGGCTGG	AATCTGGTCA	TGGTCTCCTT	CCTCATACTT	1080
GGAATTTTGG	CTCATTTTAT	CGATATCCGC	ATGGGTGCAG	GGGATTCCTT	CTTTTTAGCT	1140
TCTTGTGCTC	TCGTCTTTAG	CGTAACGGAG	TTACTGATCT	TGATTCAAGT	CGCTTCTGCG	1200
ACGGGTATCC	TGGCCTTTCT	CCTGCAAAAG	AAAAAGGAAA	GACTTCCTTT	CGTGCCCTTC	1260
CTCTTACTTG	CTACTTGTTT	GATTATTTTT	GGTAAGCTAC	TGCTTGCTCTG	ATAAAATCCA	1320
ATTTCTGCCA	TATATCCTTC	ATGAAATTAT	TTCACAGTTA	AATTATAAAT	TATTTCTTTT	1380
GTACAAAGGG	ATGATGTTAT	CAAATCGATC	TGTTCTTCTA	TCTTCTTGAT	ACTGATCAAA	1440
AAATTTTCATT	TCGACTGAAA	ATATTTTCGCT	TATAAACTGT	AAACGAATAC	TTTGTTTAGA	1500
CATTATAGTC	GCTAGACTGA	CTAGATGATT	ACTCAAAACG	ACGTCCAGAA	TACTCTTTAC	1560
TTTGCTTGGT	TTTTTAACAA	AAATTTGATC	ATCCAAGGGT	TCAATCATTT	TGTAACCTTT	1620
TTGCGCAATT	TGACGATAAA	AGTAAGAAATG	TTGCTTTGGA	GTCAATAATC	CTAACTTAAA	1680
AGCTCGATAC	TCTAAAGCCT	GTATCGAAAC	ATTCAAATCC	GACTTCAATA	AAATATAACT	1740
ATCAGGATTG	CTGACACGCT	TGCCAACCCCT	CTCTTCAAAT	TTGACTAAAA	ACTCTTCTTT	1800
TGGCAATAAA	AAACATGATG	CAAATAAATT	TGCTTCTTGC	TCCAAACGAT	CGCCATCTTC	1860
ATTCATATCT	TTATATTTAT	GTAAAAGAAT	ATGTCCTAGC	TCATGAGCTA	AGTCAAAATT	1920
TCGACGTACA	GATGATTTAT	TCGTTCCCTAA	CACAATATAA	GGTCTTCCCA	ATTTTGACCA	1980
TGCGCTATAA	GCATCAGCTT	GGCCATTAAT	TAATCGTTCC	ACGATATAGA	TGCCTGAACG	2040
TTCTAATTTA	TAAAGCAAAT	CATGATTATC	TTTTGAAATA	CCTAATTTTT	CCCTGGCATA	2100
AAGAGCCAAT	TCCTCAATGG	ATTCTCCCTT	ATGATAAGAT	TCACTCACTA	CATTACTTAG	2160
GTCATGAATT	ATAATATTAG	GTATAATTAC	AAAACTTTCA	AAATAATCAA	TCAAACATATC	2220
TACCTTATGT	AAATACATAG	TTTGAATATC	TATTGTTTTT	CGTGTTGCTA	GGTCTGCATT	2280
TCTAAAGGCA	ATTACAGAAG	AATCAAATCG	AATGCTCTCT	TCTTCCTGTT	CAAAATAAGT	2340
TAAATCAACA	TGAAATTGGT	TGGCCAAATG	CATTTTGGTT	GATAATTTAG	GTTTCGTTTC	2400
GTTGGACTCA	AACTGCCAAA	TGGCTTGTTT	CGTTAAATTA	ATTCTCTGAG	CTAATTCTGC	2460

1309

TCTACTTAAA CCATTTAACA GCCGTAATTC TTTCAATACC CGACCATTAAC ACATTTACAT 2520
 ACTCCTTACT ACTTTTGACC TTCTTGTTTT TCTATTCTTG GAATAATTTT AAAATCTTCT 2580
 GTTTCCGATA ATTCTGAAAA ATTAGGAATA TCTTGATATT TAGCTTCTTC GAAATGGTAC 2640
 GGG 2643

(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 582 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

TGACCAGTGG CAAAATGGCT ATCCAAATGC AGATGTTATT ATCGATGATA TCATCTCAGG 60
 GCAAGCCTAC GTAGCCTTGG AAGAGGGAGA ACTGCTAGCC TATGCTGCTG TGACCAAGAG 120
 TCCAGAGGAG GCCTATGAAG CTATTTATGA GGGAAACTGG CAAGCTGGAG AGTCAGAGTA 180
 TCTAGTCTTT CACCGTATTG CTGTGGCAGC AGATGTGCAG GGAAaAGGAG TTGCTCAAAC 240
 CTTCTTAGAG GGCTTGATTG AAGGTTTTGA TTATCTTGAT TTTCGCTCAG ATACGCATGC 300
 TGAAAACAAG GTTATGCAAC ATATTTTTGA AAAACTTGGT TTAAACAAG TCGGTAAGAT 360
 GCCAGTAGAT GGCGAACGCT TGGCCTATCA AAAATTAAAG AAATAATGCA AAAGAAGTAT 420
 GTAAAAATCC TCTACTCCTC ACCAATTGGT ATTCTATCAC TTGTAGCTGA TGACCATTAT 480
 TTGTATGGAA TTTGGGTTCA GGAGCAGAAG CATTTTGAGA GGGGACTAGG AGATGAAACG 540
 ATAGAAGAAG TTGTWAGTCA TCCTATTTTA GACCCAGTTA TT 582

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 554 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

CCCAAGCTAC TAAGAGACTA AACTTGCTA GAGAAGCAAG AGAAAGTGTG AATCTTTTTA 60
 ATTTATGAT GAATTCCTT TCTGCTACCA ATTTAGAGAA ATTTTCTCTA ACCAGCAATT 120
 CCCCTAGTAT AACAAGTTCA AAAAATGGAG TCAATTTATC TGCTCACGGT CCAGCAGGTA 180

1310

GCCCCGTACT TCTGAGATAA AATAGAGAGA CCCTGTAACG AACAGCAAGT CTTGAGCGTC	240
TGCCCTTTCT TCAAAATCGC TGATAAATTC TCGGTAAGAA GAAACTATAT CGTAACCTGT	300
CACATCCCTT TCGTCCAAAG CCCCCTGATA GTCAAAGCCG GTCACCTTGA GTTCCACCTG	360
AGGCAATTTT TCAGTCAGAT AACCCAACAT CCCTTGATAA TCCTTACGTT TCAAGGATCC	420
AAAGAGGATT TGAGGTCGAT AGCCTTCCTG CTCTTTTCTT TTGATAAACT CAGCCAAGCG	480
AGTCAAGGCA GGGAGGTTAT GAGCACCATC CAAATAAATC TGTGGGCGAA TACGCTCCAA	540
GCGAsCAGCC CAAT	554

(2) INFORMATION FOR SEQ ID NO: 280:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

CCGGTTTTTC AAATGAATTT CTTGGTTGTG GCTAAAAAAT ATGCTACACT ATCAATATGA	60
AAATTTTAAT CCAACAGCA AAAGAAATGA ACACAGACTT CCAAGTATC GAGGCAATTC	120
CTTTAAAACC AGAAAGTCAG GCCGTGCTTG ATGCCTTGGC TCTCTATTCT GCCAGTCAAT	180
TGGAGAGTTT CTACAAGGTA TCAGCTGAGA AAGCGGCGGA AGAATTTCAA AATATCCAAG	240
CTTTGAAAAG GCAAAGTGCT CAACACTATC CAGCCTTGAA ACTTTTGTGAT GGGCTTATGT	300
ACCGCAACAT TAAGAGAGAT AAGCTGACCG AGGCGGAACA AGATTATCTT GAAAATCATG	360
TTTTCATTAC CTCGGCTTTG TACGGTGTTG TTCCAGTCTT GTCACCCATG GTCCTCACC	420
GTTTGGAATTT TTTGATGAAA TTAAAAGTCG CTGGTAAGAC TTTGAAGAGC CATTGGAAGG	480
CAGCCTATGA TGAAACTCTG AAGAAGGAAG AAGTGATTTT CTCTCTCTTG TCATCAGAGT	540
TTGAGACTGT ATTTTCTAAG GAAATCAGAG CAAAGATGGT GACCTTCAA TTCATGGAGG	600
ATAGAGGCGG TCAGCTGAAG ATTCACTCAA CTATCTCCAA GAAAGCGCGC GGGGCCTTTC	660
TAACAGCTTT AATAGAAAAT CAAGTACAAA CTGTGGGGGAG AGCACGTCGC TTGAACTTTG	720
CTGGATTTGT TTACCGAGAA GATTTGTCAC AACCACAGGG GGATGG	766

(2) INFORMATION FOR SEQ ID NO: 281:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 901 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

CCGGCCACGG TTCCATCCAA CTTCACAGGT GTGCACTTGA TTGTGTATGT AATTGTCACT	60
AACGGTAGAA TTTCACCTAT CCCTCCTATC TGCTCGCAGT ACCCGCAGAC TTTCTGAAAG	120
AAGAAGATAA CCTACTTATC CGTTGCTATG ATTATACTAA AGTTTCTACT TTTTGTGAAA	180
TAGATTTTTA AATTTTGGC TAATTGTCTG AATCAGGGTC GGAAGTTTGA CGACCTTGTC	240
ATTGCCTAGT TTTTCGCGTG CAATTTTGAG AATGGCACCT GAGTCTTTTG AAGCAAAGAG	300
GAATTTTCCT TTGTCTGTAA AGACTTCGAA GTGGCGGCTG ATTTTGCGTC CAGTGACATT	360
GGCTCCAATC TGATTGATAT GGCTCCAAGG AATCTGGATA AATTGTTTGA CATTGACATC	420
TGGGTAAAAT TCCAAAGCCT GATCTCCGAC AAGGAATTTC CCAACTTTCC CAGCGATAGA	480
GAGGTAGGAA GTGCCTGTCTG TACTGAGGAG TACTGTTTTG TTAAGTGATT GGGCCATGCT	540
TAGTCTTCCT TACTTTCTCC AAAAAAGGCA TTGTAGAGGG CTTTAATTGC TGCTTTCTCT	600
TGGTCTTTAT TGACAACAAA CATAATAGAA ACTTCACTAG AACCTTGAGA CATCATCTGG	660
ATGTTGATTT TGTTTTCAGA TAGAGCGCGT GTCGCAGTAG CAGTCACTCC GATATGGCTC	720
TTCATTTTTT CACCAACAAT CATAATGATA GAAAGGTCGT GTTCGATTTC TGCATGATCT	780
ACTTTAGCCT TTTGAACCAA CTGACGCAGG ATTTCTTCTT CCTTGATGGG AGTTAGTTGG	840
CGAGAACGGA GAATGATAGA AAGAWCGTCG ATACCTGTTG GCATATGTTC CCAACCGATG	900
T	901

(2) INFORMATION FOR SEQ ID NO: 282:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1765 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

CCCTGTTACG TGGATAATAG GGTAAGACTG CTCAGGATTT CCTAACAAAT CCACCGCTTG	60
CTGCATTCTGA CCCAAACCTG ATCGAAAATT CAAACCAATC CGACTATGGA GCCATTCTTC	120
TACTTCAAAC ATACACATCT CCTTGACAAA AGTCCAATCA ATTATCGCAT TAAAGTATGG	180
TTACTAATAA AAACAAGGCC AGGATTTTCG TCCCGACCTC TTACCTGGTT AGCTAATAAC	240
TAGCTACTAT GAATGTGAAT ATGGGCTAAA AACATCCACT GGACGTTCCA ACTCTTCCCC	300

1312

ATTTCTGGGA GTTGGGGTAA AAATGTTTAC TGGACGTTCC AACTCTTCCC CATTTCTGGG	360
AGTTGGGCTG ATACAGTCTC CCAGACTGTA TCACTCCTCC ATAAAGCTGT TGAAGACTTC	420
TTCAATCATG TTCCATTCTG CTTCTGAGTC TTCTGGGATT GGTTGCAATT CGCCTTCTGT	480
TCCATCTTCG TTTTCGATGA ATGAGTAAGC TTGGATTTCA ACTTGTCCGT CTTCTCTTC	540
TTCTGCGTTA ACTGGTACTA GAAGAACATA GTTTTTACCA AATTCTTCTT TTCCATCAAT	600
TGTCAAAGG ATTTCAAACA AGGTTTCATT TCCTTGCTCA TCTACTAGTG TGATTAGTTC	660
ACGTTCTTCG TGGTCGTGGT TATGATCGTG TGACATAGCC TCGCCTTTAT ATTAAATTT	720
TCTATCTAAA TAATTTTGTA AAATCAGCTG AGCTGCTAAC TTATCAATGA CTTTCTTGCG	780
CTTATTGCGA CTGATATCTG CTTGTTCAAT CAACATGCGC TCAGCAGCCA CTGTTGTCAA	840
GCGTTCATCC TGATAGTCTA CTGGTAAACC AAAAACTCT TCTAGCTTTG CTCCGTAGCT	900
TGACTAGCTT CTACGCGCGG TCCACTTGTA TTGTTCATGT TTTTAGGCAA GCCCACTACA	960
AATCGTTCCA CCTTGTAAGT ATCAACCAAT TCCTTAACGC GGTCAAACC AAATTGGCCT	1020
TGTTCTTCAT TTATCTGGAT GATTTCAAGC CCTTGAGCTG TAAACCAAG CGGATCGCTA	1080
ATCGCCACCC CTACCGTTTT TGAACGACG TCCAATCCCA TAATTCTCAT AGGTTATAGA	1140
TCGACTCCTT GTCCTTTGAG GTAGTAGCGA ACCAATTCCT CAACGATTTC ATCAGCTCA	1200
TACTTACGGA TTTGATTTCTG TGCATTATTA TAACGAGGAA CGTAGGCAGG GTCTCCACTC	1260
AATACGTAAC CTACGATTTG GTTAATTGGG TTGTAAaCCCT TATCGTTCAA CGAAGCATAA	1320
ACATCTGTCA AAGTTTCGCT AATTTCTTTT TTATTGGAAT CGTCCAATTT AAAACGTACT	1380
GTTTCTTCAG TAAATCCCAT TCTAACACCC TCTTTCCTTA GAATAGTACC ATTATAGCAT	1440
AATTCCTTAC CTTCTACAAT TCAGGCAGTC TATTTATTTG GATTTTCTAT TGTTCTGTCTG	1500
CGCCATTTGC CAATCTATCT GAAATATATT TGCTTGGTTC ATTTTTCAAA AGATTTTCCA	1560
AACCAATATT CTTCAATGT TCCAAGTGGG AAGCCTTCTT GACATCCAGA ACTTGAAAAT	1620
CAAACTAGT CGTTGTTTGA AGTTCCGTTG CGCTCAATAG TTTTGTTTCA AGTTTGAAAC	1680
CTGCCAATTT ACGAGCTTCA ATGATAGACT TATCCTTCTC CTCCGCTTCA AGAAGAGCTT	1740
TTTGAGTTTC CTCCACTCCA TGTTG	1765

(2) INFORMATION FOR SEQ ID NO: 283:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

CTTATCCATT CACTTCTTG TCTGTTATTC TATAAATCTT ACTCCTAAGT ATACCACATT	60
TGCCCCCTAGA TGTGAACGAG AGAAACGCTC TAGACATTGC CAAGAAGGAA AAAAAAGGGT	120
ACAATGTAAC AAAATCAAGG GAGGTCTGGA ATGAAGAAAC AAAGCAAGTA CAAAGAGGTC	180
GTTTCCTATC TGAAAAATGG TATCGAGTCT GGACGATTTC CGACGGGTAG TCGCCTGCCT	240
TCTATCCGTC AACTGAGCCT TGA CTTTCAC TGCAGCAAGG ACACCATTC ACGAGCCCTG	300
CTGGAATTAC GGCACGAACA ATACCTCTAT GCCAAGCCTC AGAGTGGCTA CTATGTATTA	360
GAACAAGGGC AACATCAAGA CCTAGAAATC GAGGTTACCG ACGAACATGC CAGTGCCTAT	420
GACGATTTCC GACTCTGTGT CAATGAAACC TTGATTGGCC GAGAAAATA CCTCTTCAAC	480
TACTATGACA ATCAAGAAGG ATTAGAAGAC CTAAGACAGT CCATTCACAA ACTCCTCTTT	540
GAGCAAGCTC TCTACTGCAA GGCTAACCAA CTAGTACTGA CTTCTGGAAC CCAACAAGCC	600
TTGTTTATCC TCTCTCAAAT ATCCTTTCCT AGACAAGCCA AGGAAATCTT GGTGGAACAG	660
CCAACCTACC ATCGGATGAA TCGCCTCTTG ATTGCACAGG GGCTGGACTA TCAAACGATT	720
GAACGAGGCA TTGATGGGAT TGA CTTGGAG GAGCTGGAAG GCCACTTCAA AACAGGAAAA	780
ATTAAGTTTT TCTACACCAT TCCCCGATTT CACTATCCCC TGGGACATTC CTATTCTGAG	840
CAAGACAAAC GATCTATTCT TAACTTAGCT GCCAAGTATG ATGTCTATAT CGTAGAGGAC	900
GATTATCTGG GTGATTTGGA CTCCAAGAAG GGCCAAACCT TCCACTATCT TGATACAGAG	960
GAGCGTGTCA TTTATATCAA GTCCTTCTCG ACCAGCCTTT TTCCTGCCCT TCGTATTACA	1020
GCACTCATTC TTCCAAATGC TATCAAAGAA GCATTTGTGG CCTACAAAAA TATCCTAGAC	1080
TACGACAGCA ACCTCATTAT GCAAAAGGCC CTGTCACTCT ATATTGACAG TCAATTGTTT	1140
GAAAAAATC GTTTGGCTCG CTTGACCAAT CATGAATCTT ACCAAAAACA AATCGAGGAA	1200
AGGATAACTA AAACACCTTG TCCCCTTCCT CATTATTCCC TACACGATGG yTTATTGCTA	1260
GACCTGAGAC AGTATCCTAA AATCGCCAGT CTCAAACACA GTCAACTGGG cTTGGACTTC	1320
TTTGAAGAGG CCTATTTAAG CACCTG	1346

(2) INFORMATION FOR SEQ ID NO: 284:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 900 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

1314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

CTATATTCAG AATATGCCAA AAATTCGGAA TGGTATAAAT TTGCGGAGGG TTCATTTGAC	60
ATATTTAGAA AACTCCCCCA AAGAATTAAT TTTAAGAAAG ATTTTCTAG AATTTTGGCC	120
CCCTTTATTA TTAATTTGCT TAAATTAATC AATAATTATC TAGAGAATAA AGAATACGAG	180
TGGATTGACA AGAATGGAAA TATTTTTTCC TCTCTAGTAT TTTATTTAGA AGATTTAATC	240
TATCCTTGGA TTGTTAAACC TTTGGTTTTA GAGATAAATT CATTGCGTGA AAAAGGTTTA	300
CTTGAAGGGG AATCGGAGCA GCAACGGTAC AAATATTTTA TAACATTGTT TGACAAGGAA	360
GAGAATATAT TAAATTTTTA TAACAAATAT CCCGTTTTAC TGAGGCAAAT ATCGGAGTCT	420
TGTCCTCGGT TCTATACTTA TTTTATAGAA ATTTTATCAA ATTTAGAAAA TGATTTTAGT	480
GTGCTAGAAG AAGAATTAGG GCTAAGGGGG AAATTAAATG ATATAAAATT TGGAAAGGGT	540
GATACACACA GCCAAGGAAA AACTGTTTTG ATACTCTTCT TTGATGACGC GAAAATTGTT	600
TACAAGCCTA AAAATTTAAT AATCAATAAC TCACTAAATA CTATTGCTGA GTATATCCGA	660
AAGGTTGATG AAAAAATTAG GATAAGAATA CCTCGAATA TTGCTTATTC GGATCACAGC	720
TATGAAGAAT TTATTGATTA TCTACCTCTA GAGCAAAAGA AAAATTTACC TGAATATTAT	780
TATAATTTTG GTGTGCTTTT AGCATTTATA TATTTATTTA ATGGGAGTGA TATACATTTT	840
GAAAATTTAA TTTCCTATGG AGATATGCCT GTAATAATAG ACTTTGAAAC AATGTTACGG	900

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 862 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

TTATTTAGCA GAGGCAGTTT TAAATGTGAA GGATTTGGTC AGTCAAACAG TTTTTTATCA	60
GCAGATTATT GGTTTAGAAA TCCTATCTCA AACGGATACA GAGGTCGTTC TGGGACTTGG	120
AGGAAAAGCC TTGGTACACT TGATTCAAGC ACAAGAGGGT GGAGAAGTAA GGGAACATTA	180
TGGTCTTTAC CATCTGGCTA TTCTTTTGCC GACACGAAAG GCTTTGGCGG ATGTCTTGAA	240
GCACCTGACG GATTACAGA TTCCTCTTGT TGGCGGTGCA GATCACGGTT ACAGTGAGGC	300
CCTTTACTTA GAGGACTTGG AGGGAAATGG CATTGAACTC TATCGAGATA AGCCAGTTTC	360
CACATGGGAT ATTCGAGAAG ATGGACGTAT TATCGGGGTG ACTGAAGTCC TTGCGGCTCA	420
GGATATCTAT GAGTTGGGGG AAAGAGTAGA GCCTTTTATC CTAGCAGAGG GTACGAGAAT	480

1315

GGGGCATATT CATCTTTCTG TCAAGGATAG TCGAAAGTCC AGACAGTTTT ATCAAACGGT	540
GTTAGGGCTC GAGGATAAAT TCAGTGTGCC TAGTGCTAGT TGGATCGCAG CTGGGGACTA	600
CCATCATCAT TTAGCAGTCA ACGAATGGGG AGGAAAAGGT CTGGATCCGC GTAAACAAGT	660
CCTACCAGGT TTAGCCTACT ATGTCATCGA AGTCGCACAT AAAGAAGAAC TGTTAACGAT	720
TGCCCCAACGA GCACAAGAAG TTGACGCACC AATCAAATGG ATGACATCGA TCCAATTGGA	780
AATCACAGAC TCAGATGGCA TCGTGACCCG TATTCGTTTA GCTAGATAGA TGGTATGTGA	840
TGAAGGTAGA GCATCAATTG TA	862

(2) INFORMATION FOR SEQ ID NO: 286:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 650 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

TCGTTTACAA GATCGCTAAA ATGCATCTCA TGATCGCGAC CACGAATTCC AAGATAGCAC	60
GCGCTACCTC AATCATAGAT AGTTCACTTT TTTCTTGCCC AGCAAATACT TCTAATTCCA	120
AAGCGTTTCT CCTCATTTAT ACTACTATCG CCAGAGCGAA CAGACTCTGA CCTCATTTTA	180
TCATTTACTC TTTATTTTAC GATAATTTTG CGGAATAGTC AAAGGTTAAG GGGGAGAAAG	240
TGGCAGGATT AGACTAATTC CAATATAAAA CTCATTCCTT TTTCTGTTGC TCCATTTTCC	300
ACAAATCCAA GCGACTTGAA ACACCTCCTA GAAGCATGAT TGTAGGTGTA GATTTTCTTG	360
ACTCTCAATT CTTTCCATCC TTTTACTCGA GCCAATTCAA TCAAAGCACT TAGAATCTTT	420
TTTCCAAGTC CTCGATGTTG GTAAGCGGAA TTCCCAATCA CAATGGGGAG ATTATCCTGA	480
GATAGTGTA TATCCCCAAT TGGAACCAT TCTCCCTTCT CTTGACTTC AATCCAAAAA	540
AGCTCACCAT GCCGATyCAr ATAGGAATAC ATGGCTTCCA AGGTcGcTtG ACTGTAAGGA	600
AGCTTCACCC CATCTACGAG GtAAcCAAGT TCACATCCGT GATACCAAGC	650

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

GATAGCAATC CGCTTCAGAA ACTTCTCGCT TACCTCTAAC TCCGATCGCT AGTTTGGGAG	60
AAGATACTTC CATTCTCATA CTATCTGTTG GCTTTGCAGG CTGTAAAAAC AACTTTTCTC	120
TTGCTACTTC CTGAAAATCT GAATCTTGCA GTTCTTTGCT TTCAAAATAG TCCTGTACTC	180
GCTCCACATC AAAATTCCCA GCTAAAGACA GAGACATGTT TACAGGTTTG TAAAACTTTG	240
TAAAATTTTC TTGCAAATTA GTTAGATTGA TTTGGGAAAT GGACTCCTCA CTTCCAAC TA	300
TATCAGTTGC TAAAGGTGTA CCAGGATACA AATTCGCTAA AGTTGAAAAG AATAAACACG	360
AATCTGGATC ATCTTGGTAC ATTTCTCGTT CTTGCTGAAT AATATCCTGC TCTGTCAGAA	420
TGGAAGCTTC AGTAAAGTGT GCTGATGTTA CCAATTCATC AAGTAAATCT AAATTTTCTA	480
AAAAATAATC CGTTGCTGAA AAAAGATAGT TTGTTTTTGT AAAGCTTGTA AAGGCATTAC	540
TATCTGCACC TAGACTCGTA AAAGCCGACA TCAAATCACT AGAATCTTCT CTCTCAAATA	600
ATTTATGTTT AAGAAAATGA GCAATTCCTC CAGGATATTG TTTTACATCT CCGTCAACTT	660
CTGTGACAAA CGTATCTACC GAACCAAACT GTACAGTGAC ACTCCCGTAA ACCTCTTTAA	720
ATTCCTTTTT AGGCAAAAGA GCAACTGTCA ATCCGTTGGC CAAACGAGTT CGATAAACCA	780
TTTCTTTTAC AGCTGGATAG TATTTTCTT CAAAAACAAC CTTTGTCATT CTATTCCTTC	840
CATAAAGTAA ATCGCTTGTA GTTTCACATT ATTAGCTACT CTACAAATAG CATCTTTGTC	900
AATTTGTTCA AGCTTTGCAA TCCAACCTTT AAAGTCTGCT GAAGATTTTC CAAATAAGGC	960
ATTTTGATAA GCACGTTCAA TCAATGAAGA ATGATTATCT TGAGAAAGTA ACAACGACCA	1020
ACGAATCATT TCCTTGGTCT GATTTAACTC AACTCTGTA AAAAAACCTT TTTTAAATC	1080
AAGCCGTTGA TTATTCATCA ATTTACGAGC CTGGTTACG	1119

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

ACGCCCTCGC GGGGACATGA CGAATTCCCC GTTCATCACG AAGGCCGCCG AGGAGTGGGG	60
GGTGCCGTCC AAGTCAAAAG CGGCCCCACA TCGATTCACT TCCCCGACGA ACAGCCCTTT	120
CCCCAGCGT TCCTGGCTTT GCAACCGTTT CACAACAGCC TCGTAAAGTA GGCCGGACAA	180
GGCAGACGGA CTCCAAAGGA GTTCTTCCAT CTGCAAGTGC GCCTGCGTTA TGTGATCCCG	240

1317

GTCTTTTGCA TGTGTGTGGC ATGAATGCTG TTCCCAATCC CACTCCAGAA CATTCTCCTC	300
AAAAGTGCGC AACGTCGCCC TGAATGAATC CTGCCTTGTA GTCGTGACCA TTCCTATGAA	360
GGGTCGCAGA GGATTTTCCC CGAGTGCAAG CGCATCCTCC GGCTCAAATC GGGTGCATTT	420
CACAGTCCCG CTCAACGCTA GCCCGATCCC TTTTGTGGCAT GGTGACTCAA GCGTCCTTTC	480
AAACAAAAGC TCCTCATCCG CTCCAACCGG CCCGACGTAG ACGCGTAGAC CGAAGTCGTC	540

(2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1949 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

AAAGAATTCG ACCAATTCAA GGTGAGGCA TCGCAAAC TA TGGACTGTTC CCCCCTCAGT	60
TCTGGACAGA AAACGGGATA AGGTTGGCTG TGAAGCAAGC TGCCCTCCTA CCAACAATTT	120
TGGAAAGTAG GCATCAGCTG ACAATTCTTT ACAAGCATAG TCCGTTCCAT AACCTGTTAA	180
CAGTTGAAAG AGGAACTGGA CAAGGATATC TGAATCCGAA TAACGACAGT AGCGGCGTTG	240
GTCATTCGTT ACTAAATACT TAGAAATCCG CTCTTTTAGT TTCAACTGGG AAAAAAGTTC	300
CTGAAAAAAG ATAAGACCAC CATACTGGGT TAAATGACCT CCATCGAAAG ATAGTTGGTA	360
AAAAGACTTG TTTTGGAAGT GATGATTTGG TAAACTGTTC ATGTGAGTTT CCTTCTTTTT	420
TGTGTTTTTT TCTACACTTA TACCATAAAG GGGAACTCT TTTTGTCTA GTAAAAACA	480
CCCATGCGGT GAAAAAAGAA ACCATCCAGG ATCTAAGCTA AGGCAAGGAT TCTGGATGGT	540
TTTTAGATTT GGGGTGAATA ATTGGGGTTT TACAATATCA ACTCCCATGA TAGTCATGAG	600
ATGACTCTTC ACGAATTGAC GTGATGACTG TCCTTCCTTT TGCATAATTA CCTCCGAAAC	660
ACAAAAAAG GGGTAGACAA TCTAGTGTCT ACCCCCGAAA GTTTATTAAA AAAAAATCC	720
TGCCAAAGAA TTTTGGCAG GAAACCAAAT CAATTTATCA GTTTCTATCA ATCGCTTATC	780
GCTCTCAAAG ACTGGTAAAT AGGGATTCCG CAATCAAATT GCGATACTCT ATTATTTAAG	840
AGTAACTGAA GCTCCAGCTT CTTCCAATTT AGCTTTGATT TCTTCAGCTT CTGCAGTTGC	900
AACGCCTTCT TTAACAAGTG CTGGTGCACC GTCAACAAGT TCTTTAGCTT CTTTAAGACC	960
AAGACCAGTG ATTTACGTA CAACTTTGAT AACGCCAACT TTTTGTGCGC CTGCAGATGT	1020
CAATTCAACG TCGAATGAAT CTTTAGCAGC ACCAGCATCA GCTGCATCAG CTGCAGCAAC	1080

1318

AGCTACAGGA GCAGCTGCAG TTACACCAAA TTCTTCTTCG ATAGCTTTTA CAAGGTCGTT	1140
CAATTCAAGG ATTGAAGCTT CTTTAATTTC AGCAATAATG TTTTCAATGT TCAATGCCAT	1200
TGTTATTTCC TCCAAATAAG TTTTAAATTT TATAATAGTT TTTTTCGTAG CTAGkSTACG	1260
CTGTGTAGCT TAAGATTAAG CCGCGTCTTC TTTGCTTTCT GCAACCGCTT TGA CTGCAAG	1320
AGCAACGTTG CGCACTGGCG CTTGAAGTAC AGAAAGGAGC ATAGAAAGAA GTCCTTCGCG	1380
GTTTGGAAGA GTTGCAAGTG CAAGAATCTC TTCTTTAGAT GCGACAGCGC CTTCGATTGC	1440
ACCACCTTTA ATTTCAAGTG CTTCAAGCTT TTTAGAAAAG TCGTTCAAGA TTTTCGCTGG	1500
TGCGATAACA TCTTCATTAG AAAATGCTAC TGCAGATGGT CCAACAAATA CAGATGCAAG	1560
ATCTTCAAGA CCAGCTTTTT CAGCTGCACG ACGCAAGATT GAGTTTTTAA TAACTTTATA	1620
CTCAACTTCG CTTCACGAA GCTCACGACG AAGAACTGTA TCTTGCTCAA CTGTCAAACC	1680
ACGAGCGTCT ACAACGACGA TAGATGCAGC AGCTTTCATT TTTTCAGCTA tACGTCAACT	1740
AGTTCCGCTT TTTTAGCAAT AATTGCTTCA CTCATTAGTG TGTTACCTC CGTAATTATT	1800
TTGCTTGGGG AATTTTCAA AAAGAAAAAC GCGCCCAATC CTAGACACGA AAGTACAATA	1860
CGCTTCTTTT TACATGATAC GTTTTGTCTT CGGTAGGATA TTTATGAGTC GAGCTCCCCT	1920
ACTGTCTTAG GCAGTTTTTT TAGATACGG	1949

(2) INFORMATION FOR SEQ ID NO: 290:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1023 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

GGACTGTTTG ATCTTATACA GTAGCTGCTT GATCCAAGCT TTCACCGATA GCGGCTAGGC	60
GCTCGATAAC TTCAGCTTGT GTCAATTCAT TTTTGAAC ATAGCGGTTA CGTGGGTGAA	120
CACGGCACTC GTGTGAGCAT CCACGAAGGT ACTTGTCTTC ATTTTCTTCT GATGTCAAGA	180
TACGACGGTT ACAGAATGGA TTTCCACAGT TGACATAACG TTCACATGGT GTTCCATCAA	240
ACCAGTCTTT CCTACGATA GTTGGGTTGA CATGGTTGAC ATCAACGGCA ATACGCTCGT	300
CAAAGACGTA CATTTTCCCA TCCCAAAGCT CACCTTGAAC TTCTGGGTCT TTACCGTAAG	360
TTGCGATTCC TCCGTGCAAT TGGCCGACAT CTTTGTAGCC TTCACGGACC ATCCAGCCTG	420
AGAATTTCTC ACAGCGAACG CCACCTGTAC AGTAAACCAC GACACGCTTG TCCATGAATT	480
TTTCCTTGTT ATCACGGACC CATTGTGGTA ACTCACGGAA GTTGCGAATA TCTGGGCGAA	540

1319

TAGCTCCACG GAAATGTCCT AGGTCGTACT CATAATCGTT ACGTGTGTCA AGGACAACGG	600
TATCTTTATC AAGAAGCGCT TCTTTGAACT CTTTGGAGA CAAGTAAGCA CCTGTTGTTT	660
CAAGTGGGTT GATGTCATTG TCAAAGTCGT TGTCTTCCAA ACCAAGGTGG ACAATTTCTT	720
TCTTGTAAGC AACAAACATC TTCTTGAAGG CTTGTTTCATT TTCTTCGTCA ATCTTGAACC	780
AGAGTTCTTC CATTCCTGGA AGGCTGTGAA CGTAgTCCAT GTATTTTGA GTTGTTTCAT	840
AGTCACCTGA AACTGTTCCG TTAATTCCCT CGTCAGCGAC TAGGATACGG CCTTTAAGGn	900
CGATTGATTT ACAGAAAGCC AAGTGGTCTG CAGCAAATTG CTCTGCATTT TCAATTGGAG	960
TATAAAGGTA GTAAAGTAAG ACACGAATAT CTTTGTGkCaw AAGATTGTGA TCTCTTTATC	1020
TAT	1023

(2) INFORMATION FOR SEQ ID NO: 291:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3831 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

ACTATGAACA AGACCCAGAA AAAGTAGCCT TATTTCTTAA GAATTTTAAT AGTTTAAAGC	60
ACCTAGCACC TGTTTAGATT GACGAAACAG GATTCGATAC TTATTTTAT CGAGAAATATG	120
GTCGCTCATT AAAAGGTCAA TTAATAAGAG GCAAAGTATC TGGAAGAAGA TATCAGAGGA	180
TTTCTTTGGT TGCAGGTCTA ACAAATGGTG AATTAATCGC TCCAATGACT TACGAAGAGA	240
CGATGACGAG CGACTTTTTT GAAGCTTGGT TTCAGAATTT TCTCTTACCA ACATTAAACA	300
CACCATCGGT TATTATTATG GATAATGTAA GATTCCATAG AATGGGGAAG CTAGAACTTT	360
TATGCGAAGA GTTTGGGCAT AAACCTTTTAC CTCTTCCTCC CTACTCGCCT GAGTACAATC	420
CTATTGAGAA AACATGGGCT CATATCAAAA AGCACCTCAA AAAGGTATTA CCAAGTTGCA	480
ATACCTTTTA CGAGGCTTTT TTATCCTGCT CTTGTTTCAA TTGACTATAT TAGAGGCGAG	540
ACATTTTTCG GTTCTTTGTC AACTGTAGTG GGTGAAGAA AGCGAAGATC TAGAAAGGAC	600
AAATTTTCGTC CTTTCTTTTT TGAAGTTTTC AAAGTTCCTA AAACCAAAGG CATTGTGCTT	660
GATAAGTTTG ATGAGATTAT TGGTGGCTTC CAGTTTGGCG TTGGAATAAG GTAATTGAAG	720
GGCGTTGACG ATTTTCTCTT TATCTTTGAG GAAGGTTTTA AACAAAGTCT GAAACAGAGG	780
TGGAAAAGCA AGAGCTGATA GAGATTATAG TGGTGTTTAA AGTCTTCGGA ATAGCTCAAA	840

1320

AGTTTATCTA	GAATTTCTTT	ATTAGTCAAG	TGCATACGAA	AAGTAGGGCG	ATAAAATCGT	900
TTATCACTCA	GTTTCTGACT	ATCTTGTTGA	ATGAGCTTCC	AGTAGCGCTT	GATAGCCTTG	960
TATTCATGGG	ATTTCGGATG	ATGGCTTGTG	TTCTGCTCTC	AAGAACAGTT	ATGATATTGA	1020
GTTTATCAAA	GTCCTGAGCA	ATAAAGCTCA	TCTCCATCTC	CCGATTGAAA	CAGTCACTCC	1080
CCGGACTGTT	TCAACsTCCT	AGGACATAAT	CTCAGGAAGA	CGCGAAAAAT	CATGCTCAAA	1140
GTGAAAATCA	TTGTTCTTGC	GAATGACAGT	TGAAGTTGAA	ATAGACAACT	GATGATCAAT	1200
GTCGGTCATA	GAAGTCTTTT	TAATTAGCTT	CTGAGCAATC	TTTTGGTTGA	TGATACAAGG	1260
AATTTGATGA	TTCTTCTTGA	CGATAGAAGT	CTCAGCGAGC	TCCATTTTTG	AGCAATGATA	1320
GCACTTAAAA	CGGCCTTTTC	TAAGAAGAAT	TCTAGTTTGA	ATTTTTTTAT	ACTAGAAAAT	1380
CAGAACCATA	ATACCTATAT	AAAAATATTA	TAGTTCTAAT	AGGATTTACC	CAAAAGTTTT	1440
AAGGCGGTCT	TTTTAGAACT	TTAATTGTTT	GAAATTTAGG	TAGCAAATTT	GTTTCTATTT	1500
TGTCAACTTT	TCCTATTTTT	ATCTTGTTGA	GGCTGGTATT	TTAACAATTC	AGGAATTGAT	1560
AGTGAATGTG	TAAAATTTTT	TGTTAGAATA	AGTTTATAAA	AAAGAAAAGG	AGTATTTGAT	1620
TATGTTACAA	AAAATTTATG	AGCAGATGGC	TAATTTCTAT	GATAGTATTG	AAGAAGAGTA	1680
TGGTCCTACA	TTTGGTGATA	ATTTTGA CTG	GGAACATGTT	CATTTTAAAT	TTTAAATTTA	1740
TTATTTAGTG	AGATATGGCA	TTGGTTGTCTG	TAAGGATTTT	ATTGTTTACC	ATTATCGTGT	1800
TGCTTATCGT	TTGTATCTTG	AAAAATTGGT	AATGAATCGG	GGTTTTATTT	CTTGTTGAGG	1860
TAATTTTAGT	AAATTTCCGA	ACTAATTTAC	TCTTTTATGG	AAAGATGATA	GTAAATAGCT	1920
AGTAATTTTT	CTAAATCATT	TTTTAATAGT	TGGAAATAGC	AAATCTTTCT	ATTGTTTCTT	1980
CTTGATAAAA	AGGCGATTTT	TTATTATAAT	AAATTGTAAG	ATATAATTGC	AGGTGAGAGT	2040
CCTGCCATGT	ATGTGAGAAA	GGAAGAGCCT	GATGGCTCAG	ACAAGATTAT	GA CTTCAGTT	2100
GTTGTTGTAG	GTACCCAATG	GGGTGATGAA	GGTAAAGGGA	AGATTACAGA	CTTCCTTTCA	2160
GCGAATGCAG	AAGTGATTGC	ACGTTACCAA	GGTGGTGATA	ATGCTGGTCA	CACGATTGTG	2220
ATTGACGGTA	AGAAATTTAA	GTTGCACTTG	ATTCCATCTG	GGATTTTCTT	CCCTGAAAAA	2280
ATATCTGTCA	TTGGGAATGG	TATGGTTGTA	AATCCTAAAT	CTCTTGTAAG	AGAGTTGAGC	2340
TATCTTCATG	AGGAAGGTGT	AACAAC TGAT	AACTTGCGTA	TTTCTGATCG	TGCGCATGTT	2400
ATTTTGCCTT	ATCATATCGA	GTTGGATCGC	TTGCAAGAAG	AAGCTAAGGG	CGACAATAAG	2460
ATTGGTACGA	CAATTAAGGG	AATTGGTCCA	GCTTATATGG	ACAAGGCTGC	TCGTGTTGGA	2520
ATTCTGATTG	CAGATCTTTT	AGATAAAGAT	ATTTTCCGTG	AGCGTTTAGA	ACGTAACCTT	2580
GCTGAAAAGA	ATCGTCTTTT	TGAAAAATTG	TATGACAGTA	AAGCGATTGT	TTTCGATGAT	2640

1321

ATTTTTGAAG AATATTACGA ATATGGTCAA CAAATCAAGA AATACGTGAT AGATACATCT	2700
GTTATCTTGA ATGATGCGCT TGATAATGGC AAACGTGTGC TTTTGAAGG TGCACAAGGT	2760
GTTATGCTAG ATATCGACCA AGGTACTTAT CCATTTGTTA CGTCATCAAA CCCTGTAGCT	2820
GGTGGTGTGA CAATTGGTTC TGGTGTCTGGT CCAAGCAAGA TTGACAAGGT TGTAGGTGTA	2880
TGTAAAGCTT ATACGAGTCG TGTAGGAGAT GGTCCCTTCC CAACTGAGTT GTTTGATGAA	2940
GTGGGAGAAC GTATCCGTGA AGTGGGTCAT GAATATGGTA CAACAACTGG TCGTCCACGT	3000
CGTGTAGGTT GGTTTGA CTC AGTTGTGATG CGTCATAGCC GTCGTGTTTC TGGTATTACT	3060
AACCTTCTT TGAACCTCTAT TGATGTTTTG AGCGGTTTGG ATACTGTGAA AATCTGTGTG	3120
GCCTATGATC TTGACGGTCA ACGTATTGAC TACTATCCAG CTAGTCTTGA ACAATTGAAA	3180
CGTTGCAAGC CTATCTATGA AGAGTTGCCA GGTTGGTCAG AAGATATTAC CGGAGTTCGC	3240
AATTTGGAAG ATCTTCCTGA GAATGCGCGT AACTATGTTC GTCGTGTGAG TGAATTGGTT	3300
GGCGTTCGTA TTTCTACTTT CTCAGTAGGT CCTGGTCGTG AACAAACAAA TATTTTAGAA	3360
AGTGTTGGT CCTAAGAGAT TTTTAAGATT TGTTTAAGAT AGGTCGGGTA TACTATAGAC	3420
GGTTACAAGA AGACCTCCTA ACTTGTTGTA ACAAATATCC TAACTTTTC TTTTTCATAA	3480
TAATCTCCCT ATAGAGTCAC CGCATTCGGT GGCTTTTTTT GTGTTGGGAT TCATGATATA	3540
ATAATAAAAT CGATAAGTAG GAAAAGAGAA AAGAGATGTA TTATACGCTT GAAGAAAAG	3600
AAGTCTTTAT GAGGGAGGCT TTGAGAGAG CTGAGATTGC TCTTGAACAC GATGAAATTC	3660
CAATTGGTTG TGTGATTGTC AAAGATGGGG AAATCATGG TCGTGGGCAT AATGCGCGTG	3720
AGGAATTACA GCGAGCGGTT ATGCATGCGG AAATTATGGC TATAGAGGAT GCGAACTTGA	3780
GTGAGGAGAG TGCCTTGCT GGATTGCACA CTTTTGTGA CCATTGAACC G	3831

(2) INFORMATION FOR SEQ ID NO: 292:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1441 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CCGCTGTTCC AACCGCAACA TACCATAGTC CGTACGGGAT TCGAACCCGT GTTACCGCCG	60
TGAAAAGGCG GATGACTTAA CCCCTTGACC AACGGACCTG AGTTGTTATT TTCAACTCTT	120
ACTATTATAC AGTCTTTTCA AACTTTGTCA ACTACTTTTT CTAATTTTGT TTTATTTTTT	180

1322

CAACTTATAG TAAAAAAGC CAGAATTATA CTGACTCTTC TATCGCTCAT TAAACTTAGA	240
AGCACGTTCT TTTCCCCACC AATAAGGGAT TAGTTCTGCG ACTTTAACTG TTTTCTTAT	300
ATTATAGTCC ATCATGAATT CTGCATCTTT ATTTTCAGCA TTAAGCTCTA AAAGGAATTC	360
TCTACAAGCA CCGCAAGGCA TGGCTGAACT TCCACCATAA GGTGGTTTGT CTCGAAAGGC	420
TAATACTTTC TTAACCTTAG TTTGTCCTGA AAATTGGTAC ATATTGAAGA GGGCCGCCCG	480
TTCTGCGCAG AGATGGAAAA CACCACAGGT TCCCTCCATA CAGAATCCTG TAAATATTTG	540
TCCATCTCCT GCTTCTACTG CAGCTACAAC ATGATTGGCA TAAACAAAGT CTGATACTTC	600
ATGTGGATTG TATAGTTTCT GTGCTTCTTC GTACATCTTT TCCCAGATGT CCATTATTGT	660
ATCCTCTTTA TTTAGAGATT TCTTTTAGCA TGTTTTCGAT ATGCTGAATT GATTTTTCAC	720
GTCCAAGCAA GAAAATTGTA TCTGGTAATT CTGGCCCATG CATTTTCGCT GAAACTGCGA	780
TACGAATAGG CATGAAAAGA TTTTCCCTT TAATACCTGT TTCTTTTGG ACTGCTTTAA	840
TTTGTGGGAA GATATTTTCT GTCACAAATT CATCATCTGT CATCGCTTCA AGTTTGTCTT	900
TGAATGCTTC AAGAACTGTT GGAAGTGTTC CACCCGTCAT GACTTCGCGC TCTGCTTCTG	960
TCAATTCTGG GAAATCTGAG AAGAAAAGAT CTGTCAATGG GATAATCTCA TCTACTGATT	1020
TCATTTGTGG TTTATAGAGC TCAACTAATT TTTCAGCCTT GTCAGTCAA CGGCCTGCTT	1080
CCTCTAAGAA TGGTTTTGCC ATTTCAAAGA TGGTTTCAAG GTCTGCATTC TTGATATAAT	1140
CATTGCTCAT CCAGTCTAGT TTTTCTGAT CAAAGGCTGC TGGTGAATTG CTGAGGCGGT	1200
TTTCATCAA AAGTTTAATG AATTCTTCAC GAGAGAAAAT CTCATCCCCA CCACCTGGGT	1260
TCCAACCAAG AAGAGCAATA AAGTTAAAGA CTGCTTCTGG AAGGTAACCT TTCTTTCGGT	1320
AATCTTCGAT AAATTGAAGT GTATTAGTAT CACGTTTAGA TAACTTCTTA CCAGTTTCAG	1380
AGTTGATAAT CAAGTGTCAT GTGACCGAAC TCTGGAGCTT CCTCAACCTA AGAGCGGGTA	1440
T	1441

(2) INFORMATION FOR SEQ ID NO: 293:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4398 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

CGGCTTATGT AGTGGCAATC TTTCTACGTA AGCGAAACGA GGGGAGATTA GAGGCGCTAG	60
AAGAAAAAAA AGAAGAACTA TACAATCTTC CAGTAAATGA TGAAGTAGAA GCTGTAAAAA	120

1323

ATATGCACTT GATTGGACAA AGTCAAGTGG CTTTCCGTGA ATGGAATCAA AAATGGGTCG	180
ATTTATCTCT CAACTCTTTT GCCGATATTG AAAATAATCT CTTTGAAGCA GAAGGCTATA	240
ACCATTCAAT TCGTTTTCTC AAGGCCAGTC ATCAAATTGA CCAAATTGAG AGTCAAATTA	300
CTTTGATTGA AGAAGATATT GCGGCAATTC GCAATGCTTT GGCAGACTTA GAGAAGCAAG	360
AATCTAAAAA TAGTGGTCGT GTTCTTCATG CTTTGGATTT ATTTGAGGAA CTTCAGCATA	420
GAGTTGCTGA AAATTCAGAA CAGTATGGTC AAGCCTTGGA TGAAATTGAA AAACAATTAG	480
AAAATATCCA ATCTGAATTT TCACAATTTG TAACCTTGAA TTCATCGGGT GACCCTGTGG	540
AAGCCGCAGT GATTTTGGAT AATACAGAAA ATCACATTTT GGCCTTAAGT CATATTGTGG	600
ATCGTGTTCC AGCCTTG GTT ACGACGCTTT CTACAGAATT GCCAGATCAA TTACAGGATT	660
TGGAAGCCGG TTATCGTAAA CTAATTGATG CTAATTATCA TTTTGTTGAA ACGGATATTG	720
AAGCGCGTTT CCACTTGCTT TATGAAGCAT TCAAGAAAAA CCAAGAGAAT ATTCGTCAGT	780
TGGAATTGGA TAATGCCGAA TATGAGAATG GACAGGCACA AGAGGAAATC AATGCCTTGT	840
ATGATATTTT TACTCGAGAA ATTGCTGCTC AGAAAGTAGT GGAAAATCTA CTTGCAACTC	900
TTCCAACCTA TCTTCAACAT ATGAAAGAGA ATAATACTTT ATTGGGAGAA GATATTGCAC	960
GTTTGAACAA GACCTATTTA CTTCTGAGA CAGCTGCAAG CCATGTTCTG CGTATTTCAGA	1020
CAGAATTAGA GAGTTTGTAG GCAGCTATTG TTGAGGTAAC TTCAAATCAA GAAGAACCAA	1080
CCCAAGCTTA TTCAGTTCTT GAAGAAAATC TTGAGGATTT ACAAACCTCAA CTAAAAGATA	1140
TTGAAGATGA GCAAATTTCA GTTAGTGAGC GCCTGACACA AATTGAGAAA GATGATATTA	1200
ATGCACGTCA AAAGGCCAAT GTTTATGTCA ATCGTCTCCA TACTATCAAG CGATACATGG	1260
AAAAACGCAA TCTGCCAGGT ATTCCACAAA CTTTCTTGAA GTTATTCTTT ACGGCAAGCA	1320
ATAATACCGA GGATTTAATG GTTGAGTTAG AACAAAAAAT GATTAACATT GAATCTGTTA	1380
CCCGAGTTCT TGAAATTGCA ACGAATGATA TGGAAGCTTT AGAAACGGAA ACTTATAATA	1440
TTGTACAATA TGCAACTTTG ACAGAGCAAC TCTTGCAATA TTCTAACCGC TATCGCTCAT	1500
TTGATGAACG CATTCAGAA GCATTTAACG AaGCTTTAGA TATTTTGTAA AAAGAATTTG	1560
ATTATCACGC TTCATTTGAC AAGATTTCTC AAGCATTGGA AGTGGCAGAG CCTGGTGTAA	1620
CCAATCGCTT TGTTACCTCA TATGAGAAAA CACGTGAAAC GATTCGTTTT TAATAAAAGA	1680
AAAAGATTTT ATTGTGTGAG GAGCAGAATC AAATCTTTTT CTATAGTTGT GGGGAGATTT	1740
ACTTCATTTT CTCCTGAGAT TGAGTTTTTG CCCAGCCGAT TTATCCACTA CCTCAAAACA	1800
GTGTTTTATA CTCTTCGAAA ATCTTTTCAA ATCACGTCAG CGTCGCCTTA CCGTACTCAA	1860

1324

GTACAGCCTG	AGGCTAGCTT	CTTAGTTTGC	TTTTTGATTT	TCATTTAGTA	TTAAAGTGAT	1920
TTCGCCAGTC	TTATCTGCAG	CTTCAAATCT	GTACTTTGAG	TAAC TTGGTA	ACCGTCCAAT	1980
AACGAAGTCT	ATTGAAAAAT	CTCCAGACTA	GAGAACTCAC	GGATAGTTCC	TAATCTGGAG	2040
ATTTCTTATT	TGCACTTTTC	TTGTACAAC	TTAGTCCACG	GTAAATAGAC	CTCTAAAACC	2100
TCTTTGTTTA	CGAGAGTTTC	CTCGTTTGGA	AGACATTCTA	GAAGATAGGA	TAGATATTTT	2160
TCGCTATTTA	TACTAGACTA	AAATCAAAAA	GCATTATATA	ATAGTGATAT	GAAATCAACT	2220
AAAGAAGAAA	TCCAAACCAT	CAAAACACTT	TTAAAAGACT	CTCGTACAGC	TAAATATCAT	2280
AAACGCCTTC	AAATCGTTCT	ATAGTAAAAT	GAAATAAGAA	CAGTACAAAT	CGATCAGGAC	2340
AGTCAAATTG	ATTTCTAACA	ATGTTTTAGA	AGTAGAGGTG	TACTATTCTA	GTTTCAATCT	2400
ATTATATTTT	GTCTGATGGG	CAAATCTTAT	AAAGAGATTA	TAGAACTTTT	ATAGTAGATT	2460
GAAATAAGAT	GTGAACAAC	CTATCAGGAA	AGTCAAATTA	ATTTATAGAA	ATATTTTAGC	2520
AGCCAAGGTG	TACTGTTATA	GATTCAATAC	ACTATAGACT	GTAATCAAAC	AACGATTTGG	2580
CGAAATGTAA	AAAAATATGA	GGAGTTCGGA	CTCGACTCTC	TCCTTCAAGA	AACACGTGGT	2640
GGTCGTAACC	ATGCATATAT	GACAGTTGAG	GAAAAGAAAG	TCTTTCTTGC	CCGCCATTTG	2700
AAGGCTGCAG	AGGCAGGAGA	ATTTGTTACA	ATTGATGCCT	TATTTCAGGC	TTATAAAAAG	2760
GAGTTAGGTC	GTTCTTACAC	ACGTGATGCC	TTCTATCAAC	TGTTGAAGTG	CCATGGTTGG	2820
CGAAATATTA	TGCCACGTCC	AGAACATCCT	AAGAAAGCAG	ACGCTCAAAC	CATTGTCGCG	2880
TCTAAAAATA	AAATCTCAAT	TCAAGAAGAA	AAGAAAGCGC	TTTAAAACCA	GTAGACGTTT	2940
TCGTAAGGTT	CGCTTGATGT	ACCAAGATGA	GGCTGGTTTC	GGTAGAATCA	GTAAACTGGG	3000
ATCTTGTTGG	GCTCCAATAG	GAGTAGGTCC	ACATATCCAT	AGTCACTATA	TACGAGAATT	3060
TCGCTATTGT	TATGGAGCTG	TTGATGCCCA	TACAGGCGAA	TCATTTTTCT	TAATAGCTGG	3120
TAGATGTAAT	ACTGAGTGGA	TGAACGCCTT	TTTAGAAGAG	CTTTCACAAG	CTTATCCAGA	3180
TGATTATCTT	TTACTCGTTA	TGGACAATGC	TATATGGCAT	AAATCAAGTA	CCTTAAAGAT	3240
TCCGACTAAT	ATTGGTTTTA	CCTTTATTCC	TCCATACACA	CCAGAGATGA	ACCCCATTTGA	3300
ACAAGTGTGG	AAAGAGATTC	GTAAACGTGG	ATTTAAGAAT	AAAGCCTTTC	AAACTTTGGA	3360
AGATGTCATG	AATCAACTCC	AAGATGTTAT	ACAAGGATTG	GAGAAGGAGG	TGATAAAGTC	3420
CATCGTTAAT	CGGAGATGGA	CTAGAATGCT	TTTTGAAAAC	AGATGAGTAT	AAAAAGAAAG	3480
TCCTCATTTT	AATAGAAATC	ACGACTTTCT	GATGGATTTA	TAGTAAAATG	AAATAAGAAC	3540
AGGACAAATC	GATCAGGACA	GTCAAATCGA	TTTCTAACAA	TGTTTTAGAA	GCAGAGGTGT	3600
ACTATTCTAG	TTTCAATCTA	CTATATTTTT	GGAGTGATAG	AAAAGCCCTT	CATAAGCTAG	3660

1325

TCTACTTGTT	CAGGTGCGAG	AGCTTTGACA	TCTTTTTCTG	TACTTAGCCA	AGTCAGTTTT	3720
CCGTTCTCAA	AGCGTTTATA	TAGTAGCCAA	AATCCTTGAC	CATCCCAGTA	AAGGGCTTTA	3780
AAGCGGTCTT	TACGTCCACC	ACAAAAGAGA	AAGACTTGAC	CGGAGAAAGA	ATCCAATTCA	3840
AAGTGGGTTT	TAACCTACATA	GGCTAATGAG	TCTATTCCCT	GCCTCATATC	TGTCTTGCCA	3900
CAAACAAGGT	GAACCTGACC	TAAATCACTT	AGTTGAATTA	TCATAGTACA	ATACCTTTCC	3960
TCCGATAATT	ATTTTTTATC	TAGTATACTG	GAAGTTGGGG	AATTAGGATA	GATACCTTGT	4020
TATGACGCGC	TTACGTAACT	TGTAAC TAGC	TGCCTAGTTT	GATCTTTGCT	TCTTCATTGA	4080
TTAGCAGTAG	ATTTCAAAAT	GATAAAAACG	CATAGTATCA	GGTATTGAAA	TGTACTGCCC	4140
CAAAAGTTAG	ACAGAAAAAA	TCTAACTTTT	GGGGTGTTTT	TGTTATGAAA	TTAAGTTATG	4200
ATGATAAAGT	TCAGATCTAT	GAACCTAGAA	AACAAGGATA	TAGCTTAGAG	AAGCTTTCAA	4260
ATAAATTTGG	GATAAATAAT	TCTAATCTTA	GGTATATGAT	TAAATTGATT	GATCGTTACG	4320
GAATAGAGTT	CGTCAAAAAA	GGAAAAAATC	GTTACTATTT	TCCTGATTTA	AAACAAGAAA	4380
TGATTAATAA	AGTCTTAC					4398

(2) INFORMATION FOR SEQ ID NO: 294:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 718 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

AGATTTT TAG	ACTTTGTCTT	TAATCGTTTC	TTTTTAGGGA	TGATTGCGAC	ACCTTCTTTT	60
GGCTATTAAC	TTTAGCAGGA	GGGATTATCC	TTGGTCTAGC	GCCGGCTAGT	GCCACCTTGA	120
TGAGCTTATA	TGCAGAACAT	GGTTATAGCT	TTCTGGGAATA	CAGTTTGAAG	GAGGCTTGGT	180
CTCTTTACAA	GCAAAATTTT	GTCTCAAGCA	ACCTGATTTT	CTATAGCTTT	TTAGGTGTGG	240
GTCTAGTTTT	GACCTATGGT	TTGTATCTCT	TGGTGCAATT	GCCTCATCAG	ACCATTGTTC	300
ATTTGATTGC	GACCCTTTTG	AATGTCCTAG	TAGTTGCCCT	GATCTTTT TG	GCTTATACAG	360
TATCTTTAAA	ATTACAAGTT	TATTTTGCCT	TGTCCTATCG	AAATAGTCTC	AAATTATCCT	420
TGATTGGCAT	CTTTATGAGT	CTAGCAGCTG	TGGCTAAGGT	TCTCCTTGGG	ACTGTGCTAC	480
TTGTAGCAAT	TGGTTATTAT	ATGCCTGCCC	TGCTATTTTT	TGTAGGAATT	GGGATGTGGC	540
ATTTCTTTAT	CAGTGATATG	TTGGAACCTG	TCTATGAAAT	CATCCATGAA	AAATTGGCGT	600

1326

CAAAATAGAA TGAAGCAGTT TTGGCTACAT ACGCTTCTAA GAACCTATAG TTCAGTGATG	660
ATCATTATCA TTGCGAGTTT TGCAATCTTA CTCTCTTACG CTGTCTGGGA TTCACGTG	718

(2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 718 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

TCGGTACCAA AATTCTGGAT TTATACTAGC AAAGATCCAA GAGCAAATTA TTAAACAGAT	60
TTAGGTCTAG TTTTCCCTGA ATCATTAAAA GAATTTGAGA GTGAAGATAG TTTTGCAAAG	120
GAAATTTCTG CAGAAGAAGC AAATAAGATA AATGATGCTG ATGTAATCAT AACTTATGGT	180
GATGATAAAA CTCTTGAAGC TTTACAAAAA GATCCTCTTT TAGGTAAAAT AAATGCAATT	240
AAAAATGGTG CCGTTGCTGT AATTCCAGAT AATACACCGT TAGCAGCCTC ATGCACTCCA	300
ACACCACTTT CAATAAACTA TACTATTGAA GAATACCTAA ATCTTTTAGG AAATGCATGC	360
AAAAATGCGA AATAAAAAAC AAATAAACCT AGGCATAATT TTTATAATCT GCCTAGGTCT	420
TCTTATTACA ATATTTTTGT CATTAAAGCT TGGAACAAAA GAAATTAATA TCAGAGATTT	480
TTTAGCAGCT TTTGGAATGG GTAATACAAA TGATGATTTT ATTAAATCAA TTATATATAA	540
TAGAATACCT AGAACTATTT TTGCAATTTT AGCAGGTTCT AGTCTTGCCA TAAGCGGTGT	600
ATTGATGCAA TCAGTTACTA GAAACCCAAT AGCTGATCCA GGTATACTCG GTATAAACAC	660
AGGAGCAAGT CTTAGTGTAG TAATTGGTCC TTCTTTT TAG GGAATTCATC AAGCATAA	718

(2) INFORMATION FOR SEQ ID NO: 296:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GAAC TAATCA TTTTACAGG ATGAGATTTA CAGCAGAGAG TTTGAAGGCT TTATCAAAGG	60
TTTTTCTTGG CATAATGACT TTTCTCGTT TCCACTTAAT TTTGTGTCTA CTTTATTATA	120
CCAAGTCCAC SCTTAAGTTA GATAATAAAT CTAACCTAAG GAAGCTAGAA GGATGAGAAT	180
CCAGGTGGTC AAGAGTCCCA AACTTAAGCT GATGGGGACA CCCAGAATAA TTTGCTTTTT	240

1327

GAAGGCAAGG CCACGTTTCCT CTATATTGGG AAGTGAGAGT TGAATGAGAG AACCAGCTGA	300
TGAAAAGGGT GAGATATTAG TAGATAGAGC GCCAATAACG GTGGCTGTTG TGAGTAAGTG	360
AATATCAATC TGAGGATTTT GAGCACTGAT GATAGCAATG ATGGGAAAGA GGGCTGGAGC	420
TACAACGGAT AGGGTGGAAC TAAAGAGTGA CATCACTCCG GCTATCACAC AAAAGAACAG	480
AGGTAACCAG AAATGAGGAA TGGTTGTTGT CATGAGGTGC CCTATCAGTG TGAATAAACC	540
TGACTTGACC GCTAGAGACA TTAGTAAGCT CATGCCGCAG AGCATGATAA TTGTAGCCCA	600
GGGAACCTTA GCTAAAATGG CTTCTTGCTT CCCTAATTTG AGCCTTAAGG CGAGGCAGAC	660
CATGAGTATT GAGACAAAGC CAATATCAA TGTTTTTTGA TAAGTAGCTA TCCAGGCGAT	720
GTTTGGGAAA ATGAGATGCA ACAAGGGAAA AAGCCAAACC AAAACCATGC TGCTGATCAT	780
GAGCAAGGTG GTTTGTCTTT GAACCTTGCT GAGGAGTGGT GGTGGTCAA TAGTCAAGGA	840
TGAGTTTGTT CTTCCCTTAC TATAGTGACT GTAACAGGAT AATAAAAGCA AGACGATGAG	900
TGGGTAGATA ATGCTGACGA TAAAGATATG ATTGCCAAGT GAAAAAGCTT GCTCTTCCCA	960
TCCCATTGTC TTAAACAGGC CTTGAAAGAC AATGCCTGAG CTAAGGTTA TCAAATTAGC	1020
CCCTCCTGAA GCTCCCCAAT TGACGGCTTG AGCTCCAATC AAAGGGTGTT TGTCCGCTTT	1080
TTGACAGAGG GTAATCGCTA GAGGACAGCA AACGGCCATA GTAGTGAAAA ATCCAGCACC	1140
TAAAGCAGAC AAAAGGGTTG CCATCAGGTA TAAAATCATG TAGAGGGCGT TAGGGTGGGT	1200
GCGTGTGCGG TAGAGAATGT GTTGAGCCAA AACATCAAGA GTACCGTTAG TTGTTGCAAC	1260
GTTATAAAAG AGAGAGACGC TAAAAATGGT AAAAAAGAGT GAGGTGGGCC AAAAAATGAAG	1320
AAGTTCTTTG GGGCTTAATC CCATGAGAGT GGTTGCGATG AGGTAAGAAA AAGCAATAGC	1380
CAGCAGGCCA ATATTGATTT TGGTGCGGTA ACCAATTCCA ATGGCTAGAG CAATGG	1436

(2) INFORMATION FOR SEQ ID NO: 297:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1696 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

CCATTTGGGA AAGAACGTAA GAGTTTGCAG GGTGAGATTC CAGAAGAATT TTCAATGTCA	60
GCCGTTGACA TGTCTATGAT TGACCACATT CCAGATATGA TTGAAAATGG TGTGGACAGT	120
CTAAAAATCG AAGGACGTAT GAAGTCTATT CACTACGTAT CAACAGTAAC CAACTGCTAC	180

1328

AAGGCGGCTG TGGATGCCTA TCTTGAAAGT CCTGAAAAGT TTGAAGCTAT CAAACAAGAC	240
TTGGTGGACG AGATGTGGAA GGTGCCCCAA CGTGAACTGG CTACAGGATT TTACTATGGT	300
ACACCATCTG AAAATGAGCA GTTGTTTGGT GCTCGCCGTA AAATTCCTGA GTACAAGTTT	360
GTCGCTGAAG TGGTTTCTTA TGATGATGCG GCACAAACAG CAACAATTCG TCAACGAAAT	420
GTCATTAACG AAGGGGACCA AGTTGAGTTT TATGGTCCAG GTTTCCGTCA TTTTGAAACC	480
TATATTGAAG ATTTGCATGA TGCCAAAGGC AATAAAATCG ACCGCGCTCC AAATCCAATG	540
GAACATTGA CTATTAAGGT GCCTCAACCC GTTCAATCAG GAGATATGGT TCGTGCATTA	600
AAAGAAGGAC TCATCAATCT TTATAAGGAA GATGGAACCA GCGTCACAGT TCGAGCTTAA	660
GAAAGGAAAA GGAAATGATA GAGGCACAGG GTTCTTAGT GGATAAGCAA ACAAGATGCA	720
TTCATTACCA TAGCAAGCTG GATATTATTG CTTTACAATG CTATGATTGT AAAAAGTATT	780
ATGCTTGTTA TCGGTGTCAT GATTCATTAG AACATCACCC TTTTGAGCCG TATCCCTTAT	840
CTTTGATACA GGATAAGCCT ATTTTATGTG GTGTTTGTCT AAACTACTA ACATATAAGC	900
AATATAAAGA AAGCTTAAGT TGCCCTTTT GTTTTCTCG CTTTAATCCA GGTGCCCCAA	960
ATCATAAGGA ACGCTATTTT AAATAGCAAA TCATCTAGTT TTGAAGTAGG AGAAAACTCA	1020
ATTTCAAGAG AAAATGAAGT AAATCTTCCC ACAATAAAAC GCATAATATC AAGATTGTTC	1080
AATACCTGAT ACTATGCGTT TTTAAGATTT TAAAGACTTT TTTCTTTAT CTGGTATTTT	1140
GACTACTTGT TAAACTGGG TTAATTTTCG ACTGTTAAT AGTTATTATG CAAAGTCTAA	1200
AAGGTTAGAA TTGTCAAAAC AATCCGTCTA GAGTATGCGT GATGCCAACC GTGGTGGATG	1260
TTCTCAGTCA TGCCGTTGGA AGTACGACCT TTACGATATG CCATTTGGGA AAGAACGTAA	1320
GAGTTTGCAG GGTGAGATTC CAGAAGAATT TTCAATGTCA GCCGTTGATA TGTCTATGAT	1380
TGACCATATC TCAGATATGA TTGAAAATGG TGTGGACAGT CTAATAATCG AAGGACGTAT	1440
GGAGTCTATT CACTATGTAT CAACAGTAAC CAACTGCTAC AAGGCGGCTG TGGATGCCTA	1500
TCTTGAAAGT CCTGAAAAGT TTGAAGCTAT CAAACAAGAC TTGGTGGACG AGATGTGGAA	1560
GGTTGCCCCA CGTGAACTGG CTACAGGATT TTACTATGGT ACACCATCTG AAAATGAGCA	1620
GTTGTTTGGT GCTCGTCGTA AAATCCCTGA GTACAAGTTT GTCGCTGAAG TGGTTTCTTA	1680
TGATGATGCG GCGGTA	1696

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

CCGAGTTTAT TATGGTTTCT TCGGAATTTA TCTCAAAGAT TGAATTTGCT TGCAATAAGA	60
AAGAAAGTCT TTATAGTCAA AGCAAATTTA AGTATGCGAT TCGTTCGATG TTCGCAGGTG	120
CATTTTAAAC CTTCACTACT GCTGCAGGTG CAGTTGGGGC TGACTTGATT AATAAAATTG	180
CACCAGGTAG TGGACGCTTC CTCTTTCCAT TCGTTTTTGC TTGGGGCTTG GCCTACATTG	240
TTTTTTTGAA TGCCGAGTTG GTCACCTCAA ACATGATGTT CTTGACTGCT GGTAGTTTCT	300
TAAAAAAAT CTCTTGAGGA AAAACAGCTG AGATTTTACT ATACTGTACC TTGTTCAACC	360
TTATCGGAGC CTTGATAGCA GGGTGGGGCT TTGCTCATTC GGCAGCCTAT GCGAATCTGA	420
CACACGATAG TTTCATCTCA GGTGTTGTTG AGATGAAGTT AGGCCGCTCA AATGAATTGG	480
TCTTGCTTGA GCGGATTTTG GCAAATATTT TTGTAAATAT TCGGATTCCTG TCATTTATTT	540
TGGTCAAAGA TGGTGGTGCC AAACCTTGGC TTGTGTTGTC AGCTATTTAC ATGTTTGTAT	600
TCTTAACAAA CGAGCACATT GCGGCGAACT TTGCTTCTTT CGCGATTGTG AAATTCAGTG	660
TTGCTGCGGA TTCAATTGCC AACTTCGGTG TTGGAAATAT GCTTCGCCAC TGGGGTGTGA	720
CTTTCATCGG AAACCTTATC GGAGGAGGCC TCTTGATGGG TCTTCCATAT GCCTTCCTCA	780
ATAAAAACGA AGATACTTAT GTAGATTAAG AAAATGAGCA CGATTGAGTC GTGCTTTTTT	840
CATTTTCAAA ATAAGGTAAT AGCTATTTCT TATATCAAAA TATAGAAAAC TGATATTTGT	900
ArACTATAAC TCAAGGTGCT ACAATATCCT TAATAAAATA ATATGGAGGT CACCTTATGA	960
CTTGTGATTT TAAATnTGAA ACTCTACAAC TACATGCTGG TCAAGTTGTG GCTCCAGCTA	1020
CT	1022

(2) INFORMATION FOR SEQ ID NO: 299:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 663 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

CCTTAAGTAA TCTCTGATAA TATTTTCTTT ATTAGCATAG GGGAATATCG ATATAATGGC	60
TTCATTATGA GTGGCAGGAA TATCCAATAT GGCAACTTTT CCAATAGATA ATTTAAACT	120
CATTAATAAA GTTCCTTTAG GTGAAATGTC TATTTTCTTT GATTTTAATG CTAATTTAGA	180

1330

AATAGATTCT CTCGCATTAG TTACATAACC AGATATAGGC ATATCTGATA TAGATACCCA	240
AGGTATTTCA GTTCCCCAAA AAGTAGCTTC ACTGCGTGGA GGAGTTTTTC CTATTCTGAA	300
GTTAACTAGG CTAGCAAATT TAATATATCT CCATGCTTCT GGGATTTTCAT ATATAGGATA	360
AGAGGTTGTT TCGTCTTTGT TCCCATAATA AGAGTTATCA TCTCCTTGGG AAACAATAGA	420
AATGTCCAAA TCTTTCTTTT TAATCTTGCC TTCTTCAAAG AGTTTTTGTT TTTCTGCTCG	480
TATTTTTTCA AGTAAACTT CGACTGATTC ATCATTTGGG TCTTGTTCAA CTAATTTTCC	540
TTGCATAGCA TATTGAAGAA TAGATTTTTT TAGTTTATCT GGAAATTCTT TATCTAGCTG	600
TTCTAGTCTA TTATAACTTT CAGCATATTC ATCTACTTTT TCTAAAGCTG ATTCGATTGC	660
TTC	663

(2) INFORMATION FOR SEQ ID NO: 300:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 881 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

CGTCGCTGAA CATGTCAACA GCAAATTAAA CTAAACAAAC TAAAATTATG TGATACTTCA	60
CATAATTTTC TTTAGAAAAT ATTATCAGAA GAAAGTTGAG AAAAATGGCA GAAAAACAT	120
ATCCTATGAC CCTTGAGGAA AAGGAAAAAC TTGAAAAAGA ATTAGAAGAA TTGAAATTGG	180
TTCGTCGACC AGAAGTG GTA GAACGCATTA AGATTGCCCG TTCATACGGT GACCTTTCAG	240
AAAACAGTGA GTACGAAGCA GCTAAGGATG AACAAGCCTT TGTCGAAGGA CAAATCTCTA	300
GCTTAGAAAC AAAAATCCGC TATGCTGAAA TCGTCAATAG CGACGCAGTT GCCCAGGACG	360
AAGTAGCGAT TGGTAAAACA GTCACCATCC AAGAAATTGG TGAGGACGAA GAAGAAGTTT	420
ATATTATCGT AGGTTTCACT GGTGCAGATG CCTTTGTAGG TAAGGTTTCA AATGAAAGCC	480
CAATTGGGCA GGCCTTGATT GGCAAGAAAA CAGGTGATAC AGCAACCATT GAAACGCCTG	540
TTGGTAGCTA TGATGTAAAA ATCTTGAAGG TTGAAAAAAC AGCCTAAAAA CAGAAAAAGG	600
AGTGGGGAGG CGATGTGCTT CACTCACTCC TTTTCCATT TTGCTACTCT TCGAAAATCT	660
CTTCAAACCA CGTCAGCGTC GCCTTGCCGT ATGTATGGTT ACTGACTTTG TCAGTTTCAT	720
CTACAACCTC AAAACAGTGT TTTGAGCTAA CTTTCGTCAGT TTCATCTACA ACCTCAAAAC	780
TATGTTTTGA GCTGACTTCG TCAGTTTCAT CTACAACCTC AAAACCATGT TTTGAGCCGA	840
CTTCGTCAGT TTCATCTACA ACCTCAAAAC TATGTTTTGA G	881

1331

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 949 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

CCTTTTTTAA TACAAGTTAT TTTGATTTAA CCGGCTTGTC TTGAGCTGTC TGCAAAGCTG	60
TGGCAATCGT ATCTGCATAC AATTTTGCTC CTGCTTCGAT AGTGCTACTC TCACTCCCGA	120
AATGAACCTG GTCTGTTCCA GCCCAAATTT CTGGATGCTC TTTCGCAACT TGATTCCAAT	180
CTGCTATCGT AATGTAAGGT GTCTTCTCTG CCAATTCTCT CATATAGGCA GCAGCCTTCT	240
CAACGATGGC ATAGGTCTCT TTTGTCTTAT CTCCCTCATA AGGAGTCACC AAAATCATAT	300
GGTGTCCCTT AGGAAGATTT TTCACGATAC TGTCCCAGTC ATCCTTGTA TTCTCAGGAT	360
TATTTACCCC AGTCGCAATG ACCACCGTCT TAGGTAAAAA TTTATTCTGG CTATTATTTA	420
GCATGATTTC ATTTGCGGTC TTGGTTGTTA CGCTGACCTG CGCGTTAATC TGTGCTCCAG	480
GAAGAGCTGT CTGTAGTGCT GTATTTGCCC TTAAAGCCAC TGAGTCACCA ATTAACATAG	540
TGCCATCAGC AATTCCCAAA CTGTTTGCACT CTGCCCCGTT TGCCATCACC TTGGTCTGGC	600
CAATATTTGT TGCAGCTTGC TTCAAGCCAT TGACAGTCAA GTCTGTCTCA AACGCTCCCA	660
CTTGTGGTGC CAACAAGGTC ACCGTGCAGA CAATGATGGT CAAGATTCCT GTACCTGCTG	720
CAAGAATTGC GTGAATATAA GGCAGGGGAC GAAsGGTTTG GACAATAGGT GTGTTCTTGC	780
CTGCAATCCA AGGTTCCAAT ACATAAAATG ACAGACTGGC AAAGCCATAA GAACAAATCA	840
GAGTCAGTAA TACAGCAAGA AGATTTGATG TCAACTGTGA GAAAATGATA TAGAAAGGCC	900
AATGGAAAAG ATAAACCGCA TAGCTAGTAT CCGCTAAAAA GCTGATAAT	949

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

AAGATATATT TTTTACACAG AAGTATGCAA AAGTAAAGAG TGCAAAAAAT GGAATTAAAG	60
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1332

CGAAAATAAA AGCCGTGTAC AGGCGACCAA ACCAACGTAC ACGGCTAAGG AAAAATAACA	120
AAACTCAAGC AAAGGCAAGG CGCGTGGTTT TGTTAGGTAT TTAGCAAGGG GACAAACCCC	180
TTTGTAATA ATCTCCTCTT ATTTTATCAA AATTAGAGGA AAATGACAAC TTAATTTATA	240
AAAAGGAAAA ATGGAGGATA TAAATGGAAA TTCTGTCTAA AGAAATACAG TTACAGGGCT	300
TACAACTTCT TAAACAGACT CTTGAAACTT TAGTTGAGCT AGAAAAACAA CGATCTAGTA	360
AGTTAGATTT AATTCTCGT AAAGAATTAA TGGATCTGCT AGGTATAAGT GCTACAACCC	420
TTGATAACTG GGAGGATCTT GGTCTTAAAC GATATCAGAC TCCGATGGAT GGAGCTAAGA	480
AAGTATTCTA TCGTCCGTCA GATGTGTATT TATTTTtagc AATAAAATAG GAGTTATGAA	540
ATGAAAATTG TTACTTTCAA ACCAACTAAA CAAATAGACG ATGGGTTTTTA ACTGCCAGGT	600
ATTGACATTC TATTTGTCTC AG	622

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1929 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

CGCTAACTTG CAAACAAAAG AAGAACGCAA ACTCCACAAA TCCTTTACGC AGAAACTCAA	60
TCTCATCTAC TTACCTTGCT GACTTGGTAG AGTATGTTGC AGACAAAGAC TTCTCAGTAA	120
ACGTAATTTT TAAATCAGGT ACAACAAC TG AACCAGCGAT TGCTTTCCGT GTCTTTAAAG	180
AACTCTTGGT TAAGAAATAC GGTCAAGAAG AAGCTAACAA ACGTATCTAT GCAACAAC TG	240
ACCGCCAAAA GGGTGCTGTT AAGGTGAAG CAGACGCTAA CGGTTGGGGA ACATTTGTTG	300
TTCCAGATGA TATCGGTGGA CGCTTCTCAG TATTGACAGC CGTTGGTTTG CTTTCAATCG	360
CAGCATCAGG AGCTGACATA AAAGCTCTTA TGGAAGGTGC GAATGCAGCT CGCAAAGACT	420
ACACTTCAGA CAAAATCTCT GAAAACGAAG CTTACCAATA CGCAGCTGTT CGTAACATCC	480
TTTATCGTAA AGGCTATGCA ACTGAGATCT TGGTAAACTA TGAGCCATCA CTTCAATACT	540
TCTCAGAATG GTGGAAACAA TTGGCTGGTG AATCAGAAGG AAAAGACCAA AAAGGTATCT	600
ACCCAAC TTC AGCCAAC TTC TCAACTGACT TGCACTCACT TGGTCAATTT ATCCAAGAAG	660
GAACTCGTAT CATGTTTGAA ACAGTTGTCC GTGTTGACAA ACCTCGTAAA AACGTGCTTA	720
TTCTACTTTT GGAAGAAGAC CTTGACGGAC TTGGTTACCT TCAAGGAAAA GACGTTGACT	780
TTGTAAACAA AAAAGCAACT GACGGTGTTT TTCTTGCCCA CACAGATGGT GATGTACCAA	840

1333

ACATGTATGT GACTCTTCCA GAGCAAGACG CTTTCACTCT TGGTTACACT ATCTACTTCT	900
TCGAATTGGC AATTGCCCTT TCAGGTACT TGAATGCTAT CAACCCATTT GACCAACCAG	960
GTGTTGAAGC TTATAAACGT AACATGTTTG CCCTTCTTGG AAAACCAGGA TTTGAAGAAT	1020
TGAGCAAAGA ACTTAACGCA CGTCTATAAT AGAAGAAAAG AGTGGTTTGC CCACTCTTTT	1080
TACTCTCTTT ATCCATAGAA ATTGGACTCA GCCAAGACTT GTGATATAAT ATAGAAAGCA	1140
AAAAGGCAGA CGCCTAGATA ATAGGAGAAA CTATGTCAAA AGATATCCGC GTACGTTACG	1200
CACCAAGTCC AACAGGACTA CTACACATCG GAAATGCTCG TACAGCATTG TTTAATTACT	1260
TGTATGCGCG CCATCATGGT GGAACATTTT TCATCCGTAT CGAAGATACT GACCGTAAAC	1320
GCCATGTCTGA GGATGGTGAA CGTTCACAAC TTGAAAACCT TCGCTGGTTA GGCATGGATT	1380
GGGATGAAAG TCCAGAATCA CATGAGAATT ATCGCCAGTC TGAGCGTTTG GACTTGTATC	1440
AAAAATATAT TGACCAACTA TTAGCTGAAG GAAAAGCCTA TAAATCTTAC GTTACAGAAG	1500
AAGAGTTGGC AGCTGAACGC GAACGCCAAG AAGTAGCTGG CGAAACACCA CGCTACATCA	1560
ATGAATACCT TGGTATGAGT GAAGAAGAAA AAGCAGCTTA CATCGCAGAA CGTGAAGCAG	1620
CAGGGATCAT CCCAACTGTT CGTTTGGCTG TCAATGAGTC AGGTATCTAC AAGTGGCATG	1680
ATATGGTCAA AGGCGATATC GAATTTGAAG GTGGCAATAT CGGTGGTGAC TGGGTTATCC	1740
AAAAGAAAGA CGGTTACCCA ACTTACAAC TTGCCGTTGT TATCGATGAC CACGATATGC	1800
AAATCTCTCA TGTATCCGT GGAGATGACC ATATTGCTAA TACACCAAAA CAGCTTATGG	1860
TCTATGAAGC TCTTGTTGG GAAGCTCCAG AGTTCGGTCA CATGACCTTG ATTATCCACT	1920
CTGAAACTG	1929

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 708 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AAATTTAAGA AAAAGGAGAC ACATCATGTC TAAAAAAGTA TTATTTATCG TCGGATCACT	60
ACGTCAAGGT TCTTTCAACC ACCAAATGGC GCTCGAAGCT GAGAAAGCAC TTGCTGGTAA	120
AGCGGAAGTT AGCTACCTTG ATTATTCAGC CCTTCCTCTC TTCAGCCAAG ATTTGGAAGT	180
TCCAACACAT CCAGCTGTAG CTGCTGCTCG TGAAGCAGTT CTCGTTGCGG ATGCTATCTG	240

1334

GATTTTCTCT	CCAGTCTACA	ACTTCTCTAT	CCCTGGTACA	GTGAAAAACT	TGCTTGACTG	300
GCTATCTCGT	GCCCTTGACT	TGCTGTATAC	ACGTGGCGTT	TCTGCCCTTC	AAGACAAGTT	360
TGTCACAGTA	TCATCTGTAG	CCAATGCAGG	GCACGATCAA	CTTTTCGCTA	TCTACAAAGA	420
CCTCTTGCCA	TTTATCCGTA	CACAAGGCGT	TGGTGATTTC	ACTGCTGCAC	GTGTTAATGA	480
CTCTGCCTGG	GCAsACGGAA	AATTGGTTCT	TGAAGAAACA	GTCTAAACT	CACTTGAAAA	540
ACAAGCTCAA	GACTTGGTCG	AAGCTATCAA	GTAACATAACA	CTCAATAAAA	ATCAAAAAGC	600
AAACTAkGAA	GCTArCCGCA	AGCTACTCaA	gCACTGCTTT	GAGGTTGTAG	ATAGAACTGA	660
CGAGTGThnA	ACATATATAC	GGTAAGGCGA	CACTGACGTG	GCTTGAAn		708

(2) INFORMATION FOR SEQ ID NO: 305:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 781 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

CTTCTTTTCT	TGGAAATAGG	TGTATAATAC	GTTTATTAAA	TTTTTGAGGA	GTTGTCTATG	60
AAGAAAAGTT	TTATCCATCA	ACAAGAAGAA	ATTTCCCTTG	TCAAAAACAC	TTTTACCCAG	120
TATTTGAAAG	ATAAGCTAGA	AGTTGTCGAA	GTTCAAGGTC	CTATCTTGAG	TAAGGTCGGT	180
GACGGAATGC	AGGACAACCT	GTCTGGTGTG	GAAAATCCAG	TATCGGTCAA	GGTTCTCCAA	240
ATCCCTGATG	CTACTTATGA	AGTGGTGCAC	TCACTTGCTA	AATGGAAACG	CCACACCTTG	300
GCTCGTTTTG	GCTTTGGTGA	AGGAGAGGGT	CTCTTTGTCC	ACATGAAAGC	CCTTCGTCCA	360
GATGAGGATT	CCTTGGATGC	AACCCACTCT	GTTTATGTTG	ACCAGTGGGA	CTGGGAGAAG	420
GTTATCCCAA	ATGGTAAGCG	TAACATCGTT	TATCTAAAAG	AAACAGTTGA	GAAGATTTAT	480
AAGGCTATTG	GCCTGACTGA	GCTAGCTGTT	GAAGCCCGCT	ATGACATCGA	GTCTATCTTG	540
CCAAAACAAA	TTACCTTTAT	CCATACAGAA	GAATTGGTAG	AACGCTACCC	AGACTTGACA	600
CCGAAAGAAC	GTGAAAATGC	GATTTGTAAA	GAATTTGGAG	CCGTCTTTTT	GATTGGTATC	660
GGTGGCGAGT	TGCCAGATGG	TAAACCGCAC	GATGGACGTG	CACCAGACTA	TGATGACTGG	720
ACAAGCGAGT	CTGAGAATGG	CTACAAGGGT	CTAAATGGTG	ATATTCTTGT	CTGGAATGAG	780
T						781

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:

1335

(A) LENGTH: 846 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

CCCGCATCTT GTAGGGTTTT AACGGGCACG ATTTTCATAT CCGTCTTGAT TGTTTTAGCC	60
GCTTCTAGGG CTGTTTGGTA GTTGTTTTTC GCGTCCGGAT GCGCCTTTTG TTCTTCTTCG	120
CTAACAGGGT TATCAGGAGC AAAGAAAATA GCAGCACCTG CCCTAGCCGA AGCTACAACC	180
TTCTTATCAA TACCTCCAAT GTCTCCCACA TTACCATCGC GGTCAATGGT ACCTGTACCG	240
GCAACAATAC GACCATTACG AAGATCTGGG TGAGCTATTT GAGTATAGAT AGCTAGACTA	300
AACATGAGAC CAGCACTTGG ACCGCCAATA CCAGCTGTTG AAAAGCTAAT TGGGACATTG	360
CTGATTACCT CTGTACGGTC AATCAAGCCG ATTCCAATTC CATTTTGGCC ATTTTCCAAG	420
GTGATGATTT TTCCTTCTGC AGACTTGGTT TGCCCATCCT CTCATAGGT GACCTTGACG	480
GAATCCCCTA ATTTTGGAGA ACTGACGTAA TCAATCAAGT CTTTGGAAC TATCAAAGGTC	540
TGATCATTGA CTGCTGTGAC TGTATCAGAG ATATTGAGAA TCCCTTTAAA GGTTGAATTA	600
TCCGTACAT TCAAAACATA AACTCCAAAG TACTTGAGTT CGATATCCTT ACCAGCTGTT	660
TTTAGTCCTT GATACTTGGC CATATTTTGC GATGTTTGCA TGTAAGATTG ATTGATTCGC	720
ATAAATTCAA CATCGGAAGA ACCACCTGTA GTCTCCTGAG CACTACGAAT ATCTGTAAAA	780
GGTGTCAACC AAGCATAAAT CATATGAGCT AAAGTGGCAT GTTGAACACC AACCGTAACG	840
AATTGT	846

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

GCGATCTGCT TGGGCTTTTC CTATTACCTT ATCTAATAAA TAGGTACGCA GACTCATAAC	60
CATATAAAGT CCACCCCCCA TGGCACCGAC AAGAGCTACA TAAAAGAAGC TCCACAAACG	120
TCCACTTGGT TGGAAGAAAA ATCCTAACAG CCACTGGATG GTTCCTATTA ACAGAAACAT	180
GACTAGGGTC AGCAAAC TGA TTAATAATGGT TCGCTTCAAA ATCACCTTGC GCTTGACACC	240

1336

AGTTACTTTA CAAATATCCC GATACATCAA GACGTTAGGA ATGATGAGAG CAATGGTTGT	300
TGAAATCAAA GGACCATAAC TGTGGAAGAG GGCGATGGTA GGTAGTTGCA AGACTAGCTT	360
GGCAATAGAA CCATAGATAA AATAGAGAAC GGCCTTGCGG TTGCGGAACA TGGCCTGAAG	420
CATTGGAGAC AAGACCATGT ACAAGCCTAA AATAATAGAC TGCAAAACTG CAAAGACAAA	480
TAAGCCCAGA GCCAAACTAT CTGGCTTACC ATAGAAGACC GTATAAAGAG GTTCTCCTAC	540
CATAACCACT CCAACCGTTG CTGGTAGCAA GAACATAAAG AGTAGGGTGA GACTGTCCTG	600
AACGAGACGA GAAGCTGCTT TCAAGTCCCC CTTGACATAG TTTTCCGTCA AAAGTGGCAA	660
ACCAACACTC CCAATCGAAA CCCCTACAGA AATCAAAATC ATCGTGATTT TATTAGGATT	720
GGCTGAGAAA TAAGAAAACA TGACAACCAA GTCCTCATTG CTGTAGTTGG TAAACCAGCT	780
CATACTATTG ATAAAGGTCA GCTGAGTCCA AATCTGGAAG AGCTGGATG	829

(2) INFORMATION FOR SEQ ID NO: 308:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 464 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

CGAACATCTT GCTGGCTGAT TCGTCTGCCG CCATCGCAGC CCCGAACACA TTGCGACCCA	60
TGGCAAGCGG GCTCAATCCG CACATGGGAT CCGTGCCAAA GCCCCGCGTG TGCATCATTT	120
GCTCATCTAG TAACGTATGA GGTTTGCCTT CGCTGTGCGAT AAACCGATAT TCAATCGCAC	180
CACTGCTCGT TCTCCGCGGA GGGGAAACCG ACTGCGGTAG GATGAACTCC AGAGAAGAGA	240
GATCACGACC TACCAGGTGC GGCTCGTTGA AGCTGTTGCC GCTTAGCAGC AGGCTCGCCA	300
CCACGCATTC CCAGAACTCA ACGGGGGTTT GATCGGCGTT CGGTTGCTGA CTAATAACTC	360
GGTGCACGGG ATGCGAAGTG GCCACTTCTG GCACACCGTT CTTGTCTTCG TAGAGAGCAA	420
TTGGGAGGGT GGCCAGCGTT TCGGCGATGA GGCGCACGCA GGCC	464

(2) INFORMATION FOR SEQ ID NO: 309:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 982 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

1337

CCGTCTATAA TGGTAATAGA TTTTATTTGG AGGTTTTTAT GTCATTTCTA TCAAAAATG	60
GAGCAGGTAT CTTGGCCTGC CTTCTCATTT CCATCCTATC TTGGTACTTA GGAGGATTCT	120
TCCCTGTGGT TGGCGCGCCC GTTTTTGCCA TTTTCATAGG CATGCTCCTA CATCCCTTTC	180
TCTCGTCCTA TAAACAAC TG GATGCTGGTT TGACCTTTAG TTCCAAGAAG TTGCTCCAAT	240
ATGCCGTTGT CTTGCTTGGT TTTGGTCTCA ATATCTCGCA GGTCTTCGCA GTTGGCCAAT	300
CTTCACTCCC TGTCATCCTG TCCACTATCT CAATAGCTCT GATTATTGCC TACCTCTTCC	360
AGCGTTTCTT TGCCCTGGAT ACAAACCTGG CTACCTTGGT TGGAGTAGGT TCTTCTATCT	420
GTGGGGGTTC TGCCATTGCA GCGACAGgCC CGTTATTGAT GCTAAGGAAA AGGAAGTAGC	480
CCAAGCCATT TCCGTTATCT TTTTCTTCAA TGTCTTGGCT GCGCTCATCT TTCCAACCCT	540
CGGCACCTGG CTTCATCTAT CCAATGAAGG CTTGCGCCCTC TTTGCAGGGA CTGCGGTCAA	600
CGACACTTCC TCTGTAACGG CTGCCGCCAG CGCTTGGGAC AGTCTTTACC AAAGCAATAC	660
CCTCGAGTCT GCAACCATTG TTAAACTCAC ACGTACTTTG GCCATTATCC CTATCACGCT	720
CTTTCTATCC TACTGGCAAA GTCGCCAACA AGAAAACAAG CAAAGCCTGC AACTGAAAAA	780
AGTCTTCCCA CTTTTTATCC TTTACTTTAT CTTGCTCTCT CTCCTCACTA CACTACTCAC	840
CTCTCTAGGT GTGTCCAGTA GTTTCTTTAC TCCTCTCAA GAACCTCTTA AATTCCTTAT	900
TGTCATGGAC ATGAGTGCTA TCGGTCTCAA AACCAATCTG GTCGCTATGG TCAAATCCAG	960
TGGAAAATCC ATTCATCATG GA	982

(2) INFORMATION FOR SEQ ID NO: 310:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1939 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

CTAGCTGCCA ATATGATTGG GGTGCAGAAG CGCGTGATTA TCTTTAATCT TGGCTTGGTT	60
CCTGTGGTCA TGTTTAACCC AGTGCTTCTG TCCTTTGAAG GATCCTATGA GGCAGAAGAA	120
GGCTGTTTGT CTTGGTAGG TGTGAGATCA ACTAAGCGTT ATGAAACCAT AAGGCTTGCC	180
TATCGTGACA GCAAGTGGCA GGAACAGACC ATTACCTTGA CAGGCTTCCC AGCTCAGATT	240
TGCCAGCATG AGCTGGATCA CTTGGAAGGA CGAATCATTT AGGAGGAAAG CAAATGAAAC	300
GAATAGTCTT TGAACCTATT TTTATCGCAA CGACCTGGTA TATCTTTTTC CCGCCCCCTTA	360

1338

ACCTGACCAG CTGGGAATTT CTCTTCTTCC TCTGTGGGCA TTTGTTAGTT GTGGCAATAT	420
TATTTGGCTT TGGCAAGGGG ATAAACCTTG TCAAAACGGT TCATGTGCGC CACGGTAAGG	480
CGGAAGCTGC CTTAAATCTT GAGGGTTTCA AAATCAATCG GTTAGGGAAA ATTCTGTTAG	540
CTTCGATTGG AGGAATTCTT CTCTTGGCAG CTTTGGTTTc CTTGGTAACT TCCAGCATGT	600
TTCAGGCTAA AAATTATGCC AATGTAGTCA CGGTTACGGA AAAAGACTTT ACTGAATTTT	660
CTAAGAGTGA CACCAGTAAG GTTCCTATCC TAGATAGAAG TACTGCTGAA AAAATTGGAG	720
ACCGCTACTT GGGTTCCCTA ACCGATAAGG TGTCGCAATA CGTAGCGGCA GATACCTATA	780
CCCAATTGAC AATTGATGGG AAACCTTATC GGGTCACACC ACTAGAATAT GCAGACCCTA	840
TCAAATGGTT TAACAATCAA GCCAAGGGAA TCGGTGAGTA TATTAAGGTG GACATGGTAA	900
CTGGAAATGC GGATTTGGTG GACTTGAAGA CACCAATCAA GTATTGAGAC TCGGAGTATT	960
TTAACCGTGA TGTCAAACGT CACCTGCGCT TGAAGTACCC GACCAAAATC TTTAAAACTC	1020
CATCTTTTGA GGTGGACGAT GAGGGCAATC CTTTCTATGT AGCAACGGTT TACCAAAAGC	1080
AATTTGGACT TGCTGTTTCT CGTCCTGCTT CAGTCATTAT CTTGGATGCT ACAAATGGAG	1140
AAACCAAGGA ATACAGCTTA TCAGATGTTT CAGAATGGGT GGACAGGATC TATCCAGCAG	1200
AGGAAACCAT TGAGCAAATC AACTACAACG GCAAGTACAA GGACGGTTTC TTGAATGCCA	1260
TGATTTCCAA GAAAAACGTG ACCCAGACTA CCAATGGCTA TAATTACTTG TCTATCGGTA	1320
ATGACATCTA TCTCTACACA GGTGTGACGT CGGCTAATGC GGATGAGAGT AATCTTGGTT	1380
TCATCCTTGA AAATATGCGA ACAGGAGAAA TCACTAAGTA TAGCTTGGCT TCTGCGACAG	1440
AAGAATCAGC CCGTGAATCA GCAGAAGGTG CTGTTTCAAG GAAATCCTAC AAAGCAACCT	1500
TCCCAATCCT CATCAACCTC AATGACAAGC CTCTCTACAT CATGGGCTTG AAGGACAATG	1560
CTGGCTTGGT CAAAGAGTAC GCCCTGGTAG ACGCAGTCGA GTACCAAAAT GTTATCGTTG	1620
CTACTACAGT GGAAGAGATG CTCAGCAAGT ATGCCAATAA AAACGACCTT GAAATTGACA	1680
ATGCAACGAC AGAAAGCATC AATGGAGTAG TAGCAGACCT CAAATCAGCT GTTATCAAGG	1740
GAGACACTGT CTAATTCTTT AAAGTTGATG GCAACATCTA CAAGGTCAAG GCTTCAGTAT	1800
CCGATGACCT TCCTTACCTT GAAAATGGTA AAACCTTCGA AGGTCAAGTA GGAAAAGACA	1860
ATTATCTCAA GACCTTTAAG CTACGGTAAA AATAGGTTTT TTTCAGAAAG TATATGTTAT	1920
AATAAGGTAA ATTAAGCCG	1939

(2) INFORMATION FOR SEQ ID NO: 311:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 907 base pairs
 - (B) TYPE: nucleic acid

1339

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

CCTGCTAATA GAGAGAAAGA CTAGGAGTAG AAGTAAGCCA ATTAAATAAT GAGAAAGTTT	60
CATACCCCGT CCTTTCATGT AGATTTGGTA TCGAAAGATA TCTGCGGATA TAAATGTAAC	120
ATTATTTTTC TAATCTGTCA ATAAAATTTT TGACAATTTA ATAAATACAA CAAGGAGAGA	180
GCAACAAGAC TTTCTCCTTT GTTATCCTAT TCTAAAATGT TTTTACCTTA ATCTGATAAA	240
ATAATATCTT CGAGGGAGTA GCTAGCCGTC CAATCAAGAT ATTGTTTAGC TTTTGAAGCA	300
TCTGCTAGGA CACTGGCTGG GTCACTAGCA CGTCGAGCAA CAATCTCGTG TGGGATTTTT	360
TAATTTAGTA ATTCTTCAGC AGTTTTAAAG ATTTCTTTGA TAGTATAGCC TTTTFTAGTT	420
CCTAAGTTAA AGATTTGAGA AGAACTGTCT TCTTGAAATA GGTAGTTCAT TCCTTTAACA	480
TGAGCCTATG CAAGGTCCAA GACATAAATG TAATCTCGAA TACATGAACC GTCACGTGTA	540
TCGTAGTCAT CTCCAAATAT TTTTAAGCTA TCATTTTGTC CCAATGCGGT CTTGTTGATA	600
TTTGGAATGA TGTGAGTTGG ATTTTTCACA CGCAGACCGT TTGAAGCATC CATTTCAGCC	660
CCAGCAACAT TAAAGTAACG GAAAATAACA TATTTCCAGT CGTAGCGATT GGCCATCCAG	720
TAAATCATTC GTTCGCCCAT CAGTTTTGTC TCTGCATAAG GGTTGACAGG GTCGAGCAGG	780
GTATCTTCAG TCACCGGCTT GTCAATACAG TTATTTCCAT AGAGAGAAGC AGTCGAAGAG	840
AACATGATTT TTTGAATGCC AACTTCAGAT AAGACTTTGA GAACTTGTTT CATAACCAGCA	900
ACGTTGG	907

(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2170 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

CCACATAAAG GTAAATATCT TTTGTACTAT CTTGGGCATC CAAGAAAAGC AATTGGGCAA	60
TAACAGAGTT AGCCATATTG TCTTCAACCG GACCTGTCAG CATAATGATG CGGTCTTTGA	120
GAAGACGTGA GTAAATATCG TAAGAACGTT CTCCACGGCT TGTTTGTTCA ATAACTACAG	180
GAATCATTCA TTTCTCCTTT TGAGTTTTAA TTTTGTTGGT CAAATGACTG AAGATAAGAC	240

1340

TATTATAATA	TCTTGGTCAA	AAAAGGTCAA	ATTTTTTGCTC	TGCTTTCATT	AGACAGAAAC	300
AAAAACCCAA	CCTCCTTTCG	TGACTGGAAA	TACTTTTCCA	AGTCATTCTT	CTTTTCGATC	360
TTATTTTGTA	CCGAACAAGC	GGTCTCCAGC	ATCTCCAAGA	CCTGGAACGA	TATAACCGTG	420
TTTCGTTCAA	CGTTCATCCA	AGGCTGCTGT	AAAGATTTCT	ACATCTGGAT	GAGCTTCTTG	480
AAGGGCTTTT	ACACCCTCTG	GAGCAGATAC	AAGGCAGACA	AATTTGATAT	TTGATGCGCC	540
ACGTTTTTTA	AGAGAATCAA	CAGCCAAGAT	TGCTGAGCCA	CCTGTTGCCA	ACATTGGGTC	600
TACTACAAAA	ATTTGACGTT	GGTCAATGTC	CTCAGGCAAT	TTCACCAAGT	ATTCAACTGG	660
TTGAAGTGTT	TCTTCATCAC	GGTACATACC	GATGTGGCCA	ACTTTAGCAG	CTGGAACCAA	720
GTTCAAGAGA	CCATCAACCA	TCCCGATACC	TGCACGCAAG	ATTGGGACGA	TGGCCAATTT	780
CTTACCTGCC	AATTGTTTTT	GAAGTGTGTT	TGTAATTGGT	GTTTCGATTT	CCACATCTTC	840
TAGTGGAAGA	TCACGAAGTA	CTTCATACCC	CATCAACATT	GCAATCTCAT	CTACTAGCTC	900
ACGAAAAGCT	TTTGTAGAAG	TATCTGTACG	ACGCAAGATT	GACAATTTGT	GTTGAATCAG	960
TGGGTGATTA	ATAACTTCAA	TTTTTCCCAT	TTTTGGAATT	CCTTCTTTCA	ATTTATTCTT	1020
CTTATTATAC	CAAAAAACGG	TTTAAAAATC	TTTCTAAACC	ATTTATTTTT	GATAATTTTT	1080
ACATTAGATC	AGCCTCTTTA	AGAGCTGTCT	GTAAGTGTCT	AAGTGGTAAA	TGGGTCAATT	1140
CTGTCCCTTT	TTCTTGATAA	AGGTATTGGG	CGTAGTCGTC	CATTCCGTAC	TGGTTGATAT	1200
AAACCACGCG	CTTGCAGCCG	ACCTGAAGCA	ATTGTTTTGT	ACAGTTGAGA	CAAGGAAAAT	1260
GGGTACATA	GGCTGTAAAG	CCTTTGGGAA	CACCACGCTC	AGCACCTTGA	AGGATAGCAT	1320
TGACCTCAGC	GTGAAGGGTG	CGAACGCAGT	GGCCTTCAAT	GACCAAACAT	TCGTGATCAA	1380
TACAATGCTC	AGTCCCTGAC	ACCGAACCAT	TGTAACCAGT	GGAAATAACC	TTATTATCTT	1440
TTACCAGAAT	CGCGCCCACT	TTAGCACGTT	TACAAGTGGA	ACGATTCGCA	ATTAGTAGAG	1500
CTTGGGCTGC	AAAATACTCA	TCCCAGGCCA	GTCTTTTTTC	AGTCATCTCT	TTTCTCCTTT	1560
TTCTCTATTT	TTTAAAAAAT	GGTAAACCTA	AATCTGCAAT	CTTTTCAGCT	GGTACCTTCA	1620
TGCCATCCTT	GATCCATTTT	AGAAGGACAG	AGACGATGGC	TGAGCTCCAG	AAGGAATGAA	1680
GATAAGAGCT	GACACCTTTT	GATTTCCCAT	GGTATTTTTT	TAGAAATTCC	TGCATGGCTT	1740
GGACAAAGAT	TTTTTCCAGA	TGGTAATCCA	AGGCCAATTG	AATTACTCTA	GCTTCCTTTC	1800
TGGCCTCCCG	GAAAAGGTGA	ACCCAAACCA	AATAAAGGTC	TGTCTTTAAA	TCGTAATGAT	1860
GCAGCTGTTC	CATAATATTG	TGGACAGTTC	GTTTAAAGAC	GCTCTCTAAA	ATTTCTCTCT	1920
TGGAGTCATA	ATTGCGATAA	AAGGCCGCAC	GCGAAACACC	TGCACGTTTG	ACCAATTCAG	1980
AAATACTAAT	CTTGGTCAGT	TCCTTTTTTT	CCAAGAGTTG	CAAGAGGGCT	GTTTCAATGG	2040

1341

CTTCTCTGGT TAATAAATTG GATTCTTGGT TTGATTTTCT GAGATTTTCA AGAGACTTTT 2100
 CAGAGATTCT ACGTTCAGAC ATAACATTTT CTTTCTACTT GTCACAACAG ACGGATGATG 2160
 CTTTTGTTTC 2170

(2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 539 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

ATCTGCACGA ATCAGGGCTT TCTAAGTGAC TATTTCCACC GAAATATTAT TTATATCAGG 60
 AGGACATTCA TATGTCACGT TATACAGGAC CATCTTGGA ACAAGCTCGT CGTCTTGGCC 120
 TTTCACTTAC AGGTACAGGT AAAGAATTGG CACGTCGTAA CTACGTACCA GGACAACACG 180
 GACCAAACAA CCGTTCTAAA TTGTCAGAAT ACGGTTTGCA ATTGGCTGAA AAACAAAAC 240
 TTCGTTTCAC TTACGGTGTA GGTGAAAAAC AATTCCGTAA CTTGTTCGTA CAAGCTACAA 300
 AAATCAAAGG CGGAATCCTA GGTTCACACT TTATGCTTCT TTTGGAACGT CGTTTGGATA 360
 ACGTTGTTTA CCGTCTTGGT CTCGCGACTA CTCGTCGTCA AGCTCGTCAA TTCGTAAACC 420
 ACGGTCACAT CCTTGTGAC GGGAAACGCG TTGATATCCC ATCATrCCGC GTAACCTCAG 480
 GTCAAGTGAT CTCAGTTCGT GAAArATCAT TGAAAGTTCC AGCAATCCTT GAAGCAGTA 539

(2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 667 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

CCGGTTTGC TCCTTCTCTA CGGCTACGAC GTGATGTATC TCTGATGATA TCCACTGTTT 60
 CTGTAGCAGG CGTAGGTGTT TCTGGACCTG CTTGTTCTGC TTTTCTCTCT GCCGTCGTAT 120
 AGGAAACAGC TACCCTTGTT GGGGTTTCAT TGTATTCTCT TTCAAGTTTC TTAGGTCTAA 180
 CAGGACCTGG ACCTGGTCTT GATCCACTTT CTTCCGCTGG AGAAGAAGGT ACATCTTGAC 240
 TTGGATGACT TGGAACACCA GGAGTTTCTC TTTGAATCTC ATCTGCTGGA GAAGCTGGTA 300

1342

CACCTTGACT TGGGTGAGTA GGCACGGTAG GAGCTTTTCT CATAATCTCC TCTACCGTTG	360
ACAAGGAATC AGCCATGAGT TCTTCAGTTG AAGGTTTCATT TGCAGGAGTG CGAACTACTG	420
CCTCATCTTC TTTCAGAACT TCATCATAGC CTTTTACTTT TTCTAAATCT CTCAGAATCT	480
GCTCTTTAAA GCGTAATTTT TCTTCTGCTC TTGACTTTTC ACTCAAAAGT TTTTCCTCCT	540
TGTTGAGAAT CCATAATATT AGAGCTGAGA AGTCCAAAAA AAGCAATCTA TGATACTTTT	600
CCTAACGGAT TTTGTCATTT CCCAGACCAT ATCATACCAT GTTTCCTCTG CAAAGGTTGA	660
CTGGGAA	667

(2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

GGGAAGCCAA GGTATTTTAT CGGATGAAGT TGTTACTAGT TCTTCACCGA TGGCTACAAA	60
AGAGTCTTCT AATGCAATTA CTAATGATTT AGATAATTCA CCAACTGTTA ATCAGAATCG	120
TTCTGCTGAA ATGATTGCCT CTAATTCAAC CACTAATGGT TTAGATAATT CGTTAAGTGT	180
TAATAGTATC AGCTCTAATG GTACTATTCG TTCCAATTCA CAATTAGACA ACAGAACAGT	240
TGAATCTACA GTAACATCTA CTAATGAAAA TAAGAGTTAT AAGGAAGATG TTATAAGTGA	300
CAGAATTATC AAAAAAGAAT TTGAAGATAC TGCTTTAAGT GTAAAAGATT ATGGTGCGGT	360
AGGTGATGGG ATTCATGATG ATCGACAAGC AATTCAAGAT GCAATAGATG CTGCAGCTCA	420
AGGGCTAGGT GGAGGAAATG TATATTTTCC TGAAGGAACT TATTTAGTAA AAGAAATTGT	480
TTTTTTTAAA AGTCATACAC ACTTAGAATT GAATGAGAAA GCTACAATTC TAAATGGTAT	540
AAATATTAAG AATCACCCCTT CCATTGTTTT TATGACAGGT TTATTTACGG ATGATGGTGC	600
GCAAGTAGAA TGGGGCCCAA CAGAAGATAT TAGTTATTCT GGTGGTACGA TTGATATGAA	660
CGGTGCTTTG AATGAAGAAG GAACTAAAGC AAAAAATCTA CCACTTATAA ATTCTTCAGG	720
TGCATTTGCT ATTGGGAATT CAAATAACGT AACTATAAAA AATGTAACAT TCAAGGATAG	780
TTATCAAGGG CATGCTATTC AAATTGCAGG TTCGAAAAAT GTATTAGTTG ATAATTCTCG	840
TTTTCTTGGG CAAGCCTTAC CAAAACGAT GAAGGATGGG CAAATCATAA GTAAGGAGAG	900
CATTCAGATT GAACCATTA CTAAGAAAAGG TTTTCCTTAT GCCTTGAATG ATGATGGGAA	960
AAAATCTGAA AATGTGACTA TTCAAAATTC CTATTTTGGC AAAAGTGATA AATCTGGGGA	1020

1343

ATTAGTAACA GCAATTGGCA CACACTATCA AACATTGTCG ACACAGAACC CCTCTAATAT	1080
TAAAAATTCAA AATAATCATT TTGATAACAT GATGTATGCA GGTGTACGTT TTACAGGATT	1140
CACTGATGTA TTAATCAAAG GAAATCGCTT TGATAAGAAA GTTAAAGGAG AGAGTGTACA	1200
TTATCGAGAA AGCGGAGCAG CTTTAGTAAA TGCTTATAGC TATAAAAACA CTAAAGACCT	1260
ATTAGATTTA AATAAACAGG TGGTTATCGC CGAAAATATA TTTAATATTG CCGATCCTAA	1320
AACAAAAGCG ATACGAGTTG CAAAAGATAG TGCAGAAaTWT TTAGGAAAAG TATCAGATAT	1380
TACTGTAACA AAAAAATGTAA TTAATAATAA TTCTAAGGAA ACAGAACAAC CAAATATTGA	1440
ATTATTACGA GTTAGTGATA ATTTAGTAGT CTCAGAGAAT AGT	1483

(2) INFORMATION FOR SEQ ID NO: 316:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

CCTGAACGCT TTTTATATAA TATCATAAAG CCAATCTGAT TTATCAAGTG TGTCTAAGCG	60
ACGCGAATTA AAATTCATTG CATACTCCAT CGCTTCTAAA AAATCATT TTGAAAAGAC	120
GTAAAAATCA TCTAAATTCT GACTCCAATA TAATAACAAA ACCAATCCCA TAATATCCTC	180
TGGTTGATTA TTCAATAAAT TTAAGTTGGT TTCATAAAAC CCTGGAGTTC CAAATAGAGG	240
CAACTTTTTT TCTTCAATTT GAGTTTCTTT CCTTAGGGCA TGCTCAAAGT CTATAATATA	300
AATATTATTT CTATTATCAA TAAGTATATT ATTAAATGAT AAATCTCTAT AGGAAAGATT	360
ATATTTGGAG TTTATTATCT CCATATAATC AATTAATGTT AAAAACCAAT CATACGAGCC	420
ACTAACCATA TTATACTCGC TTAATTTATC TGCAATAATA AACTCAAATT CCACAAAATA	480
CGAATTCTTT ATGTAAAAAT CGTTAAAAAC TTTTGGAGTA AATTCCTCCT TTTCCAATTC	540
TACTAATATT TCTCTTTCAT TTATTAAACG ATTCACAGAA TCTCTATTTG TAAAATCAAC	600
CAACGATAAA TCACTAGCTT CTTTAAATAA AGAATAAACT CGCTTTTGAG TATTAAATAC	660
TTTATAAACT CCACCTTTGG CATTTT TAGA AATCACTTCC AAAATAATAT ATTGATCAGG	720
AATAGTGTTA TATCTTGGAA TATAGTAATC CCTTATTGGA ACATTCACAT TTGAAGGGAT	780
TTTCTTATCT CTTTATCCT TGAAAGTGCT ATCTTTTACG AACTCCCCAT ATCTGTAATA	840
TACAACCTCG CTAAGTTGAA ATCTGAAATC TGATGGTATG TTTACACCCT TTACACCTTT	900

1344

ATACAATATT	TCTAATTTGT	GTAACAAACG	TTGAAACTCT	TTATTATCTT	TTGGATAAAT	960
TGTAATGAAT	TTCCCGACTT	GTGAATAACC	ATTAAGCCCT	GTATTTTGCA	AAGAAAGTTC	1020
TTTAATGCTA	ACCAAAATTT	TGAAATTTAT	CTTCTTCTCT	CTAGAAAATA	TAAAATCAAA	1080
GAATTTTTTA	GCAACCAAAT	TAGCATTTAA	TATTGAAGCG	CTCAGGTGTA	TTTTAAATCC	1140
CTTAGATTGG	GTGATATTAG	ACGGCAAATT	ATATAACCAA	TGTTCATCAC	TAAAATTATC	1200
ACTAATTTTA	TATTCTAATA	ATAAATTATG	GTATGCGTCT	TCTATTTTCT	TTTCATAGTC	1260
CAAATAGTTT	AAATACTTTT	CGTAATTCAT	ATTAAGAAAT	CTTCTCCATA	AATTTTCTAG	1320
CCATCATTTA	AAGCCAAACA	ATTTAAAGCG	TGATAATAAA	TGTTGATAAT	CAATGTAACT	1380
TTCAGTCCTC	TATTTTGTA	TTCTTCACC	AATAATTTTA	TGCTATATCT	ATTTTCTCGA	1440
GGCAATTTAT	AGGACTTCAA	GATAAAACCA	TAAAAGAGAT	AAGTATTATA	ATCTGACAAT	1500
CCAGTTTCAG	AATAATTTT	TAGAAAAATA	TCTAGTGATT	CTGATAATTC	ATCCGGAATA	1560
ATTCTTTTAA	CATCGTATTT	ATTTTTCATA	TCGGCCACTC	TTCTTAAAA	AGCTCACAAAT	1620
AAAATTTTAA	ATTTCTATAC	AACAATCCGA	GAGTAGTCTC	ACAATTTGAA	CATTTTACAT	1680
CACTCTTAAT	ATATAAAAA	TGAATTAATC	AGAAACCTCT	GAATAAGATT	TCCTAATTAA	1740
TTCACCTTCT	ATATCATAGT	AAGGAATTCT	ATTATCCCTA	ATTGAAAATT	GAAATTTTAT	1800
GTTTTATATA	TTAACAATTA	TGCGGATTGT	AAATCTTGTC	TAACAAAATG	GCAAGTGCTA	1860
CTATGTGCCC	CAGAAGGCGA	TGCAACGCTA	TTTTGAATTG	AAAGAGCATA	ATCATCCATA	1920
TCATTTAAGT	CACGGATTAG	CAATGCTTCC	TTCTCTCTTC	CGACAATTCC	AAATTTTCTA	1980
ATTACCTTTT	CAGGATTATC	AAAAAATTCT	CCAACAACCT	CCATATTTC	TTGAAGTTCA	2040
TTCAAGAAAG	CTTTCATTTG	ACTACTCATT	ATATAGCTCC	TTTTCTATTA	CTTTATTTGG	2100
AATCAAAACT	TACTTGTTACA	TTGGAAACAC	CTCTATTCTA	CGCTTTCATA	TTGCTGCATG	2160
ACACTTTCAA	AATCAAATTG	CTAAAAATAA	TTTTTTTAAAG	CTTAATTTAG	ATTTAATTAC	2220
ATATATCTCA	AAAAATTGTT	TTGAAATTAG	TAAATTAAAA	TAGGTTTCTG	TACTTATAGG	2280
AACTAGTTAT	AAAAACTTCG	CCCATCATAA	AATATCTATT	TAAGTAAAC	AAAAATTTTA	2340
TAATTTTTTG	ATTTTAAAGT	GACTATAATC	TCCTATCTAT	AAATACCATT	CGCAGGACCT	2400
GGATCAATCC	CTCTAGCCAT	CTTATGAACT	TGAGTTCCTC	CAGACAGTCC	CGG	2453

(2) INFORMATION FOR SEQ ID NO: 317:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1049 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CCAATTTGAA GGCTCTAAAA CAATGGAAAA GTGCTACACA GATGTGACAG AATTTGCCAT	60
TCCAGCagTA CTCAAAACT TTACTTATCA CCAGTTTtag ATGGCTTTAA CAGCGAAATT	120
ATTGCTTTTA ATCTTTCTTG TTCGCCTAAT TTAGAATAAG TACAAACAAT GTTGGAACAG	180
GCATTCAAAG AGAAGCACTA TGAGAATACG ATTCTCCATA GTGACCAAGG CTGGCAATAC	240
CAACACGATT CTTATCATCG GTTCCTAGAG AGTAAGGGAA TTCAAGCATC CATGTCACGC	300
AAGGGCAACA GCCCAGACAA CGGCATGATG GAATCTTTCT TTGGCATTtT GAAATCGGAG	360
ATGTTTTATG GTTATGAGAA GAACTTTAGA TCTTTAGAAA ACCTTGAACA AGCTATTGTG	420
GACTACATTG ATTATTACAA CAACAAGAGA ATTAAGGTAA AGCTAAAAGG ACTTAGCCCT	480
GTGCAATACA GAACTAAATC CTTCGGATAA ATTAATTGTC TAACTTTTGG GGTGCAGTAC	540
ATTTTTGGTA TATATAAAAT TTGTAGGAGC TATATCTACA ATTTTATATT CCCAGTTTAT	600
GGATGTAACT TACTATATTC ACAATGTTAT CCAGTGTTTT TTCTCTAATA TTTAAGGAGT	660
GTTCTGTTTC TCGAATAAAT TCTTCAAAGT TTAACCCGTC AACTTGTTCC TGAACAAGAA	720
AATAATCATC CACGATATAA AATTCATCAG TTAAATTAGT AGTATAACTT TTATCGGCTA	780
ATTTTTTTAG CATGTGAGCT TCATTTTTTA TATCATCAAG AGCTGTCCAT TCTCCTTCAG	840
CATCATAATT CACAAAAGGT CTTGACTGCT TGATGATTAC TTTTtGCCCG TCCGATTTTC	900
TAATTGCCCG ATAAACATTT CCTTTATTtG ATCTCTTAAT AATTTTTTCC ATTTTGTATT	960
TATTTATTGC AGAGTCCTTA CTTGAAACTT CACATGTGGT TTGAAAATAA ATCCTTTTTT	1020
CTTCTTCTGA AAATAAATCC ATTTTCCGG	1049

(2) INFORMATION FOR SEQ ID NO: 318:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 776 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

TTAGTTGGTT AGAATCAGAA AATCGCCGAA GTGGTTATTT ATTTTTGAAT AAATTTAACG	60
AACCAATTAC AGCAAGAGGA GTTGCTCAAC AGTTAAAAA TTATGCTGAT AAATACAAAA	120
TGAATCCTAA AGTAATTTAC CCTCATTCTT TTAGGCATTT ATTTGCTAAG AATTTTTTAG	180

1346

CGAAGTATAA TGATATTGCC TTGCTTGCAG ATTTGATGGG ACACGAAAGT ATAGAAACTA	240
CTCGAATTTA TCTAAGGAAA ACAGCTACTG AACACAAAAA TATTGTAGAT AAAATTGTTA	300
ATTGGTAAAA AATAACAGGT GGTCAAACCTG ACTACCTGCT ATTTTGTGA TTATGGCTCT	360
TATTATGGGA ATATACCTAT GAATTGGGTT GTTATAAAAA TAAAAGATAT TTTTCAATA	420
AATACAGGTC TTTCTTACAA GAAGGGCGAT TTAAGCATTA ATAATAAAGG TGTAGAATT	480
ATACGTGGTG GTAATATTAA GCCTTTAGAA TTTTCTCTGT TGGATAATGA TTACTACATT	540
GATACACAAT TCATCTCCTC TGAGCAAGTT TATTTAAAC ATAATCAGCT AATAACACCT	600
GTATCAACCT CTTTAGAACA TATTGGAAAG TTTGCAAGAA TCGAGAAAGA CTATGATGGT	660
GTTGTGGCTG GTGGATGTAT TTTCCAATTA ACACCATTCTG AAAGTGCAGA GATGATGTCA	720
AAATGTCTAT TATGTAACCTT GTCCTCTCCG TTATTTTATA AACAAATTGAA AGCAAT	776

(2) INFORMATION FOR SEQ ID NO: 319:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 658 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

TGCAATGCGG CGGCTGCATA CGCTTGATCC GGCTACCTGC CCATTCGACC ACCAAGCGAA	60
ACATCGCATC GAGCGAGCAC GTACTCGGAT GGAAGCCGGT CTTGTCGATC AGGATGATCT	120
GGACGAAGAG CATCAGGGGC TCGCGCCACC GAACTGTTCG CCAGGCTCAA GGCGCGCATG	180
CCCGACGGCG AGGATCTCGT CGTGACCCAT GGCGATGCCT GCTTGCCGAA TATCATGGTG	240
GAAAATGGCC GCTTTTCTGG ATTCATCGAC TGTGGCCGGC TGGGTGTGGC GGACCGCTAT	300
CAGGACATAG CGTTGGCTAC CCGTGATATT GCTGAAGAGC TTGGCGGCGA ATGGGCTGAC	360
CGCTTCCTCG TGCTTTACGG TATCGCCGCT CCCGATTCGC AGCGCATCGC CTTCTATCGC	420
CTTCTTGACG AGTTCTTCTG AGCGGGACTC TGGGGTTCGA TGTCGACAGC CCGCCTAATG	480
AGCGGGCTTT TTTTTCCTGA GGCTGGACGA CCTCGCGGAG TTCTACCGGC AGTGCAAATC	540
CGTCGGCATC CAGGAAACCA GCAGCGGCTA TCCGCGCATC CATGCCCCCG AACTGCAGGA	600
GTGGGGAGGC ACGATGGCCG CTTTGGTCCC GGATCAATTC GCGCGACCGG ATCGATCC	658

(2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1475 base pairs
 - (B) TYPE: nucleic acid

1347

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

CCGGCTTAAT TTTTAGAAAA CGTGGGCAGG GAACCTTTGT TCTCTCTCGT GGCAGCTCAA	60
AAAGAAAATT AATCGTTCCA GAAAGAGATA TCCGGGGACT GACAAAAATA TCTGAAGATG	120
CTCATTCTAC AATTGACTCG AGGATTATTC ACTTCAAATT AGAATTTGCA AATGAATTTT	180
TAGCAGAAAA ACTACAGGTC GCTTTGCAGA GTCCAGTTTA TAATATTTAC CGCCTGCGTA	240
TTATTGACGG TAAACCTTAT GTTCTGGAAC AAACCTTATAT GAGTACCGAT GTTATTCCAG	300
GTATTACTGA AGATATTTTA CAAAAATCGA TTTACAATTA CATTGAAGGA AAGTTAGGAT	360
TGCATATTGC CAGTGCTACA AAAATCTTAC GAGCTTCTTC TAGTTCAGAA AATGAGCAAC	420
ATTACTTGCA GCTCCTTCCA ACGGAACCGG TATTTGAAGT AGAACAAGTG GCTTATTTGG	480
ATAACGGAAC TCCGTTTGAG TACTCGATTA GTCGTCATCG CTATGATTTA TTTGAATTTA	540
ATTCTTTTGC ATTACGACAT TCCTCCTAGG AGAAAATGTG AAAATGAAGC CAATCTTTTA	600
CAGACTCTAG TTTAAGAAAA ATTTAAACA GGGCAAGAAG GTCCCATCTA TGCTTAAATG	660
GTTTCTCTTT TCTAAATAAG ATGGCTTTAA AAGAGTGATC GTTGTATCCA TCATGTTGAA	720
AAATATCTTC GTATAGCTTA TAGAGTAGGT ACTGAAATTG TTCACCTGAT CTAATTCTTA	780
TAGTTATTTA GTTTTAAATA GTGTTTCAAA CATTCTTACA CTGACGAGAA GTTTTTGAGT	840
CTTTTCTTGT AACACATATA GTATACTGTG GTTAGAATAG TAGACTGTGA CTTCTAACAA	900
ATTGCTAGAA ATGAATTTCA ATCTCCCAAT TTATTTGTTC ATATCTTCTT TTAATATATT	960
AAATAAATTC TAAATCATAA TCATTTAAAA AAATTTTATT TTTTATTTT CATTACGAAT	1020
AATATAGATG AAGGGGAAAG AGTATGAAAA CAGAACTGTT TCTTTTGCTA TTAGTTCAAA	1080
AGGAGAAAAA ATGAAAGTAG AAAATATTTT GTATAGGGTG GATCATCGTA AATTGTTTGA	1140
TAATATTTCT TTTGATACTT CGAGTTCAGA CGTGACATTA ATTACTGGTA AAAATGGTAC	1200
AGGAAAGTCA ACTTTACTAT AGTAGATTGA AACTAGAATA GTACACATCT ACTTCTAAAA	1260
TATTGTTAGA AATCGATTTG ACTATCCTGA TCTATTTGTC CTGTTCTTAT TTCATTTTAC	1320
TATATCTCAA ATTGAGTATG ACGAAGTGCG CTCCCATGTC CTGGGAACGC ACTTTCTTCA	1380
TATTTTTCAT ATTCTTGAAT CCATCGATAA AGACTATTGG GATGAATTTT TAAAGTTGAA	1440
CTAATCATTT TTACAGGATG AGATTTACAG CAGAG	1475

(2) INFORMATION FOR SEQ ID NO: 321:

1348

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 560 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GAAATATATA TACTTCATCT TAATAGTGAG CAAGCTAAAC TTAGCATTTC ATGCCCTCAT	60
ATGGGATGTT CTTTGACTAA ATAATATGAT TATCGAGATA TATCTGGATA AATGAACTAA	120
TAAGTCTGAC GCGTAGACTT ATCAAAGTCA TTGGCATAACA CCACTATGAA CTCGTTGGTC	180
TGTTCAAATC CCAACACATT ACCTGAGAAG AAAGTTGCAA TGTTGTTTTT GGTGCGGGTT	240
TGAATTTAAA AAATTTGTTA TGTAGTACCT AATCTAAGGA ATTAGAACAA TGCCTCTAAT	300
TTTTCTTTAA TACACTGAAA CATTGATGAT TCTGGCTGTA TTTTGTGAAAC AGCTCTTCTT	360
TGCTCCTGGA AAATATCTTC AGAAGTTATA TTCTCTATTC CTAACGCTAC TTGAGTTTTT	420
TTTCTAAAAT ATTCTTTTCC GTTGCCATCT TTAGAAAAAT CATAACCTTC CCTATCTACG	480
CTGTTACACA AATTAGCTAA AAAA _r ACTCT GGGGTGGGA AAGGAAGATA AGAA _a CGTAT	540
TTAGCCCATATA ATCTATAAAG	560

(2) INFORMATION FOR SEQ ID NO: 322:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 643 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

CCGCCCCGCC ACCGCTGCCT ATCCTCGGGA GAGGGTCACC TGGAGTGAAC CTAGAACGAT	60
AGACACGGTG CGGTACGACC TCGTACTACT TTCGCCGACG GCCTCGTCCG TTGTCATCCA	120
CGAACTGATC GGACATGGGT GCGAACACTT CAGAGAAAAA ATCGTTGGAC TGCCTGTCCG	180
GCCTGAGGAA CTACGGGTGG TGGCTTTTCC GAAGAACGGC TCCGGGTTTG ATGACGAGGG	240
TACACCCTCC GAAGAGATTG TACTTGTGGA GAACGGCATT GTGAGGCACG CTGTCAGGGA	300
TCGGGCGACT GGAGGAATGG CGCCTTTTTC CGGTTTGACC AAAGTGGCAT CACATGGTGT	360
CAAACCTGGC TCAAGATGTA CGCATCTCAA GCGGAAGGG GAATCGTCAC AGGAAGGAGT	420
TACCGGAGTA CCCGCCGAAC GCACCGTTTG GATAGAGCAT TTTTCTGCAG CGAACTACCA	480
TTCAGGTCGA GCCTTTTTC GGTCTGGCCT TGCCTGGGTA GGCAGCCGAG AAGAACTCTT	540

1349

ATATCCCTTA ATGCCTTTCA CCATGTCAAT TGATATCTAC GAACTGGCCA GCTTATTGTG 600
GCATTTAGAC GGTCAAACGG AACGAGCACG TAGGGTACTG TGC 643

(2) INFORMATION FOR SEQ ID NO: 323:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

GGTACCCACT CATTCTTGAT GAATTGTGAA CAGTTGCCCT TGGGTCGTTT TGCGAGTTGA 60
AGTCAAGAAG AGGAAAAAAA CAAAAGGAG AAATACTCAT GGCAGTAATT TCAATGAAAC 120
AACTTCTTGA GGCTGGTGTA CACTTTGGTC ACCAACTCG TCGCTGGAA' CCTAAGATGG 180
CTAAGTACAT CTTTACTGAA CGTAACGGAA TCCACGTTAT CGACTTGCAA CAACTGTAA 240
AATACGCTGA CCAAGCATAC GACTTCATGC GTGATGCAGC AGCTAACGAT GCAGTTGTAT 300
TGTTCGTTGG TACTAAGAAA CAAGCAGCTG ATGCAGTTGC TGAAGAAGCA GTACGTTCAG 360
GTCAATACTT CATCAACCAC CGTTGGTTGG GTGGAAGTCT TACAACTGG GGAACAATCC 420
AAAAACGTAT CGCTCGTTTG AAAGAAATTA AACGTATGGA AGAAGATGGA ACTTTCGAAG 480
TTCTTCCTAA GAAAGAAGTT GCACTTCTTA ACAAACAACG TGC GCGTCTT GAAAAATTCT 540
TGGGCGGTAT CGAAGATATG CCTCGTATCC CAGATGTGAT GTACGTATtTG ACCCACATAA 600
AGAGCAAATC GCTGTTAAAG AAGCTAAAAA ATTGGGAATC CCAGTTGTAG CGATGGTTGA 660
CACCAATACT GATCCAGATG ATATCGATGT AATCATCCCA GCTAACGATG ACGCTATCCG 720
TGCTGTTAAA TTGATCACAG CTAAATTGGC TGACGCTATT ATCGAAGGAC GTCAAGGTGT 780

(2) INFORMATION FOR SEQ ID NO: 324:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 624 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

CGGGAAAAAT CAGATTGTGG GTTCAGATAT CGAATTAGCC AAGGCTATCG CAACAAAAT 60
AGGTGTCGAA TTGGAAGTAT CTCCCATGAG TTTTGATAAT GTACTGGCTA GTGTTCAATC 120

1350

AGGAAAAGCC GACCTTGCCA TATCAGGTGT TTCTAAGACA GATGAACGGA GCAAGGTGTT	180
TGACTTTTCC ATTCCCTACT ATACTGCAAA AAATAAACTC ATTGTCAAAA AATCTGACTT	240
GACTACTTAT CAGTCTGTAA ACGACTTGGC GCAGAAAAAG GTTGGAGCGC AGAAAGGTTT	300
GATTCAAGAG ACGATGGCGA AAGATTTGCT ACAAATTCT TCCCTCGTAT CTCTGCCTAA	360
AAATGGGAAT TTAATCACAG ATTTAAAATC AGGACAAGTG GATGCCGTTA TCTTTGAAGA	420
ACCTGTTTCC AAGGGATTTG TGGAAAATAA TCCTGATTTA GCAATCGCAG ACCTCAATTT	480
TGAAAAAGAG CAAGATGATT CCTACGCGGT AGCCATgAAA AAAGATAGCA AGAAATTGAA	540
AGAGGCAGTT CGATAAAACC ATTCAAAAGT TGAAGGAGTC TGGGGAATTA GACAAACTCA	600
TTGAGGAAGC CTTATAAGCA TCCA	624

(2) INFORMATION FOR SEQ ID NO: 325:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

TCTTATGAAG CCGAAGCGTG ATTTATGGCG GATAGGTTTG GTCTGCAGAA AGTGACAAAT	60
CTAGTGCCAT CAGCGTATAT GGAATCTnTG GCTGAGAAAC AGTCCCGGGG TGAAGTACT	120
TATGAGCAGG TTTATGAGGA TGCAACGGCT TATCATCATA CCATTGATGC GAGTACAGAG	180
GAGGCAGACT TGGTTTCTCT ACGTATTGTA GAACTATTGT CTCGAAGAGG CTTTAGCTTC	240
AGTCCTGCGA TCTTACTTGC TATTCATAAG GAGTTGTTTC AAGATATATT TGAACCCTCG	300
ATTCCGGTAG GTCAATTTTCG TCAGACTAAT ATCACAAAGA ATGAACCTGT TTTGAATGGT	360
GAAAGTGTTG TGTACTCTGA TTAATCCATG ATTCAAATGA CCTTGGATTA TGATTTTAAT	420
CAGGAAAAAC AAGTTGCATA TGCGACACTA ACCCAGGCGG ATATGGTTAA AAAAATCCAG	480
CATTTTATTT CAGGAATCTG GCAGATTCAT CCATTTTCGCG AAGGAAACAC TCGGACGGTA	540
ACGGTATTTT TGATTCAGTA TCTTCGTGAG TTTGGTTTTG ATATTGATAA TACACCATTT	600
CAGCAACATT CCAAGTATTT TCGTGATGCC TTAGTGTTAG ATAATGCAA GATTTTACAG	660
CGACGTCCTG AGTTTTTAAC AGCTTTTTTT GAAAATCTCT TGCTCGGTGG TCAAAATGAT	720
TTGTCTTCAG AAAAAATGTA TCTAGATTTA GACCTCGATC TTTCATAATC CTAATACTGA	780
GTAAACATTG AATTTTAGGA AAAAATGAAG TAAATATTCT CACAAGAAAA CGTATATCAT	840
CAAAGTTTGG CTCTTTGTCA ATTGTAGTGG GTTGAAGAAA AGCTAAGTTC GAGAAAGGGC	900

1351

AAATTTTCGGC CTTTCCTTTT TGATGTTTCAG AGCGATAAAA ATCCGGTTTT TTGAAGTTTT	960
CAAAGTTTCG AAAACCAAAG GCATTGCGCT TGATAAGTTT GATGAGATTA TTGGGCGCTT	1020
CCAGTTTGGC ATTAGAATAG TGTAGTTGAA GGGCGTTGAT AACCTTTTCT TTATCTTTGA	1080
GGAAGGGTTT AAAGACAGTC TGAAAAATAG GATGAACCTG CTTAAGATTG TCCTCGATAA	1140
GTTGAAAAA TTTCTCCGGG TCCTTATTCT GAAAGTGAAA CAGCAAGAGT TTGAAGAGCC	1200
GATAGTGATG TATCAAGTCT TGTGAATAGC TCAAAAG	1237

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

TTTGATTTTT CTGAATTAGA AGAGATTGAA TTGCCTGCAT CTCTAGAATA TATTGGAACA	60
AGTGCATTTT CTTTGTAGTCA AAAATTGAAA AAGCTAACCT TTTCCTCAAG TTCAAAATTA	120
GAATTAATAT CACATGAGGC TTTTGCTAAT TTATCAAATT TAGAGAAACT AACATTACCA	180
AAATCGGTTA AAACATTAGG AAGTAATCTA TTTAGACTCA CTACTAGCTT AAAACATGTT	240
GATGTTGAAG AAGGAAATGA ATCGTTTGCC TCAGTTGATG GTGTTTGTGTT TTCAAAAGAT	300
AAAACCCAAT TAATTTATTA TCCAAGTCAA AAAAATGACG AAAGTTATAA AACGCCTAAG	360
GAGACAAAAG AACTTGCATC ATATTCGTTT AATAAAAATT CTTACTTGAA AAAACTCGAA	420
TTGAATGAAG GTTTAGAAAA AATCGGTACT TTTGCATTTG C	461

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

TAACATTTAG GTACCTCTTC TTAACAAAGT TCAATAGTAA CAATTAATAT TTAAACAAT	60
ATATCAAACA TCAATGACTA GAATACTTGC ATCATCCTTC TTTCCATAGA TTGGATCAAT	120
AGCAGAAGAA TTAAATCTCA TCTTAATTAA CTCTCAAAA GTTTTATTTT GATTATTTTG	180

1352

ATAGAATTCA TAAAAGCCAT CGCTCATTAA AACAAATTTGT TCACTAGTAA CATCTATTTG	240
ATTAATAATA GCATGGTCTA AAAATCTCTC ATCCAACGAA CCTATCCAGT ACCCACTCGG	300
TTGATTAGAT AATTTTCTGA TTTTTTGTA AATAATTTT TTATTTAAAA CACTATTTGT	360
ACCAATTGAA TCTTTTATCT CATTTTCCC TTTTCAAAT AAGTTATCTA CTCTATGATC	420
AGTTATTTCC ATTTCTGTTA CTAACATGAC GCAGTCACCT AGCATCATAT ACTCCAACCT	480
TTTTTCTGAA AGTTTAGCAA ATATTGGTAA GCGATAATAT AGTATATTGA AACTAGAATA	540
GTACACCTCT ACTTCTAAAA CATTGTTAGA AATCGATTTG ACTGTCCTGA TTGATTTGTC	600
CTATTATTAT TTCATTTTAC TATACTCTGT TAATTTATAT GAGTTTAAAC CGATTTTCATC	660
TTTAACCTCG AGTAAAGCAG TTTCAAATAT TTGTTTAAGA GTTTTTGATT CTTTACAATT	720
AACCGACAAA CTTTCTGATA AAATATGTAC AACTTCTGAG ACTGAATAAC CTATCTCCTC	780
TTTAGAATTA TATAAATCTG TAGCTCCACC AATAATCCAA AAATACTGAT TTTGTGAACC	840
TACAATATCC TCATTTTCTA CGGAACCTCC TTGTATCGAA CAAATTTTAT TTATCTTTAC	900
CATAATACTT CAACCCTTTT AGTGTCAAAA GTAAACCAAT TCCTGTCACT GTTAAGAATA	960
GTTCCATAAT CTTATTCGAA CCAGTCTTTG GTAATTTTGT TTTkACATCT ACTATyTCTT	1020
TAGATTTATT AATATGATTT TCAGTTTCTC TGCCATCTCC AACTATTTTA TAGTTTACTT	1080
CTTCTGTCTT ATTATCTTGT TTATTGTCGA TCTTGTCATT CATTTGTCTA TTATCTTTAC	1140
TTGAGTTAAA CTCTCCGTTT TTCTGGTTAC TATCAATTAC ATTATTTGAA TTAGATTGTT	1200
TTTCCTCTTT GTTTTTTTCT TTTTCGTTTT TATCACTTAA ATTATTTGTT ACAATTTTGT	1260
AAAGCCCATT CTCCGTTACA ATATTGAAAT TACCATCGCT ATCACGTATA ACAGGTTCTT	1320
TCCCATTTGC ATTAGATTTG ATGAATGATA TATACTTACC GGATAAATTA TAAAATTGGT	1380
TATTTAAAC GGTATTTTA CCCTTTGAAT CCTCAATAAC AATTCCTTCT TTACCC	1436

(2) INFORMATION FOR SEQ ID NO: 328:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 646 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

CCGGCAGACA GGAGAAGGTG TTAAATATCA ATCTCAAATG GTTCGTCAAT GGTTTCTGAT	60
ACGTATTTTC CGTCTTCTT CCGTTGCTTG ACACACTCTG TGAGGAGATA TTCGATTTGC	120
CCATTGACTG AACGAAAGTC GTCTTCTGCC CATGATGCGA GTGCAGCGTA TAACTTTGTT	180

1353

GAGAGTCGAA GGGGGATCTG CTTTTTTTTTA GCTTCAGCCA TCTTTAGTAA AGGCTTCCTG	240
TGTTGACAAT TGGTTGTGCA TCATGATTGC CACAAAGAAC GACAAGGAGA TTTGAAACCA	300
TGGCAGCTTT TCGTTCTTCG TCAAGTTCTA CCAATTCCCC TTCATTGAGC CGTTCTAGTG	360
CCATTTCAAC CATTCTTACA GCACCATCTA CAATCATCTT CCGTGCATCA ATAATGGCAG	420
ATGCTTGTTG GCGTTGAAGC ATAACGGCAG CAATTTCTGG AGCATAAGCT AGGTAAGTGA	480
TACGTGCTTC AAGGATTTCC AAGCCAGCAT CCTCAACACG ACTTTGGATT TCTTCACGAA	540
TACGGGTAGC AACAATTTTCG CTAGAGCCAC GGAGACTACC TTCATCTGCG TGCCCATCAC	600
CCGGAGTATC CACATTAGGA GACACATCGT AAGGATAGAT GCGGAC	646

(2) INFORMATION FOR SEQ ID NO: 329:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1653 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

GTTGCAGGTG CAGTAGGTGT TACTTCAGAT ACATTTGAAC GTGCAGAGGC TCTTTTGTAG	60
GCAGGAGCGG ATGCGATTGT TATTGATACT GCACATGGTC ATTCTGCAGG TGTCTTGCCT	120
AAAATTGCCG AGATTCGTGC TCATTTCCCA GATCGGACTT TGATTGCTGG AAATATTGCT	180
ACTGCTGAAG GTGCACGTGC CCTTTATGAA GCGGGTGTAG ACGTTGTTAA GGTTGGTATT	240
GGACCAGGTT CTATCTGTAC TACTCGTGTG ATTGCTGGTG TTGGTGTTCC GCAAGTAACA	300
GCTATCTACG ATGCTGCAGC TGTTGCGCGC GAATATGGTA AAACGATTAT TGCTGACGGT	360
GGGATCAAGT ATTCTGGAGA TATTGTAAAA GCACTTGCTG CAGGTGGAAA TGCTGTTATG	420
CTTGGATCTA TGTTTGCTGG AACTGATGAA GCTCCAGGCG AACTGAAAT CTTCCAAGGA	480
CGTAAATTCA AGACTTACCG TGGTATGGGA TCAATTGCTG CTATGAAGAA AGGTTCAAGC	540
GACCGTTATT TCCAAGGTTT TGTCAATGAA GCAAACAAGC TTGTTCCAGA AGGAATTGAA	600
GGTCGTGTTG CTTATAAAGG AGCGGCAGCT GATATTGTTT TCCAAATGAT TGGTGGTATT	660
CGCTCTGGTA TGGGTTACTG TGGTGCAGCT AACCTTAAAG AACTACACGA TAATGCTCAA	720
TTTATTGAAA TGTCTGGTGC TGGTTTGAAA GAAAGCCATC CTCATGATGT GCAAATTACT	780
AATGAGGCAC CAAATTATTC TATGTAAAAA ACAATGAAAA GAACTCCAGT GAAAACAGGA	840
GTTCTTTTAC AATGTTGTCA ATTTCCATTT ACAGCAGCTT TACCATCCTG AATAGTGAAG	900

1354

ATACTTAGAT TTTCTGGCAG ATTTTGAAGA TGGTCTAAGC TTGTTGTTGT GATAAAGGTT	960
TGGATTGATT GAGAAATCGT TTCTAATAAT TTAACTGTC TAGTGTTGTC AAGTTCACTC	1020
ATCACATCGT CAAGCAGTAA TATAGGAGAT TCTGTGGTAA TGCTTTCCAT TAATTCGATT	1080
TCTGCTAATT TTATCGAGAG GACGAGACTA CGATGTTGAC CTTGGCTTCC GAAACTAGCA	1140
TCCATCCCAT TTATATAAAA AGAAATGTCA TCTCGATGAG GACCGACACC AGTATTCTTT	1200
TTAAATAAAT CTCTGGATCT ACTTTTTTCT AAAGCAATTT TGAAAGATTC GGATAAGTTT	1260
TGTTTGTGAG TTATATTGAC AGAAGATTGA TAGGATATTG ACAACTCTTC GATCTGATTA	1320
GAGAGTTCAA AATGTTTCTT ACGCCCAAAT GATTCTAGTT TTTTATGAA ATCTAAGCGG	1380
TGATTCATTA CACGACATCC ATAATCAACT AGCTGATCAT CTAACACAGA AAGGAATGTT	1440
TCATCTATTT TTTGAGCTGA TTTTAGGTAA GTGTTTCTTT GCTTTAGGAT GTGGTTATAA	1500
TTGGTTAAGT CAGATAAATA GATTGGCTTA ATTTGCCCAA GTTCCATATC AATGAATTTT	1560
CGTCGAATCG AAGGTGCTCC TTTAATTAGT TGTAATCTT CAGGAGCAAA TAAGACAACA	1620
TTCATGTGTC CTACATAATC TGAAAGGCGT GCC	1653

(2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

GAAACACTGT ATTTCAAAGC ATTTTTTGTT AGTTTAAAAT TACTCCCAT CTTCTTTTCC	60
AAACGTACAA TATATCCAAA ACCATTCAA ATACTAGATT CTATTTTTTA TAATATCACT	120
AAATCCACCT AATTATAGGA CGTTTTCAGA TTTTGTAGTCC CAGTCCCAGT ACCGGAGAAA	180
TATTGTTTTA ATATAATATC TCTTTTTGTC TTCTAAGCTC TTAAAAGCAA AAGAACAAGT	240
AAAGAGTCAA GACAAGGATA AAAAGTCCAT ATTAGGGCAA ATAAAAAGCT TTAAGACAGA	300
TGACAAATCT AAGTCAAATA AGAAAGACCA TAGCAAAGGT GCAGAGAGAT AAATATTGGC	360
GGTCTTCGGA CTGCCTTTAT TTTTTTATCC ATTTTTCAAA TCAAATTTAT TCAGACTATA	420
TATGCACATA TAACTTAAA TTCATATAAA AACATGGCTT GTAAAAAATT ACTTTAATCA	480
CAATAATCGC ATTTAAAATT GTGATGTTTG CAAGCTAAAT TACGGACTTC ACTTGGAAGT	540
TTTCCCTTGT ATCTTTTATA ATAGATAGAA AATTTGCTGG CAGATGAATA TCCAACAGAT	600
TCTGCTATCT CTTTATAGG TAGTTCAGTG TTTAAAAGAA GAGTTTCAGC TACATTCATT	660

1355

CTTTTTCTTT GAGTGTACTC TGTAATGCTT TGACAATATT TTTCTTAAA TAAATTTTTT	720
AATTTAGTAC CACTCATTTT AGATATTTTT TCAAGCGTGC CTTGATTTAC ATTCTGTGCA	780
AAATGATCAT CTAAGAATCT TGCTACATCT TCAAGTGCTT TATCATCATC AATTTCAATT	840
TTATATTTTT TTCTATTTAA GTATGTGTCA ATTACTATAC TTATCCATTC ATTTGCCTTT	900
GCTTTAAAGA AAAAATCAGC GGCAGGAGCG TCCATCTTAC AATTTAATAT TTCCATTGCC	960
ACTCTTTCTA AGGCCTTTGT AAGTATTATT TGATTCGGTT GAAGCAAGGT TGAATAAAAA	1020
GATTCTGGAT TAATGTAAAT AGATGCTAAA TGTTTTTCTA TTAGCTCTTT TTTAAAACcm	1080
ATGGAAACAG CAAGATAACA ACAATTCTCG TGTAATAAAA AAACAAAATT ATCTTTTATA	1140
TTATCAAAAT CAAAAGTACA TAGAGAGTTT GCGGTAATAG TTTGATACGG ATTAACTTT	1200
TCTCCGTTTG CACTGACAAT GTAAGTTGAA TAAATTGAAA CATAGTCTGA CATACTATAA	1260
GTGCTATTTT GAACTACTTC CTCTTTGATA TAAAAATCAT GTATATCGAT AATGAAGATG	1320
CCTCCTTCAT AAAACCGGTA	1340

(2) INFORMATION FOR SEQ ID NO: 331:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 607 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

TATGTTCTGT ATGAGTTTTT AAGTAGGAAA AACGTGCTAA CCTCTCAGAT TTTGGAACTT	60
GTAAAAGAAA CTCTTTTTTC ACCCGTAGTA GTTGATAATG GGTTTGATCC GGCCTTATTT	120
GAAATTGAGA AAAACAATT GCTAGCAAGT TTAGCAGCTG ATATGGATGA TTCTTTTAT	180
TTTGCACATA AAGAATTGGA TAAATTGTTT TTTCATGATG AACGTCTTCA ATTGGAATAT	240
AGTGATTTAC GAAATCGTAT TTTAGCTGAA ACTCCACAAA GTTCTTATTC TTGTTTCCAA	300
GAATTTTATG CCAATGATCG AATAGATTTT TTTTCTCTAG GTGATTTTAA TGAGGTTGAA	360
ATTCAAAATG TATTAGAATC ATTTGGCTTT AAAGGTCGAA AAGGAGATGT GAAGGTTTCA	420
TATTGTCAAC CTTATTCTAA TATCCTTCAG GAAGGTATGG TTCGGAAAAA TGTGGGACAA	480
TCCATTTTGG AATTAGGTTA TCATTACTGT TCTAAATATG GTGATGAGCA ACATTTACCC	540
ATGGATTGAA TGAATGGTTT ACTTGGTGGA TTTGCTCACT CTAAGCTCTT TACAAATGTC	600
CGGGAAA	607

1356

(2) INFORMATION FOR SEQ ID NO: 332:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 900 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

TTAAAATACC GAATTTTGTG TTGTCCTCTA TTTCAACATT GTGAATCGCC TCAGGCAGAG	60
AACCGATACT AAAGATATAA CCAAATAGT TGTCAATTGC TTTACCGATA TCAATCTTAT	120
TGGTTAAATC AAAATCCAGT TCGTCAATTG CGCCATCGAT GTCTTGATTG ATTTCCAAAA	180
GTTTTGTAAT GAGGTTACCC GTACCGCCTG GGATAATCCC TAACTTAGGA ATGTAGTCTC	240
TCTCATCAAT ACCTGAAATG ACTTCATTGA CAGTTCCATC TCCACCAAAC ACAACCACTG	300
CATCATACTG CTCACGAGAA GCTTCTTCAG CAAAATGTGT TGCATCCAGC GCTTTTTCGG	360
TAATTTTGGT TTCAACATAT TCAAAGTATT CTTTGTGCTTT ATTCTCCAGC TTTTCTTTGT	420
AATCCAAAGC CTTCTCGCCA CCAGAAGTAG GGTTGATAAT TACCATTGCT TTTTTCATTG	480
ATTTTATCCT TAATTTTAAA CAGAAATGTT TACATTTTCGT CGTATGCAAG TAAATGTAAT	540
CCTATTATAC AATGAAAATA CAGAAAAGAG AAATCTGACG TACTGGAGAT TAATACGCTT	600
TTATTCTATT TTCCCATCGC CTAACATCAT CCTTTAAGGG TTCATCCAAG TAAGAATAGG	660
CCTTATCCTT GATCCAATCA GGAATACCGT AAGCTGCCTC TGCTAwGCTA CAAGTGATTG	720
CTGCGAGAGT ATCACTGTCT CCACCAAGTG AGATGGCATT TCTTATCGCA TCTTCGAAGT	780
CTCTACTTTC AAGAAAGGCG ATAATGGCTT GAGGGACAGT TTCCTGACAT GTTTCGTTAA	840
AACGATAGTT AGGACGGATT TCATCTAAAG TTTGAGATAG ATTGTAATCG TATTCTTTTT	900

(2) INFORMATION FOR SEQ ID NO: 333:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

CCTTTCTGGC AACTGGTCT TGGAATACGG CAAAACCTCT GAAAATATCT ATGCTGGAAT	60
GGACGAGGAA TACCGTCGTT ATCAGCCTGC CATCATCACT TGGTACGAAA CAGCCAAACA	120
TGCTTTTGAT CGCGGACAGA TTGGCAAAAT ATGGGTGGAA TCGAAAACGA CCTCAAGGGC	180

1357

GGTCTCTACA GCTTTAAATC CAAGTTCAAT CCGACCATTC AGGAATTCGC TGGTGAGTTC	240
AACCTGCCAA CTAATCCTCT TTACCACCTC TCCAATCTGG CCTACACTCT CAGAAAGAAA	300
CTGCGCAGaA GcATTAAACAG AAAGGAAGCC TATGACCTTT AAACCTTCTCA GCCAAGAAGA	360
ATTCATCCAG CATACTCAG CTAGATCCCA ACGCTCTTTT ATGCAGACCG TAGAAATGGC	420
AGAGCTGCTG AGCAAGCGTG GCTTCAGTAC CCAGTATGTC GGCTACACTG ACCCACAAGG	480
GAAGGTAGTG GTGTCAGCTG TCCTCTACAG CATGCCTATG ACTGGTGGCC TTC	533

(2) INFORMATION FOR SEQ ID NO: 334:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 544 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

CCAGCAAACCT AGGAAGCTAG CCGTAGTTGC TCAAAGCACA GCTTTGAGGT TGTAGATAAG	60
ACTGACGAAG TCATGTACAA AACACTGTTT TGAGGTTGCA GATAGAACTG ACGAAGTCAC	120
TCAAAACACT GTTTTGAGGT TGCAGATAGA ACTGACGAAG TCACTCAAAA CACTGTTTTG	180
AGGTTGCAGA TAGAACTGAC GAAGTCAnnA ACCACACCTA CGGCAAAGTG AATCTGAAGT	240
GGTTTGAAGA GAGTACAACT TGTCTTTTAG AAAAGGAGCC TATAATGAAA GTCTTTCAGC	300
ATGTAAATAT CGTGACTTGT GATCAAGATT TCCATGTTTA TCTTGATGGA ATCTTAGCAG	360
TCAAGGATTC TCAAATCGTC TATGTCGGTC AAGATAAGCC AGCGTTTTTA GAGCAAGCTG	420
AGCAGATTAT AGACTATCAG GGAGCTTGGA TTATGCCTGG TTTGGTCAAT TGTCACACCC	480
ATTCTGCAAT GACAGGTCTG AGAGGGATCC GAGATGACAG CAATCTCCAT GAATGGCTCA	540
ATGA	544

(2) INFORMATION FOR SEQ ID NO: 335:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

CCAGGAACTC AAATGTAAGT AGGGGTTCTT TTTTGTATA TTTTCAAAT AACGCCTCTA	60
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1358

CACTATTTGT AGCAAATTCA CCAACTACAG TTGTATCTTA GTTAAAATAA GTTAGAATAT	120
GTAAGTGAGT ACCAGATATA CCAAGACATC GTCACCATCT AAGGTATATT CAAAATACAA	180
AAGTTGACCA ACTAGATTTC TGAATATCCT TATATATCCA TTCTTAAAAT TGGTTTAAAT	240
AGCGTAGTCT TTAAACTAG TTTTGAGAAT CCAAAAAATC TTCCTACATA TGTAAGAAGA	300
TTTTTTAGTT CAGAATGATT AGATTTAGCT AATGGATACC TATCCTACC	349

(2) INFORMATION FOR SEQ ID NO: 336:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

CTCCGATAAC CACACCAGCA ATGGAAATAA TTCCATCGTT AGCATCAAGA ACACCCGCAC	60
GCAGGATATT TAAACGACCT GCAAAATTTG AATCAATTTT GTGATTTGTT TCTGACGCTA	120
AATTTCAAGT TCAAGTTAGC CATCAAGAAG TCTTCTCTGG GTGACTTGTA GTCCAAGCAT	180
TTTTTAGGAT AGTTGTTAAT CCACTTTTCG ATGAATGCGA CTTCTTTGGG AGTCATTTTC	240
TTGGTTCCCT TAGGTAACCA TCTACGAATG AGCCTGTTGT GATTCTCATT AGTTCCCGGG	300
ATCCTCTAGA GTCGACCTGC AGGCATGCAA GCTTGGCACT GGCCGTCGTT TTACAACGTC	360
GATGACTGGG GAAAACCTG GCGTTACCCA ACTTAATCGC CTTGCAGCAC ATCCCCCTTT	420
CGCCAGCTGG CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAG	480
CCTGAATGGC GAATGGGGCC TGATGCGGTA TTTTCTCCTT ACGCATCTGT GCGGTATTTT	540
ACACCGCATA TGGTGCACTC TCAGTACAAT CTGCTCTGAT GCCGCATAGT TAAGCCAGCC	600
CCGACACCCG CCAACACCCG CTGACGCGCC CTGACGGGCT TGTCTGCTCC CGGCATCCGC	660
TTACAGACAA GCTGTGACCG TCTCCGGGAG CTGCATGTGT CAGAAGTTTT CACCGTCAATC	720
ACCGAAACGC GCGAAACGAA AGGGCCTCGT GATACGCCCTA TTTTATAGG TTAATGTCAT	780
GATAAGGATG GTTTCTTAGA CGTCAAGTGG CACTTATCGG GGAAATGTGC GCCGAGACCC	840
TATTTGTTTA TTTGTCTAAA TACATTCAAA TATGTATCCG CTCGTGAGAA AATAAACCTG	900
ATAAATGCGT CAATAATATT GAAAAATGAA GAGTATGAGT ATTCTACATT TCCGTGTCGC	960
CCTTATACCC TTTTTTGCGG CATGTTGCCT TCCTGTTTTT GCTCACCCAG AAAACGCTGG	1020
TGAAAGTTTA AGATGCTGAA AAATCATTTG GGTGCACAAC TGGGGTTACA TCCAACGGGA	1080
ATCTCCAnCA GCAGTTAAGA TCCTCTGACA GTTGTACACG CCGCAAGAAC TATTCCCGAT	1140

1359

GAATGAGCAA CTTTAAAG TCCTGCGAAT GTTGGGGCGG TAATAATCCC CGTGTTGTAG 1200
GCCCCG 1206

(2) INFORMATION FOR SEQ ID NO: 337:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 813 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CTGCTCAACT CAGACAGTCA AATTTCTGAC TTTACCAAAA GAACCATCAA AAAAGTTGCT 60
GAAAAAGGCC ATCAGGTTAT TATTACGACA GGTGCCCCCTT ACCGTATGTC AAAAGATTTT 120
TACCGTGAAC TGGGCTTAGA CACTCCTATG ATTAACCTCA ACGGATCCCT TACTCATTTA 180
CCAGACCAAG TTTGGGATTT TGAAAAGTGT TTGACTGTAG ACAAAAATA TCTGCTAGAT 240
ATGGTTCAAC GTTCAGAGGA CATTCAAGCC GATTTTATCG CTGGAGAATA TCGTAAAAAA 300
TTCTACATTA CAAATCCCAA TGAAGAAATT GCCAATCCCA AACTATTTGG TGTAGAAGCT 360
TTCCAGCCTG AAGATCAATT CCAGCCTGAA TTGGTGACCA AGGACCCTAA CTGTATCCTC 420
TTGCAGACTA GAGCCAGTGA CAAATATTCC TTGGCAAAAG AAATGAACGC CTTCTACCAG 480
CATCAACTTT CTATCAATAC CTGGGGAGGT CCGCTCAATA TCCTTGAATG TACCCCAAAA 540
GGTGTCAACA AGGCCTTTGC TTTGGACTAC TTGCTCAAGA TAATGAATCG TGACAAAAAA 600
GATTTGATTG CCTTTGGAGA TGAACACAAT GATACCGAAA TGCTCGCTTT TGCTGGGAAG 660
GGTTATGCCA TGAAAATGC CAATCCAGAG CTACTCCCTT ATGCAGATGA GCAAATTTCC 720
CTTACCAACG ACCAAGATGG GGTGCCCCAA ACCCTACAAG ACTTATTCTT ATAACCTATA 780
CTGATACTCA ATGAGGGGCA AAGAGCGAAC TTA 813

(2) INFORMATION FOR SEQ ID NO: 338:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 683 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

CCTAGATAAA TGATATAATT CTATTATTGT TCGTAAAAAT TAAAAGGAGA TTGATGATGG 60

1360

ACAAATTATT TAAACTAAAA GAGAACGGTA CAGACGTTTCG TACAGAGGTT CTCGCTGGTT	120
TAACAACTTT CTTTGCAATG AGCTATATTC TCTTTGTAAA CCCACAAATA CTTTCACAAA	180
CAGGAATGCC TGCTCAGGGC GTCTTCCTAG CGACGATTAT TGGTGCAGTA GCGGGTACCT	240
TGATGATGGC TTTTATGCT AACTTACCTT ATGCCCCAAGC GCCAGGTATG GGA CTCAATG	300
CCTTCTTTAC CTTTACAGTT GTATTCGGGC TTGGTTATTC TTGGCAAGAA GCCCTAGCTA	360
TGGTCTTCAT CTGTGGGATT ATTTCAATTGA TTATTACCTT GACAAATGTT CGTAAAATGA	420
TCATTGAATC GATTCCCAAT GCTCTTCGCT CAGCTATTTTC AGCTGGTATC GGTGTCTTCC	480
TTGCCTATGT AGGGATTAAG AATGCTGGAC TTTTGAAATT CACGATTGAT CCAGGCAACT	540
ATACTGTTGT AGGAGAAGGG GCTGACAAAG CTCAAGCAAC GATTGCAGCA AACTCTTCAG	600
CAGTTCCAGG ATTGGTCAGC TTTAATAATC CAGCTGTTTT AGTGGCTCTT GCAGGACTTG	660
CCATTACTAT CTTCTTTGTC ATC	683

(2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 852 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

CTACTTTACA TGGAAGTAGT CACTGAATTC CAGTTAGAAA TTACTTTGTA ACTACGTTTT	60
GAGGAGGAGT AAAATGCTTT CCTACGTTTCG ATATTACCCA CTAGCGATAG CTAAATTAAT	120
GTGTCTGTGC TCTCCTAAAA TCTGCTGATT TATTACTGAC TAATACAGGA GGTTTTTTTT	180
ATGgACAGAC AATCATATCT GCTATTGGTG TTTATATTTTC CACCAGTATC GATTATTTAA	240
TTATTTTAAT TATTTTATTT GCACAGCTAT CACAGAATAA ACAGAAATGG CATATTTATG	300
CGGGGCAATA TCTAGGCACA GGCTTACTTG TAGGGGCGAG TTTAGTTGCT GCTTATGTCG	360
TTAATTTTCGT GCCTGAAGAA TGGATGGTTG GATTGCTTGG TTTAATCCCT ATCTATTTAG	420
GGATTCGCTT TGCAATTGTT GGAGAAGATG CGGAAGAAGA AGAGGAAGAA ATTATTGAAA	480
GATTAGAACA AAGCAAGGCA AATCAACTGT TTTGGACAGT TACATTGCTG ACAATTGCGT	540
CTGGCGGAGA TAATTTAGGT ATCTATATAC CTTATTTTGC TTCGTTAGAT TGGTCACAGA	600
CCCTCGTGGC CTGCTTGTG TTTGTAATCG GCATAATTAT CTTTTCGAG ATTAGTCGGG	660
TGTTATCCTC TATTCGTTA ATATTCGAGA CAATTGAAAA ATACGAGCGA ATCATTGTGC	720
CCTTAGTATT CATTCTACTT GGA CTATACA TCATGTATGA AAATGGCACG ATAGAGACTT	780

1361

TTCTGATCGT GTAGATTTTT TTGTTTCACT AGGGATTTAG CCCGAGCTCA AATCAGCTCT 840
CTGATTTTCA GA 852

(2) INFORMATION FOR SEQ ID NO: 340:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

CCGCACAAAA GCGCATAGTA TCAAGATTCT ATAAAGCCTT GATACTATGC CTTTTTAATG 60
GATAAATAGT TAGTCTTTTT TAAAGACCGG ATCTTTCAAA CTCTGCATAC TGGCATTGAT 120
CACCGCGCCT AGGATAACAA TTTTAGCAAT CAAGATAAAC CAAAACATCA TAACAACAAG 180
AAGAACGGAA CCTAAAATTC GGACATCCAC CAAATGATGG ACATAGTAAT TGAGATAACT 240
AGAGAACAGA GTTAGTAAAC CTAAAATCAC TAAGAGAACA AAGGCACTGC CTGGTAGGGT 300
ATAGCTAATT TTCCTGTTAG ATAGATTGGG AAGAAAATAA TAAAGCATGA CCAAGATAGC 360
AAAGAGGAGG GCGTAAATCA GAGGACCTGC CAACCCTTGT AAAGCCTGAT AGATAATGCC 420
ATCTTTTGTC CAATAATGAG CAAGTAAAGC CAAAATCATC TGACCATAA AGATCAAAAA 480
CAAGGCAAAC GCAAAGAGGA GCTGCAACCA AAAGTACTA GGAGACTTAG CATCTGATGG 540
GAAATAAGTC CACGACTCTT TTCGACGCCA TAAGCCTTGT TAAAAGCTTT TTGCAAGAAA 600
TTCATAGATT TTGAAAAACT CCATAACGCC GATAAAACAG AAAAAGCTCA TAAACCTGTT 660
GAAGGTTGCG TCAAGACTTC TCTGGCTATT TTTCCACAC CTTTCATAGAG GCTTGGGGGG 720
CAGACGTCTT TCATAAGGCC CAAAATTCTT CCCA 754

(2) INFORMATION FOR SEQ ID NO: 341:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 707 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

GGGGATAACT CTAGGAGTAC CGCTATTACT CGACTTAATG AGTGCACAAG AAGTCAGGAT 60
TTTTATGCAG GTTGGGCGCT TCATCAGACA GGGAAGATTT ACAGCGACTA TTATGGAAGT 120

1362

CAAGGTTTGC TTTATTATTT GCTGACTTAC GTGAGTCAGG GCGGATTTTT CTTTGCCATC	180
TTTGAGTGGT TAGCCTTGGT AGCAGGAGGA TTTTTCCTTT TTAGATCAGC GGACACCTTG	240
ACAGAGCAAG GAGACCAAGC TGGACATCTG GTGACTATTT TTTACATGCT AGTTACAGGT	300
CTTGCTTTTG GTGGAGGCTA TGCGACTCTT TTAGCGCTTC CTTTCTTATT CGCAGCCTTT	360
AGTTTAGTTG CGGCTTACCT AAGCAATCCA AGCCATGATA AGGGATTTGT ACGGATTGGG	420
CTAGCTTTGG CAGGCGGATT TTTCTTTGCT CCCTTATCAT CGCTCCTGTT TATTGCTGTA	480
GTGAGTTTAG GCTTGTGGT CTTTAACCTT GGGCATAGAC GCTTTGCGCA TGGGTTTTAT	540
CAGTTTCTTG CAGTGGCTTT AGGTTTTTCA CTTGTCTTTT ATCCAACCTGC CTACTATAGT	600
GCTGCAACAG GAAGTTTTGG GGATGCGWTT AGTGGTATTC GTTATCCTAT TGACAGTATT	660
CGCTTTGATT TTA CTCTAA AATTTTAGAG AATATGTTTT TTTAAGG	707

(2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 762 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

GGATTTTGAA AAACCATACC GATTTGACGA CGTATATTCC AAACATTTTC CTCAGTCAAA	60
CGTTGGCCAT CAATTACAAT CTCTCCGGAT TCTGCTTCCA GTAAGCCATC AATTAATCGA	120
ACCGTCGTTG ATTTACCACT ACCATTATGC CCTACAATCG AAAGCCATTC TCCACGTTTC	180
ACGTGAAAgT AATATCCTTC ACATCGTAGT AGTTCTGATT TTCTTTATAG CGAAAAGAAA	240
GATTTTTTAC ATCAATTATT GATTTCAATTT CGAACCAAAT GTCCCTTTAA ATACATAGGC	300
ACTACCCTTG AAATAGTCAT AGCCAGAGTA GATAGTGAAA AATAAGGCTA CATAAAGTAG	360
AACTTGACCA AGCAAAGTCC AATGTAATAG CAAGAAAATA ATGGCAAACA TCTGACTAAA	420
AGTTTTAATT TTTCCAGGCA TTGCTGCTGC TAAAATTGTT CCACCAGTTT CAACCAATAA	480
AAGCCTTAAA CCTGTCACAG CTAACCTCACG ACAGATAATC ACTGCAACAA TCCAAGCCGG	540
AGCCATACCT AACTCAATCA ACATAATAAA AGCCGACATA ACTAGTAACT TATCCGCCAT	600
AGGATCTGCA AATTTACCAA AATTACTGAC CACATTCCAT TTACGAGCTA AATATCCATC	660
TAAATAGTCG GTAATACTGG CAACAGCAAA GATAATAGCT GCAACTATAT GACTCTCTAT	720
CGAATTCCT ATCGTTAAAA TAAAGATAAA AATAGGTATA AA	762

(2) INFORMATION FOR SEQ ID NO: 343:

1363

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 482 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

CTTTTGATAC ACTTAAACTA TGAATACAAA TCTCAAGCCC AAAC TTCAGC GTTTTGCTTC	60
TGCGACTGCC TTTGCCTGTC CTATCTGTCA AGAAAATCTG ACTCTGTTAG AGACTAATTT	120
CAAGTGCTGC AACCGTCATT CTTTTGACTT GGCGAAATTT GGCTATGTCA ATCTAGTCCC	180
TCAAATCAAG CAATCTGCTA ACTACGACAA GGAAAATTTT CAAAACCGTC AACAAATCCT	240
AGAAGCCGGC TTTTACCAAG CTATCTTAGA TGCTGTATCT GACTTGCTTG CAAGCTCAAA	300
AACTACCACA ACAATTTTGG ATATCGGTTG TGGTGAAGGA TTCTATTTCTC GCAAACTACA	360
AGAAAGTCAC TCTGAAAAAA CTTTCTATGC CTTTGACATC TCCAAAGATT CAGTCCAAAT	420
CGCGGCTAAA AGTGAACCCA ACTGGGCAGT CAATTGGTTC GTTGGCGACT TGGCACGACT	480
TC	482

(2) INFORMATION FOR SEQ ID NO: 344:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 520 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TTTATTTTAA TAAAGTCAAT ACCTGTCTTT ACTTTTCTT AAAAAAGTT TATTATGTTC	60
TTTAAGGAGG TGTAACACAT GAAAATAAAT AATAAACTCG TTGGAGAACG TATTCAAAAT	120
ATCCGTTTAA GCCATGGCGA CTCTATGGAA AAATTTGGAG AAAAATTTAA TACTAGCAAA	180
GGTACAGTTA ACAACTGGGA AAAAGGTCGC AATTACCAA ATAAAGAAAA CCTACTAAAA	240
ATTGCATCTA TTGGAAAAAT GAGTGTGAA GAGTTACTCT ACGGCGATTA CAATACTTAT	300
CTACACTTAA AGATTATGGA TTTAGCTCCT GAATGTATAA AAAATTATGA TGAGTATAAC	360
TCTTTACACG ATGATATAAC AAATAAAGCG TTACAGATCG CTCAAATAC CATTTCTAAG	420
ATTGATTATC AAATTTTACA CGAAACGATC AAAAAATTTA TTGATTAGC TATCGAACAA	480
TCGAGAGATT TGCAAGGAAA TTTGTTGAAA AATAACGGGT	520

1364

(2) INFORMATION FOR SEQ ID NO: 345:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1003 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

GCATCAAATC CGCCATCAAA GAAGTTCTCT GGATTACCA AGACCAGTCA AATAGCTTAG	60
AAGTGCTTAA TGACAAGTAC AATGTTCACT ACTGGAATGA CTGGGAAGTT GGAGACACGG	120
GAACCATTGG TGAGCGCTAT GGTGCCGTTG TTAAGAAACA CGACATTATC AATAAGCTTC	180
TCAAACAGTT GGAAACCAAT CCTTGGAACC GCCGCAATAT TATTTGCTC TGGGATTACC	240
AAGCTTTCGA AGAAACAGAT GGGCTGCTCC CGTGCGCCTT TCAGACCATG TTTGATGTTT	300
GGCGTGTTGA TGGGGAATC TATCTGGATG CGACCTTGAC CCAGCGCTCC AATGATATGC	360
TGGTGGCCCA CCACATCAAC GCTATGCAGT ATGTGGCTTT GCAGATGATG ATTGCCAAAC	420
ATTTTGGCTG GAAGGTTGGG AAGTTCTTCT ACTTCATCAA CAACCTCCAT ATCTATGATA	480
ATCAATTTGA ACAAGCTCAG GAATTGCTCC GTCGGGAGCC GTCAAAGTGC CAACCACGCT	540
TGGTTTAAA TGTTCCTGAT GGGACTAATT TCTTTGATAT CAAAGCAGAA GATTTTGAGT	600
TGGTGGATTA TGACCCTGTT AAGCCACAGT TGAAGTTTGA CCTAGCTATT TAAAAGAATA	660
GAAAAAAGAA GTTGAGAATA ATCCCAACTT CTTTGTGTTT TTAACGTGAT ACGCGGCGAC	720
GAGCTGCTTT TTTACGGTTT TCTTCGATGA AAGCTGCTTT TTGCTCTTCT GGTTCGATTA	780
CTTTCTTTTT AAATGCGTAT ACTGCACCTG CAACGGCAGC GACAGTTCCT GCGACACCTG	840
TTACAAGACC TTTAGCGAAT CCTTTAGCCA TGAGTCTTCC TCCTTTATAT TCTCAATCAG	900
CCAGCCTCCT CAAGAGGTCA CATTTTCTG ACTGACCTTT TTGTGTTATA ATAATAGTAA	960
CGAAAAAATG GGAATTTTTC AAGGAAAAA GATGAGAACA AAA	1003

(2) INFORMATION FOR SEQ ID NO: 346:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 750 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

CCGCACGTAC TATTCCAGAT GCCGAGGAAG TGGACCTCAT CCTCGTTGGC GCAACTGGTC	60
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1365

TCAACGCCTT TGAACGCCTC TTGGTCGGCT CTTCATCTGA ATACATACTC CGCCATGCTA	120
AGGTCGATTT GCTGGTTGTG AGAGAACAAG AAAAAACCTT ATAATCACAA AGAAAAGGAG	180
CCCCTAGCTC CTTTTTGTTT ACGATTTATT TCTCTCTTTA TGGCGTTCGT AAGCCTTGAG	240
CTGGCGCTGC AGTTCCTTTT TAATAGCAGG TTCTGGAGCA TATTTTTCTT CCCAATTATC	300
TGGTTTTAAG ATTTTATGGG TCACTGGATC AAAATGAGCC TTGCCATCTG GAAAAATTTT	360
CCCCATATTG GCCTGATGGA CAATATCAAA AATACGTTCT GGGTCCACCC CCATCAAGAC	420
AAACTGCCG TAGGTGAAGT AAAGCGTGT C AATCAAGGCA TCCACTTGCC CTATCAAATC	480
TTGCTGAGCA GGTGTCTTCT TGGCTACTTT ATCTGCTGCC TTATCAAGGG CCTGATGAAG	540
TTGCGATACA GCTTGACCAA AATCTTCTTC AGAAGGACTG GCTGCTCGAA CAAACTCCAC	600
CAATTCTTCT ATTTTAAAAC CAGCCCTATG GGTTCACCC TCTAAATCCC AAGCTCGAGG	660
TTCTTCTTGG GTTCGTTTAT CCATCATGTG GTGGAAAGTC TTGACCTTAT TGAAATGATA	720
GTCACGGCTG ACAAAGACTT TTTCTGAAGA	750

(2) INFORMATION FOR SEQ ID NO: 347:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 596 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

CGCAACATAC GGATAACCTC CAAAGAATAT TTTTATATTA TAGCAAAGCT TTAAATTGAA	60
TGTTAGAGTC TTGTTCAAAA CAATCATCAA AACCACGTGG ATGATGGTAT TCTACTAAGT	120
GTTGATCTTG AGGATAAGTG TACTTACCGC CAACTTCCCA GATAAATGGA TGGAAATCGT	180
ATTGCAAGCG ATCTTTTCGC ATTTTCCAAA GTTCTAGAAT CTCATTAGTA GAAGCCATGA	240
AGTTAGACCA GATATCATAG TGAAC TGGA TAATGACTTT GGTACGCAGA TTTTCTGCCA	300
TACGAAGAAG GTCGATAGAT GTCakTTTGT CTTGGATACC TACCGGATTT TCACCATAGT	360
TATTCAAAGC AACATCAATT TTAAAGTCTT TACCATGTTT TGCAAAATAG TTTGAGAAGT	420
GAGAATCTGC ACCATGATAG ATGGTTCCAC CTGGTGTTC AAAGATATAG TTAACAGCCT	480
TTTGAGCCAT TTCTTCATCT GTAACAGCCA AGCCAGCAgT TCACCGCCTG TCTCATCAGC	540
ACCGTTCACT GGGAGAGTTA CCAAGCAAGT ACGGTCAAAT GATTCTACTG CATGAA	596

(2) INFORMATION FOR SEQ ID NO: 348:

1366

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 673 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

CAGAGTCAAC AGCCTGAGTT GAAGGCAACT TTAGACACAG CAGTTACGAC AGCTGAATGA	60
GCTCCTCCAT CAGTTTTTTC TTTAATGAGT CCAGCTACAT CTTCAACTTC GAGGCCGTTA	120
ATCACAATGT CAGCGCCTAC TTCTTTTGCA AGGGCAAGTT TGTCATTGTT GATATCGACT	180
GCGATAACAT GAGCATTGAA TACTTTTTTA GCGTATTGAA CAGCGAGGTT ACCAAGTCCA	240
CCAGCACCGT AAAGAACAAC CCATTGGCCT GGTTCAACTT TTGCTTCTTT GATAGCTTTA	300
TAGGTTGTTA CTCCAGCACA TGTGATAGAA GAAGCTTGGG CTGGATCAAG TCCGTCAGGA	360
ACTTTGACAG CATAGTCAGC AGTTACGATA CATTGTTTCAG CCATACCACC GTCTACTGAG	420
TAGCCAGCAT TTTTCACTGT ACGGCAAAGG GTTTCGCGAC CAGTTGTACA GTATTGCGAA	480
GTGCCACATC CTTCAAAGAA CCAAGCAACG CTGACGCGGT CACCGACTTT AAGGCTTTTC	540
ACATCTGGAG CAATCTCTTT AACGATACCG ATACCTTCGT GCCCAAGAAC ACGTCCTGGG	600
ACTTGACCAA AGTCACCATG AGCAACGTGG AGGTCGGTGT GGCAAACGCC CACAGTATTC	660
ACTTCTACAA GTG	673

(2) INFORMATION FOR SEQ ID NO: 349:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

GTACCCTACA AATGCTTTAC AGTATGGGTT GAGGGTGGTC AATGGAACTA TGGAGTAGGT	60
TGGACAGGAA CTTTGGATA TTCTGATTAC TTACATTCTA CTCGATATCA TACAGCAACT	120
GTTAGACATG GGGGTAGAAC CTCTAAGGAT TATGCAAAAC CTGAGGCATG GGCTAGAGCT	180
TCCCTCACCA AGATTCCG	198

(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 891 base pairs
(B) TYPE: nucleic acid

1367

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

GCTTCTTCTA TAGACAAAAA TATCATGGGT AAAATAATCA AGGCTATAGC TAGAAGGAGG	60
GACCAATCCA CTACTAATCC TAAGAACAAA AACTCAAGA GAGCAGAAGA GAGAGGTTCA	120
CTGGCACTGA TAACGGCAAC CACCAAAGGA GAAACCAAGG ACACAGCCTT CATGGAAATG	180
AAAAAAGCAA AAGCCGTTCC AAAGAAAGCG ATAATGAGGC AAATCAAGAT ACTCCAAATA	240
TCAAGAGTAA AGGAAAGCTG ATAAACCGGC GAGAGGACAT TGCTAAACAA ACCTGCCAAA	300
ATCATCCCCC ACCCAACCGT AGGAACAAAA CCATAACGCT TAGCAAAAGG TTGGGGCAAG	360
ATAACATTAA ACATAACACC CATGGCACTC AGCAAACCTG TTATAAGAGC TAGCGGCGTC	420
ATGGATAACT GAGAGAGGTC TCCCTTTGTC GCCATCAAGC AAACACCCAG CATGGCAACC	480
AAAACATAGA AAACAGCGCT TTTTGACGCT CGTTTTTGAT AAACCAAGCG ATTGTAAAAG	540
AGGATAAAGA CAGGGCTAAT AACTGTAAA ATAGTTGCTG TCGTAGCATT TGAGTATTCT	600
ACACAGAGAT AGAAAAATA CTGAACTGAA AAAATCCCCA AAATAGCATA GGCTAAAAAG	660
GGCAGGTAAT TTTTCTTGTC TCGCCAAATA TCTAGCACTT GCGATTTTAA TTGTATTGCA	720
GACCAAATGA GTACAAGACT CCCTGCCAGT GTCAAACGCA TAGAGGTAAT CCAGCCCGAA	780
GACACCTGAT AATGAGTAAA GAAGTACTCT CCTAAAATTC CACAGATTCC CCATATTAAG	840
CCGGATAGGA GCGAATAAAT TTTTCCGTTA ACAATCTTTT TCTGATACTG A	891

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

GAAAGCGTTC AATAGAACAT TGCTTTTTTA TTTTtagagt AAGCTAAGCG CTTCAGCATC	60
TGCGATGATG GTTACATCAG GGTGATTTTG GAGGCTACTT GCAGGTAGGT TCTCAGTCAC	120
TGGGCCAGAT ACTGTTCCGG CAATGGCTTC TGCTTTCGAC TCACCGTAAG CAAAAAGAAT	180
AATAGACTTG GCATCCAAAA TGTTTTTAAT CCCCATTGAA ATAGCTTGGG TTGGGACGTC	240
TTCAATCTTG GCAAAGAAGC GTGCATTGGC TTCGATAGTA GACTGGTCAA GTTCTACTAG	300

ATGCGTTTGA CTGTCAAATG GAGTG 1368 325

(2) INFORMATION FOR SEQ ID NO: 352:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

CAAGAGCAGT TTGATGATTT TTGATAAGCA TGCGAATTTA AAATACAAAT ATGGCAATCG	60
CAAGTTTTGG TGTAGAGGCT ATTATGTAGA TACGGTAGGC CGTAATCAGA AAGTGATAGC	120
TGAATATATT CAGAATCAAT TACAAGAAGA CAGAGTAGCA GACCTAGCTC ACGTTATTCG	180
AGTCAGTAGA TCCGTTTACT GCGGAAATAA ATAAGAGGAA GTAACGTnAA GTGCTTTAGC	240
ACCTGCTCGG GAAAGTGGTG CCGGAGGAAG CTATTTTCAGG ATGCTTTGGC CCTGGCCGGT	300
AGAAGCGTTA TAGCCGCAGA CTACGACACT TCACACTGGT GGT	344

(2) INFORMATION FOR SEQ ID NO: 353:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 692 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CCCTATCCCT GCTATTGGGG CTGCTCTCAT TGCTGCTTTG GCACAAATCA GTCTTCCAAT	60
TGGACCTGTT CCCTTCACTC TGCAAACTT TGCAATCGGC TTGATTCTAC TGTCTTTAGA	120
CCGAGAGAGG CTGTACTTTC TGCTGGACTC TATCTTCTTC TAGGTGCTAT CCGTCTTCCT	180
GTCTTTGCAG GAGGTGGAGC TGGTTTTTCAG GCTTTAGTTG GCCCTACTGC AGGCTATCTT	240
TGGTTTTATC TCGTTTACTC TGGACTTACT TCCTCTCTAA CCAACAGCAA GAGTGGTGTT	300
GTAAAGATTT TTCTTGCAA CCTCTTGGGT GATGCCCTTG TCTTTGTCGG CGGGATTCTC	360
AGCTTGCATT TCCTAGCTGG AATGGCATT GAAAAAGCTC TTGCTGTGGG GGTCTTCCC	420
TTTATCATTC CAGACCTTGG CAAACTTCTA GCTATTAGTT TTATTAGCCG TCCCCTACTT	480
CAACGCCTTA AAAATCAGGC TTACTTTACT AACTAAAAA GGATATCGAG TTATCATGAC	540
TCAATATCCT TTTCTTTTAT TTTGAAACT TATACTCAAT GAAAATCAAA GAGCAAATA	600
GGAAGCTAGC CGCAGGCTnG CAAAACACTG TTTTGAGGTT GTGGATGAAA CTGACGAGTA	660

1369

AnATCTCATA CATACGGCAA GGCAAAGCTG AC

692

(2) INFORMATION FOR SEQ ID NO: 354:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1005 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

GTGATGGACT ACTGGTTCAA AACGCATCCA GAAGATTTTT TCGATAATGT CGGACCTCTT	60
GTAGCCAGTA ACTTTTTTCA TACTTACACC GAAGATTTCC ACTTGATGAA GGAAATTGGA	120
GTTAATTCTT TCCGCACTTC CATCCAATGG AGTCGACTCA TCAAGAATTT AGAGACAGGT	180
GAGCCTGATC CAAAAGGTAT TGCTTTCTAC AATGCCATCA TTGAAGAAGC TAAAAAGAAC	240
CAGATGGATC TTGTGATGAA TTTACATCAT TTTGATTAC CAGTGGAAC TCTTCAAAAA	300
TACGGTGGTT GGGAAAGCAA ACATGTAGTG GAGTTATTCG TGAAGTTGC CAAGACTGCT	360
TTACATGCT TTGGAGATAA GGTTCATTAC TGGACAACTT TCAATGAGCC AATGGTCATT	420
CCAGAAGCAG GGTACTTATA TGCTTTCCAT TATCCAAATC TAAAAGGAAA GGGAAAAGAG	480
GCCGTACAAG TCATCTATAA TCTAAACCTT GCTAGTGCAA AAGTGATTCA ACTATATCGC	540
TCATTAGAAC TTGATGGAAA GATTGGGATT ATTTTAAACT TGACACCTGC TTATCCAAGA	600
AGTAATTCTC CAGAAGACTT AGAAGCAAGT CGATTTACAG ATGACTTCTT TAACAAAGTC	660
TTCTTGAATC CAGCTGTAA AGGAACTTTC CCAGAAAGAT TGGTAAAACA GCTAGAGAGA	720
GATGGCGTGT TATGGAGTCA TACCGAAAAA GAGCTTCAAC TGATGAAATC AAATACGGTT	780
GATTTTCTTG GAGTAAACTA CTACCATCCA AAACGTGTTC AAGCACAAGC AAATCCTGAG	840
GAATATCAGA CGCCCTGGAT GCCAGACCAA TACTTCAAAG AGTATGAATG GCTGGAGCGT	900
CGCATGAATC CATATCGTGG TTGGGAAATT TTTCCGAAAG CCATTTATGA TATTGCTATG	960
ATTGTGAAGG AAGAATATGG TAATATCCCA TGGTTTATCA GTGAA	1005

(2) INFORMATION FOR SEQ ID NO: 355:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 973 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

1370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

CCGACAAGCA ATATTAAAAA GAGTAAACTA TTAAC TAGTT AATTAACCGG TTTATTACTT	60
TATAGTGAAT CAAATATACT TAAGAAAAGA GGAAAGAATG AAAATTAATA AAAAATATCT	120
AGCAGGTTCA GTGGCAGTCC TTGCCCTAAG TGTTTGTTCC TATGAGCTTG GACGTTACCA	180
AGCTGGTCAG GATAAGAAAG AGTCTAATCG AGTTGCTTAT ATAGATGGTG ATCAGGCTGG	240
TCAAAAGGCA GAAAACTTGA CACCAGATGA AGTCAGTAAG AGGGAGGGGA TCAACGCCGA	300
ACAAATTGTT ATCAAGATTA CGGATCAAGG TTATGTGACC TCTCATGGAG ACCATTATCA	360
TTACTATAAT GGCAAGGTTT CTTATGATGC CATCATCAGT GAAGAGCTCC TCATGAAAGA	420
TCCGAATTAT CAGTTGAAGG ATTCAGACAT TGTC AATGAA ATCAAGGGTG GTTATGTCAT	480
TAAGGTAAAC GGTAATACT ATGTTTACCT TAAGGATGCA GCTCATGCGG ATAATATTCG	540
GACAAAAGAA GAGATTAAAC GTCAGAAGCA GGAACGCAGT CATAATCATA ACTCAAGAGC	600
AGATAATGCT GTTGCTGCAG CCAGAGCCCA AGGACGTTAT ACAACGGATG ATGGGTATAT	660
CTTCAATGCA TCTGATATCA TTGAGGACAC GGGTGATGCT TATATCGTTC CTCACGGCGA	720
CCATTACCAT TACATTCCTA AGAATGAGTT ATCAGCTAGC GAGTTAGCTG CTGCAGAAGC	780
CTATTGGAAT GGGAAGCAGG GATCTCGTCC TTCTTCAAGT TCTAGTTATA ATGCAAATCC	840
AGCTCAACCA AGATTGTCAG AGAACCACAA TCTGACTGTC ACTCCAACCTT ATCATCAAAA	900
TCAAGGGGGA AACATTTCAA GCCTTTTACG TGAATTGTAT GCTAACCCTT ATCAGAACGC	960
CATGTGGGAT CTG	973

(2) INFORMATION FOR SEQ ID NO: 356:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 843 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

GGTCGCATCT GCAATATCTG TCGCCTCCAC ATAAGCGACA CCAGCCTTGT CTGCTGCCCCG	60
TTTGACACGT TCTGCAGATT GACCCAGGAT GACCATCTTC TTGAGTCCAG TAATGTCTGG	120
CACCAATTCG TCAAACATCAT TGCCACGGTC CAAACCACCT GCAATCAAGA CGACCTTGCT	180
GTTGTCAAAT CCTGACAAGC TTTTGTAGTA GCCAAGATAT TAGTTGATTT ACTGTCGTTA	240
TAGAATTTAA CACsCTTGAT GTCATCCACA AACTGGAGAC GGTGTTTGAC ACCACCGAAG	300
GCTGAAAGAG TTTCTTGAT GGTGTTGATTG TCCACATCAC GAAGCTTGGC TACAGCAATA	360

1371

GTCGCAAGGG CATTTCAC ATTGTGGCTA CCTGGAACAC CGATTCATT CGCTGCCATG	420
ACTACTTCAC CACGGAAGTA GAGTTGACCA TCTTCCAGAT AAGCTCCATC AACCTTTTCA	480
AGTGTTGAAA ATGGTACAAC AGTGGCTTCT GTCTTGGAAG TCAAGTCTTT TGCCAAGTCT	540
TGATTAAAGT TCAAGACAAG GAAATCAGCT GCTGTCATCT TGTTCTGGAT ATTCCACTTG	600
GCTGCTACAT ATTCCGAAAA TGACCCATGG TAGTCGATAT GAGTTGGCAT GAGGTTGGTA	660
ATAACCGCAA TCTCTGGATG GAATTCTTGA ACACCCATGA GTTGGAAGA AGAAAGTTCC	720
ATAACAAGCG TGTCCTTATC TGATGCTATT TGAGCAACCT GACTAGCTGG ATAGCCGATA	780
TTCCCTGATA AAAGACCATG TTGGCCAGCA GCAGTCAAAA CTTCCCGGGn TCCTCTAGAG	840
TCG	843

(2) INFORMATION FOR SEQ ID NO: 357:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 807 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

TTTTTTTAT ATTTTTTTTA TTTATTATTT TTTGGCAAAA AAGACCAATT TGCTTTGGAG	60
CATTGCTTCT GCATTAAATT GTCTATTTTT GCTCGTGCTG TTACGCTCTT TGTATCATGT	120
ATTAAC TAGC AAGTGCAACT TGCAAACTAC TAGTAAGAGG AGAAAAACAA AATGGTTATG	180
ACTGACCCAA TCGCAGACTT CCTAACTCGT ATTCGTAATG CTAACCAAGC TAAACACGAA	240
GTACTTGAAG TACCTGCATC AAACATCAAA AAAGGGATTG CTGAAATCCT TAAACGCGAA	300
GGTTTTGTAA AAAACGTTGA AATCATTGAA GATGACAAAC AAGGCGTCAT CCGTGTATTT	360
CTTAAATACG GACCAAATGG TGAGAAAGTT ATCACTAACT TGAAACGTGT TTCTAAACCA	420
GGACTTCGTG TCTACAAAAA ACGTGAAGAC CTTCCAAAAG TTCTTAACGG ACTTGGAATT	480
GCCATCCTTT CAACTTCTGA AGGTTTGCTT ACTGATAAAG AAGCACGCCA AAAGAATGTT	540
GGTGGTGAGG TTATCGCTTA CGTTTGGTAA AATCAAGATA CAAAGCTCGT AAAGAACAAA	600
GCAAAATTAG GAAGTTGGAG AAGTTTGT TT ACAAACAGGC CAACTTATCT ATTTTGCACA	660
GTTCTTAGAG CGTGTTCA GT TCAGCTCTTG AGCTAAGTAA GTATCTGAAC CCCGTGAAAA	720
CTGGCCGTGC TGGCATGTTT GGGTAACAGG AGAnAATAAA CATGTCACGT ATTGGTAATA	780
AGTTCAGCTA AGGCCTTCGT AAAAGTT	807

1372

(2) INFORMATION FOR SEQ ID NO: 358:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 653 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

CCCAGTATTT TTGTCCAAGC ACGACCAGAA AAGGATGATA CAGATCTGGA ATTGGCTCTC	60
TTAACCATCT tTGAACAAAA TCCTCAGGCT CAGGTCAC TA TTTTCGGTGC CTTGGGTGGC	120
CGTATTGACC ATATGTTGGC CAATGTCTTT CTGCCTAGCA ATCCTAAGTT GGCACCCTAT	180
ATGCATCAAA TAGAAATTGA GGATGGGCAA AACTTGATTA CTTATTGTCC AGAAGGAATC	240
AGTCAGCTAG AACCTCGTTC AGACTACGAC TATCTAGCCT TTATGCCAGT TCGGGATAGC	300
CAAGTATGAG TTGACAGAGG AAAATTTTTT CTTTAAAAAA GTGTACGCTT CTAACGAATA	360
TATAGATAGG GAAGTGTCCG TAACTTGCCC AGATGGTTAT GTGGTCGTAC TGCATAGCAA	420
GGACAGGAGG TAGGATGGAA AGTTTACTTA TTCTATTATT AATTGCCAAT CTAGCTGGTC	480
TCTTTCTGAT TTGGCAAAGG CAGGATAGGC AGGAGAAACA CTTAAGTAAG AGCTTGGAGG	540
ATCAGGCAGA TCATTTGTCA GACCAGCTGG ATTACCGCTT TGACCAAGCC AGACAAGCCA	600
GCCAGTTAGA CCAAAAAGAT TTGGAAGTGG TTGTCAGCGA CCGTTTGCAA GAA	653

(2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 641 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CACCATGTGA TGTGACGCTG GCCACAGCTG TCAGAAATCT GGCGAGCCAT CGTGTGCAAT	60
GACTCTTCCC GATGTAATCT TGTTCATAGT CCTTTGATGA ATATGTTCAA GCTGTAGAAG	120
GTGCGCTTCC TGAACACTTA TCAACTGTTA CAGGCGAGTT GACCAGTCAG GAAACAGATG	180
GCTGGTACAC ACTTGCCAAC ACTTCTTCAT CCCGCATTTA CCTAAAACAA GCCTTCCAAG	240
AAAATAGCAA CCTCCTAGAG CAAGTGGTAG AACCTTGAC TATTATCACT GGTGGACACA	300
ACCACAAGGA CCAGTTGACC TATGCTTGGA AAACACTTTT GCAGAATGCG CCACATGATA	360
GTATCTGTGG CTGTAGCGTG GACGAAGTTC ACCGCGAGAT GGAAACGCGT TTTGCCAAGG	420

1373

TCAACCAAGT AGGAAACTTT GTTAAAAGTA ACTTGCTCAA CGAGTGGAAG GGTAATAATTG	480
CTACGGATAA GGCTCAAAGT GACTATCTCT TTA CTGTCAT TAACACAGGC TTGCATGATA	540
AGGTCGATAC TGTCAGCACA GTGATTGATG TGGCGACTTG TGATTTCAAG GAATTGCACC	600
CAACAGAAGG CTACAAAAAG ATGGCTGCTC TTATCTTGCC G	641

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1958 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CCTCAAGGCC AATTGAAGG CTCTAAAACA ATGGAAAAGT GCTACACAGA TGTGACAGAA	60
TTTGCCATTC CAGCAAGTAC TCAAAAGCTT TACTTATCAC CAGTTTTAGA TGGCTTTAAT	120
AGCGAAATTA TTGCTTTTAA TCTTTCGACT TCACCCAAGT TAGAACAAGT ACAAACAATG	180
TTAGAACAGG CATTCAAAGA GAAGCACTAC GAGAATACGA TTCTCCATAG TGACCAAGGC	240
TGGCAATATC AACACGATTC TTATCATCGG TTCCTAGAGA GTAAGGGAAT TCAAGCATCT	300
ATGTCACGCA AGGGCAACAG CCAAGACAAC GGTATGATGG AATCTTTCTT TGGCATTTTA	360
AAATCCGAAA TGTTTTATGG CTATGAGAAA ACATTTAAT CACTTAACCA ATTGGAACAA	420
GCCATTATAG ACTATATTGA TTA CTACAAC AACAAACGAA TTAAGGTAAA ACTAAAAGGA	480
CTTAGTCCTG TGCAGTACAG AACTAAATCC TTTGGATAAA TTAATTGTCT AACTTTTTGG	540
GGTCAGTACA AA ACTCTTGC TACTATGCGT TTTATTATTG AAAGACTTAT TGGACTTTCT	600
CTCAAATCGA GTTTTTACTC AATTTTCTTA CTTGATTGGG ATTGAAATTC CAATTAATTT	660
CTCTGAGTAG AGTGTCTTGA TATTGGCTTC ATCAACAGAG GCCTTATCAA TTTTACGTTT	720
CAAGAAAAAT TCTTGAATGG TTTCGATTTT AGGCTCACGA ATAGCACGGT GTTTGTTTGA	780
GATGAGGATT TCATAGTGAA GCGGAGCTTG GGTA AAAATA ACATCTGTAT TCCCTGCAGA	840
ATAAACCTCA ACAAGGGTTG CATCGGTACT TTCTAGCTGA CTTTTTACAA GTTGCGAGTG	900
TGAGTTTGTC GTATTGATAA GCTTCATAAT ATTTCCCTCCG ATTTTCTAAT TCTATTATAG	960
CACTTTTTGA ATAAAGTCGC TTGATTTATA CTCAATGAAA ATCAAAGAGC AA ACTAGGAA	1020
GCTAGCCGCA GGCTATACTT GAGTACGGTA AGGCGACGCT GACGTGGTTT GAATTTTATT	1080
TTCGAAGAGT ATTAGCCAAT CTTATGCTGT TTTTCCAAG ATTCAATGGC CCATTTATGG	1140

1374

CTACCACGTT TAAGGTTTTT GATAGCCTCG TCAATAGGGA ACCAGGCAAT ATGATTAAAG	1200
TTTTCTAGTG GCTTTTGTAC TTCTTTGAAA GGAGTTGCTT CATAGAGGTA GGCAGGATTG	1260
TAGTAGTAGG TATCACGATG ACGAGAATAG AAATATTCGT CAGCTTGTCC GTAATAGGTA	1320
CCAATTTCTG CTGTGAAACC AAGCTCTTCA ATCAACTCAT GCTTTAGGGC TTCCTGATGA	1380
TTTTCACCTG CTTCAATTTT TCCACATGGT AGGAACCAAG CACCATTTGG TTCTTGAACA	1440
AGAACAATTT GTTTTTGTTC AGGATTAGGG ATAAGTGCAT ATACGCCATA GCGAGCAATA	1500
TAGTCTGTAT TCACTTTTTT TCTCCGAAAG TTGGGTTTGC CATTGCATTT TCCTCATTAT	1560
CTAGTATCGT TATTATTATA GTGAAATGAA CCAAAAATAG TACACAATGT GGTATAATCT	1620
TCTTATGGCA TATTCAATAG ATTTTCGTAA AAAAGTTCTC TCTTATTGTG AGCGAACAGG	1680
TAGTATAACA GAAGCATCAC ACGTTTTCCA AATCTCACGT AATACCATTT ATGGCTGGTT	1740
AAAGCTAAAA GAGAAAACAG GAGAGCTAAA CCACCAAGTA AAAGGAATAA AACCAAGAAA	1800
GGTTGATAGA GATAGACTTA AAAACTATCT TACTGACAAT CCAGACGCTT ATTTGACTGA	1860
AATAGCTTCT GAATTTGGCT GTCATCCAAC TACCATCCAC TATGCGCTCA AAGCTATGGG	1920
tACACTCGAA AAAAAAAGA ACTACACCTA CTATGAAC	1958

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 851 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

TATGAAATTA AGTTATGATG ATAAAGTTCA GATCTATGAA CTTAGAAAAC AAGGATATAG	60
CTTAGAGAAG CTTTCAAATA AATTTGGGAT AmACAATTCT AATCTTAGGT ATATGATTAA	120
ATTGATTGAT CGTTACGGAA TAGAGTTCGT CAAAAAAGGA AAAAATCGTT ACTATTCTCC	180
TGATTTAAAA CAAGAAATGA TTAATAAAGT CTGACATGAA GGCTGGACTA AAGATAGAGT	240
TTCTCTTGAA TACGGTCTCC CAAGTCGTAC GATACTTCTT AACTGGCTAG CACAATACAG	300
GAAAAACGGG TATACTATTG TTGAGAAACC AAGAGGGAGA GTACCTGAGA GCGGAGAATG	360
CCATCCTAAA AAAGTTAAGA GAACTCCGAT TGAAGGAGGA AAAAGAGAAA GAAGAAAGAC	420
AGAAATTGTT TAAGAATTAA TGACTGAGTT TTCGTTAGAT CTTCTTTTAA AAGTCATTAA	480
ACTAGCTCGT TCGACCTACT ACTATCACTT GAAACAGCTA GATAAACCAG ATAAGGACCA	540
AGAGCTTAAA GCTGAAATTC AATCCATTTT TATCGAACAC AAAGGAAATT ATGCTTATCG	600

1375

TCGGATTTAT TTAGAACTAA GAAATCGTGG TTATCTGGTA AATCATAAAA GAGTTCAAGG	660
CTTGATGAAA GTACTCAATt TACAAGCTAA AACGCGACAG AAACGAAAAT ATTCTTCTCA	720
TAAAGGAGAC GTTGGCAAGA AGGCAGAGAA TCTCATTCOA GGCCAATTTG AAGGCTCTAA	780
AACAATGGAA CAGTGCTACA CAGATGTGAC AGAATTTGCC ATTCCAGTAA GTACTTAAAA	840
GCTTTACTTA T	851

(2) INFORMATION FOR SEQ ID NO: 362:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

GGGTAGAATC GATATCTCCA ATGAGTTGGT tTAGCTGGTG AAACGTAAA AAGATTTCGw	60
CCAATTCAAG GTTGAGGCAT CGCAAATAT GGACTGTTTC CTCGTCAGTT CTGGAAAGAA	120
AACGGGATAA GGTGGCTGT GAAGCAAGCT GCCCTCCTTC CAACAATTTT GGAAAGTAGG	180
CATCAGCTGA CAATTCTTTA CAAGCATAGT CCGTTCCATA ACCTGTTAAC AGTTGAAAGA	240
GGAAGTGGAC AAGGATATCT GAATCCGAAT AACGACAGTA GCGGCGTTGG TCATTCGTTA	300
CTAAATACTT AGAAATCCGC TCTTTTAGTT TCAACTGGGA AAAAAGTTCC TGAAAAAAGA	360
TAAGACCACC ATACTGGGTT AAATGACCTC CATCGAAAGA TAGTTGGTAA AAAGACTTGT	420
TTTGGAAGTG ATGATTTGGT AAACGTTCOA TGTGAGTTTC CTTTCTTTTT GTGTTTTTTT	480
CTACACTTAT ACCATAAAGG GGAACTCTT TTTTGTCTAG TAAAAAACAC CCATTGGGTG	540
AAAAAAGAAA CCATCCAGGA TCTAAGCTAA GGCAAGGATT CTGGATGGTT TTTAGATTTG	600
GGGTGAATAA TTGGGGTTTT AGCTGCTTGC GGCCAATCAG GTTCAGATAC AAAAAGTTAC	660
TCATCAACCT TTAGTGGAAT TCCAAGTACA TTTAACTATC TATTAGACTA TTACGCTGAT	720
AATATAGTCA ATTGAAACAA GAACAAGACA AAAGAGCCTC ATAAAAGGTA TTGCAACTTG	780
GTAATACCTT TTTGAGGTGC TTTTGTGATAT GAGCCCATGT TTTCTCAATA GGATTGTACT	840
CAGGTGAGTA GGGAGGAAGA GGTAAGGTT TATACCCAAA CTCTTCACAC AAGAGTTCTA	900
ACTTACCCAT TCTATGGAAT CTTGCATTAT CCATAATAAT AACCGATGGT GTGTTTAATG	960
TTGGTAAGAG AAATTTCTGA AACCAAGCTT CAAAAAGTC GCTCGTCATC GTCTCTTCGT	1020
AAGTTATTGG AGCGATTAAC TCACCATTTG TTAGACCTGC AACCAAAGAA ATCCTCTGAT	1080

1376

ATCTTCTTCC AGATACTTTG CCTCTTCTTA ACTGACCTTT TAATGAGCGA CCATATTCTC	1140
GATAAAAATA AGTATCGAAT CCTGTTTC	1168

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4483 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GTCAGCTTCA GCAAGCCCAT CAGCTTCTGA ATCTGCATCA ACCAGTGCGT CCGCTTCAGC	60
GTCAACCAGT GCGTCGGCTT CAGCGTCGAC AAGTGCTTCG GCTTCAGCAT CAACGAGTGC	120
GTCGGCCTCA GCAAGCGCAA GTACCTCAGC GTCAGCTTCC GCCTCAACCA GTGCGTCGGC	180
TTCAGCAAGC ACAAGTGCGT CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC	240
GAGTGCGTCT GAGTCAGCAT CAACGAGTAC GTCAGCCTCA GCAAGCACAT CAGCTTCTGA	300
ATCTGCATCA ACCAGTGCGT CAGCCTCAGC ATCGACAAGC GCCTCAGCTT CAGCAAGTAC	360
CAGTGCTTCA GCCTCAGCGT CGACAAGTGC GTCGGCCTCA ACCAGTGCAT CTGAATCGGC	420
ATCAACCAGT GCGTCAGCCT CAGCAAGTAC TAGTGCATCA GCTTCAGCAT CAACGAGTGC	480
ATCGGCTTCA GCATCAACCA GTGCCTCGGC TTCAGCGTCA ACCAGTGCGT CAGCTTCAGC	540
AAGTACCAGT GCTTCAGTCT CAGCATCAAC AAGTGCTTCA GCCTCAGCAT CGACAAGTGC	600
CTCGGCTTCA GCAAGCACAT CAGCATCTGA ATCAGCGTCG ACAAGCGCCT CAGCTTCAGC	660
AAGTACCAGT GCGTCAGCCT CAGCGTCGAC AAGTGCGTCA GCCTCAGCAA GTACTAGTGC	720
ATCAGCTTCA GCATCAACGA GTGCATCGGC TTCGGCGTCA ACCAGTGCAT CAGAGTCAGC	780
AAGTACCAGT GCGTCAGCTT CCGCATCAAC AAGTGCTTCG GCTTCAGCAA GCACCAGTGC	840
GTCGGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCCTCA ACCAGTGCGT CAGCCTCAGC	900
AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTGCGTCC GCTTCAGCAA GTACTAGCGC	960
CTCAGCCTCA GCGTCAACAA GTGCATCGGC TTCAGCGTCA ACGAGTGCGT CTGAATCGGC	1020
ATCAACGAGT GCGTCCGCTT CAGCAAGTAC TAGCGCCTCA GCCTCAGCGT CAACAAGTGC	1080
ATCGGCTTCA GCATCAACGA GTGCGTCCGC TTCAGCAAGT ACTAGCGCCT CAGCCTCAGC	1140
GTCAACAAGT GCATCGGCTT CAGCGTCAAC GAGTGCGTCT GAGTCAGCAT CAACGAGTGC	1200
GTCAGCCTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCGT CAGCCTCAGC	1260
ATCGACAAGC GCCTCAGCTT CAGCAAGTAC CAGTGCGTCA GCTCAGCGTC GACAAGTGCS	1320

1377

TCrGCTTCAG CAAGTACCAG TCGGTCAGCC TCAGCAAGTA CCAGTGCKTC AGCCTCAGCG	1380
TCGACAAGTG CGTCGGCCTC AACCAGTGCA TCTGAATCGG CATCAACCAG TCGGTCAGCC	1440
TCAGCAAGTA CTAGCGCCTC AGCCTCAGCA TCAACGAGTG CGTCCGCTTC AGCAAGTACT	1500
AGTGTCATCAG CTTTCAGCAAG TACTAGCGCC TCAGCCTCAG CGTCGACAAG CGCCTCAGCT	1560
TCAGCAAGTA CCAGTGCGTC AGCCTCAGCG TCGACAAGTG CGTCGGCTTC AGCAAGTACC	1620
TCAGCGTCTG AATCAGCATC AACAAGTGCG TCGGCTTCAG CATCAACGAG TGCATCAGCT	1680
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG	1740
AGTGCTTCAG TCTCAGCGTC AACCAGTGCC TCTGAATCCG CATCAACAAG TGCCTCGGCT	1800
TCAGCAAGCA CCAGTGCTTC GGCTTCAGCG TCAACGAGTG CGTCTGAGTC AGCATCAACG	1860
AGTGCGTCAC CTCAGCAAGC ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCACTTC	1920
CGCATCAACA AGCGCCTCGG CCTCAGCAAG TACAAGTGCT TCAGCCTCAG CATCAACCAG	1980
TGCATCAGCT TCAGCCTCAA CAAGTGCTTC AGCCTCAGCG TCAACCAGTG CCTCGGCTTC	2040
AGCAAGTACC AGTGCGTCAG cTTTCAGCAAG CACAAGTGCG TCAGCTTCAG CATCAACCAG	2100
TGCTTCGGCT TCGGCATCAA CAAGTGCTTC AGCATCAGCA TCAACGAGTG CGTCAsCTCA	2160
GCAAGTACTA GTGCATCAGC ATCAGCATCA ACCAGTGCAT CAGCCTCAGC AAGTATCTCA	2220
GCGTCTGAAT CGGCATCAAC GAGTGTCATCA GCATCAGCAT CAACGAGTGC ATCGGCTTCA	2280
GCGTCAACCA GTGCATCAGT CTCAGCAAGC ACCAGTGCGT CGGCTTCAGC ATCAACCAGT	2340
GCCTCAGCCT CAGCAAGTAT CTCAGCGTCT GAATCGGCAT CAACGAGTGC GTCAGcCTCA	2400
GCAAGTACTA GTGCATCAGC ATCAGCATCA ACGAGTGCAT CGGCTTCAGC AAGTACCAGC	2460
GCCTCAGCTT CAGCAAGCAC CAGTGCGTCA GCCTCAGCAA GTACCAGCGC CTCAGCCTCA	2520
GCAAGCACCA GTGCCTCAGC TTCAGCAAGT ACCAGTGCGT CAGCCTCAGC GTCGACAAGT	2580
GCGTCGGCTT CAGCAAGTAC CTCAGCGTCT GAATCAGCAT CAACGAGTGC ATCAGCTTCA	2640
GCATCAACAA GTGCTTCAGC TTCAGCAAGT ACCAGTGCGT CGGCTTCAGC ATCAACGAGT	2700
GCTTCAGTCT CAGCGTCAAC CAGTGCTCTT GAATCAGCAT CAACAAGTGC CTCGGCTTCA	2760
GCAAGCACCA GTGCGTCGGC TTCAGCAAGT ACTAGTGCAT CGGCTTCAGC ATCGACAAGT	2820
GCGTCTGAAT CGGCATCAAC GAGTGCTTCG GCTTCAGCAT CAACGAGTGC GTCAGCCTCA	2880
GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCGT CCGCTTCAGC GTCAACCAGT	2940
GCGTCGGCTT CAGCGTCGAC AAGTGCTTCG GCTTCAGCAT CAACGAGTGC GTCGGCCTCA	3000
GCAAGCGCAA GTACCTCAGC GTCAGCTTCC GCCTCAACCA GTGCGTCCGC TTCAGCAAGC	3060

1378

ACAAGTGCGT CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTGCGTCG	3120
GCCTCAGCAA GCGCAAGTAC CTCAGCGTCA GCTTCCGCCT CAACCAGTGC GTCGGCTTCA	3180
GCAAGCACAA GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT	3240
GCGTCTGAGT CAGCATCAAC GAGTACGTCA GCCTCAGCAA GCACATCAGC TTCTGAATCG	3300
GCATCAACCA GTGCGTCAGC CTCAGCATCG ACAAGCGCCT CAGCTTCAGC AAGTACCAGT	3360
GCTTCAGCCT CAGCGTCGAC AAGTGCGTCG GCCTCAACCA GTGCATCTGA ATCGGCATCA	3420
ACCAGTGCGT CAGCCTCAGC AAGTACTAGT GCATCAGCTT CAGCATCAAC GAGTGCATCG	3480
GCTTCAGCAT CAACCAGTGC CTCGGCTTCA GCGTCAACCA GTGCGTCAGC TTCAGCAAGT	3540
ACCAGTGCTT CAGTCTCAGC ATCAACAAGT GCTTCAGCCT CAGCATCGAC AAGTGCCTCG	3600
GCTTCAGCAA GCACATCAGC ATCTGAATCA GCGTCGACAA GCGCCTCAGC TTCAGCAAGT	3660
ACCAGTGCGT CAGCCTCAGC GTCGACAAGT GCGTCAGCCT CAGCAAGTAC TAGTGCATCA	3720
GCTTCAGCAT CAACGAGTGC ATCGGCTTCG GCGTCAACCA GTGCATCAGA GTCAGCAAGT	3780
ACCAGTGCGT CAGCTTCCGC ATCAACAAGT GCCTCGGCTT CAGCAAGCAC CAGTGCGTCG	3840
GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA GTGCGTCAGC CTCAGCAAGT	3900
ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCCGCTT CAGCAAGTAC TAGCGCCTCA	3960
GCCTCAGCGT CAACAAGTGC ATCGGCTTCA GCGTCAACGA GTGCGTCTGA ATCGGCATCA	4020
ACGAGTGCGT CCGCTTCAGC AAGTACTAGC GCCTCAGCCT CAGCGTCAAC AAGTGCATCG	4080
GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCGTCA	4140
ACAAGTGCAT CGGGTTCAGC GTCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTGCGTCA	4200
CCTCAkCAAG CACATCAGCT TCTGAATCTG CATCAACCAG TGCGTCACTT CCGCATCAAC	4260
AAGCGCCTCG GCCTCAGCAA GTACAAGTGC TTCAGCCTCA GCATCAACCA GTGCATCAGC	4320
TTCAGCCTCA ACAAGTGCTT CAGCCTCAGC GTCAGACCAG TGCCTCGGCT TCAGCAAGTA	4380
CCAGTGCGTC ACTTCAGCAA GCACAAGTGC GTCAGCTTCA GCATCAACCA GTGCTTCGCG	4440
TTCGGCATCA ACAAGTGCCT CAGCATCAGC ATCAACGAGT GCG	4483

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

1379

GTACCTCAGC GTCCTTCCGC CTCAACCAGT GCGTCCGCTT CAGCAAGCAC AAGTGCGTCA	60
CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TCGGTCGGCC TCAGCAAGCG	120
CAAGTACCTC AGCGTCACTT CCGCCTCAAC CAGTGCGTCG GCTTCAGCAA GCACAAGTGC	180
GTCAsCTCAG CAAGTATCTC AGCGTCTGAA TCGGCATCAA CGAGTGCGTC TGAGTCAGCA	240
TCAACGAGTA CGTCAGCCTC AGCAAGCACA TCAGCTTCTG AATCGGCATC AACCAGTGCG	300
TCAGCCTCAG CATCGACAAG CGCCTCAGCT TCAGCAAGTA CCAGTGCTTC AGCCTCAGCG	360
TCGACAAGTG CGTCGGCCTC AACCAGTGCA TCTGAATCGG CATCAACCAG TCGGTCAGCC	420
TCAGCAAGTA CTAGTGCATC AGCTTCAGCA TCAACGAGTG CATCGGCTTC AGCATCAACC	480
AGTGCCCTCGG CTTTCAGCGTC AACCAGTGCG TCAGCTTCAG CAAGTACCAG TGCTTCAGTC	540
TCAGCATCAA CAAGTGCTTC AGCCTCAGCA TCGACAAGTG CCTCGGCTTC AGCAAGCACA	600
TCAGCATCTG AATCAGCGTC GACAAGTGCG TCGGCCTCAA CCAGTGCATC TGAATCGGCA	660
TCAACCAGTG CGTCAGCCTC AGCAAGTACT AGTGCATCAG CTTTCAGCATC AACGAGTGCA	720
TCGGCTTCGG CGTCAACCAG TGCATCAGAG TCAGCAAGTA CCAGTGCGTC AGCTTCCGCA	780
TCAACAAGTG CCTCGGCTTC AGCAAGCACA TCAGCATCTG AATCAGCGTC AACCAGTGCT	840
TCGGCTTCAG CAAGTACCAG TGCTTCAGCT TCAGCATCAA CCAGCGCCTC GGCCTCAGCA	900
AGCACCTCAG CTTCTGAATC GGCCTCAACC AGCGCCTCGG CCTCAGCAAG CACCTCAGCT	960
TCTGAATCGG CCTCAACCAG CGCCTCAGCC TCAGCATCAA CGAGTGCTTC GGCTTCAGCA	1020
AGCACAAGCG CCTCGGGTTC AGCATCAACG AGTACGTCAG CTTTCAGCGTC AACCAGTGCT	1080
TCAGCCTCAG CATCAACAAG TCGGTCAGCC TCAGCAAGTA TCTCAGCGTC TGAATCGGCA	1140
TCAACGAGTG CGTCTGAGTC AGCATCAACG AGTACGTCAG CCTCAGCAAG CACAAGTGCT	1200
TCAGCCTCAG CAAGTATCTC AGCGTCTGAA TCGGCATCAA CGAGTGCGTC CGCTTCAGCA	1260
AGTACTAGCG CCTCAGCATC AGCGTCAACA AGTGCTTCGG CTTTCAGCGTC AACGAGTGCG	1320
TCTGAGTCAG CATCAACGAG TACGTCAGCC TCAGCAAGCA CATCAGCTTC TGAATCTGCA	1380
TCAACCAGTG CGTCAGCCTC AGCATCGACA AGCGCCTCAG CTTTCAGCAAG TACCAGTGCG	1440
TCAGCCTCAG CAAGTACCAG TGCTTCAGCC TCAGCGTCGA CAAGTGCGTC GGCCTCAACC	1500
AGTGCATCTG AATCGGCATC AACCAGTGCG TCAGCTCAGC AAGTACTAGT GCATCAGCTT	1560
CAGCATCAAC GAGTGATCG GCTTCGGCGT CAACCAGTGC ATCAGAGTCA GCAAGTACCA	1620
GTGCGTCACT TCCGCATCAA CAAGTGCCTC GGCTTCAGCA AGCACATCAG CATCTGAATC	1680
AGCGTCAACC AGTGCTTCGG CTTTCAGCAAG TACCAGTGCT TCAGCTTCAG CATCAACCAG	1740

1380

CGCCTCGGCC TCAGCAAGCA CCTCAGCTTC TGAATCGGCC TCAACCAGCG CCTCGGCCTC	1800
AGCAAGCACC TCAGCTTCTG AATCGGCCTC AACCAGCGCC TCAGCCTCAG CATCAACGAG	1860
TGCTTCGGCT TCAGCAAGCA CAAGCGCCTC GGGTTCAGCA TCAACGAGTA CGTCAGCTTC	1920
AGCGTCAACC AGTGCTTCAG CCTCAGCATC AACAAGTGCG TCAGCCTCAG CAAGTATCTC	1980
AGCGTCTGAA TCGGCATCAA CGAGTGCGTC TGAGTCAGCA TCAACGAGTA CGTCAGCCTC	2040
AGCAAGCACC TCAGCTTCTG AATCGGCCTC AACCAGTGCG TCAGCCTCAG CATCGACAAG	2100
CGCCTCAGCT TCAGCAAGTA CCAGTGCTTC AGCCTCAGCG TCGACAAGTG CGTCGGCCTC	2160
AACCAGTGCA TCTGAATCGG CATCAACCAG TCGTTCAGCC TCAGCAAGTA CTAGTGCATC	2220
GGCTTCAGCA TCAACCAGTG CCTCGGCTTC AGCGTCAACC AGTGCGTCAG CTTTCAGCAAG	2280
TACCAGTGCT TCAGTCTCAG CATCAACAAG TGCTTCAGCC TCAGCATCGA CAAGTGCCTC	2340
GGCTTCAGCA AGCACATCAG CATCTGAATC AGCGTCGACA AGCGCCTCAG CTTTCAGCAAG	2400
TACCAGTGCG TCAGCCTCAG CGTCGACAAG TCGTTCAGCT ACAGCAAGTA CTAGTGCATC	2460
AGCTTCAGCA TCAACGAGTG CATCGGCTTC GCGTCAACC AGTGCATCAG AGTCAGCAAG	2520
TACCAGTGCG TCAGTTCACG CATCAACAAG	2550

(2) INFORMATION FOR SEQ ID NO: 365:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

ACCCAGCAAG TACTAGTGCA TCGGCTTCAG CAAGCACCAG TCGGTCGGCT TCAGCATCAA	60
CCAGTGCCTC AGCCTCAGCA AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCGTCAC	120
CTCAGCAAGT ACTAGTGCAT CAGCATCAGC ATCAACGAGT GCATCGGCTT CAGCAAGTAC	180
CAGCGCCTCA GCTTCAGCAA GCACCAAGTG GTCA _s CTCAG CAAGTACCAG CGCCTCAGCC	240
TCAGCAAGCA CCAGTGCCTC AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA	300
AGTGCGTCGG CTTTCAGCAAG TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT	360
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTATCTCAG CGTCTGAATC GGCATCAACG	420
AGTGCGTCCG CTTTCAGCAAG TACTAGCGCC TCAGCATCAG CGTCAACAAG TGCTTCGGCT	480
TCAGCGTCAA CGAGTGCGTC TGAGTCAGCA TCAACGAGTA CGTCAGCCTC AGCAAGCACA	540
TCAGCTTCTG AATCTGCATC AACCAGTGCG TCAGCCTCAG CATCGACAAG CGCCTCAGCT	600

1381

TCAGCAAGTA CCAGTGCCTC AgCCTCAGCA AGTACCAGTG CTTACAGCCTC AGCGTCGACA	660
AGTGCCTCGG CCTCAACCAG TGCATCTGAA TCGGCATCAA CCAGTGCCTC AGCCTCAGCA	720
AGTACTAGCG CCTCAGCCTC AGCATCAACG AGTGCCTCCG CTTACAGCAAG TACTAGTGCA	780
TCAGCTTCAG CAAGTACTAG CGCCTCAGCC TCAGCGTCGA CAAGCGCCTC AGCTTCAGCA	840
AGTACCAGTG CGTCAGCCTC AGCGTCGACA AGTGCCTCGG CTTACAGCAAG TACCTCAGCG	900
TCTGAATCAG CATCAACAAG TGCCTCGGCT TCAGCATCAA CGAGTGCATC AGCTTCAGCA	960
TCAACAAGTG CTTACAGCTC AGCAAGTACC AGTGCCTCGG CTTACAGCATC AACGAGTGCT	1020
TCAGTCTCAG CGTCAACCAG TGCCTCTGAA TCCGCATCAA CAAGTGCCTC GGCTTCAGCA	1080
AGCACCAGTG CTTCCGCTTC AGCGTCAACG AGTGCCTCTG AGTCAGCATC AACGAGTGCG	1140
TCAGCCTCAG CAAGCACATC AGCTTCTGAA TCTGCATCAA CCAGTGCCTC AGCTTCCGCA	1200
TCAACAAGCG CCTCGGCCTC AGCAAGTACA AGTGCTTCAG CCTCAGCATC AACCAGTGCA	1260
TCAGCTTCAG CCTCAACAAG TGCTTCAGCC TCAGCGTCAA CCAGTGCCTC GGCTTCAGCA	1320
AGTACCAGTG CGTCAGCTTC AGCAAGCACA AGTGCCTCAG CTTACAGCATC AACCAGTGCT	1380
TCGGCTTCGG CATCAACAAG TGCCTCAGCA TCAGCATCAA CGAGTGCCTC AGCCGG	1436

(2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 735 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

GCAGTTGCCA CACCGTGCTG ACCAGCACCC GTTCCTGCGA TAATTTTCTT TTTACCCATG	60
CGTwTGCAA GCCAACTTG TCCTAAGGCA TTGTTAATCT TGTGGGCTCC TGTATGGTTA	120
AGGTCTTCCC GTTTGAGATA AATCTTGCTC CGCCAATATG CTGGGTCAAG TTTTTTGCGT	180
AATAAGAGG AGTTTCACGT CCTACGTACT GCGCAAAAG CTGGTTTAAT TCCTCTTGGA	240
AACTTGGGTC TGCCTGACTT TCACGGTAGG CCTTCTCAA CTCCAAACT GCTGTCATCA	300
ATGTTTCTGG GACAAAACGT CCGCCGAATT TTCCGTAAAA TCCATCTTTA TTTGGTTCCT	360
GATATGCCAT GCTTTACCCT CTCTATAAAT CTTCTAATCT TTTCATGATC TTTTGTCCA	420
TCTGTCTCCA CTCCGCTCGA TACATCTACT GCATAGGGAG TAAAGTGTTG AATTGCTTTT	480
ACTACATTAT CTTCAATAAG GCCACCTGCG ATAAAGAAGG GCTGTGCTAG TCCAGTCGTA	540

1382

TCCAGTTGAC	CCCAATCAAA	GGGCTGGCCA	CTTCCTGCCA	CAGGGGCATC	AAAGAGTAGA	600
TAATCTGCCT	GAGAATTGGG	GACATGCCCCA	TTTCCATCTA	CCTGCACAGC	CTGAATACTG	660
GCACAAGGCA	AATTCTCAAA	TAAATCATCT	GCCACCTGAC	CGTGAACCTG	AACCAAGTCC	720
AAGCCGGGGA	TCCTC					735

(2) INFORMATION FOR SEQ ID NO: 367:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1702 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

TACTAGCGCC	TCAGCCTCAG	CGTCAACAAG	TGCATCGGCT	TCAGCATCAA	CGAGTGCCTC	60
CGCTTCAGCA	AGTACTAGCG	CCTCAGCCTC	AGCGTCAACA	AGTGCATCGG	CTTCAGCGTC	120
AACGAGTGCG	TCTGAGTCAG	CATCAACGAG	TGCGTCAGCC	TCAGCAAGCA	CATCAGCTTC	180
TGAATCTGCA	TCAACCAGTG	CGTCAGCCTC	AGCATCGACA	AGCGCCTCAG	CTTCAGCAAG	240
TACCAGTGCG	TCAGCCTCAG	CGTCGACAAG	TGCGTCGGCT	TCAGCAAGTA	CCAGTGCCTC	300
AGCCTCAGCA	AGTACCAGTG	CGTCAGCCTC	AGCGTCGACA	AGTGCGTCGG	CCTCAACCAG	360
TGCATCTGAA	TCGGCATCAA	CCAGTGCCTC	AGCCTCAGCA	AGTACTAGTG	CATCAGCTTC	420
AGCATCAACG	AGTGCATCGG	CTTCAGCATC	AACCAGTGCA	TCAGAGTCAG	CAAGTACCAG	480
TGCGTCAGCT	TCCGCATCAA	CAAGTGCCTC	GGCTTCAGCA	AGTACTAGCG	CCTCAGCCTC	540
AGCGTCAACA	AGTGCTTCAG	CTTCCGCGTC	AACCAGCGCC	TCGGCCTCAG	CAAGTATCTC	600
AGCGTCTGAA	TCGGCATCAA	CAAGTGCCTC	GGCTTCAGCA	TCAACGAGTG	CATCAGTCTC	660
AGCAAGCACC	AGTGCGTCGG	CCTCAGCAAG	CACCAGCGCG	TCTGAATCCG	CATCAACCAG	720
TGCCTCAGCT	TCAGCAAGTA	CCTCAGCATC	TGAATCAGCA	TCAACAAGTG	CATCGGCTTC	780
AGCAAGCACA	AGTGCTTCAG	CCTCAGCAAG	TATCTCAGCG	TCTGAATCGG	CATCAACGAG	840
TGCGTCCGCT	TCAGCAAGTA	CTAGCGCCTC	AGCATCAGCG	TCAACAAGTG	CTTCGGCTTC	900
AGCGTCAACG	AGTGCGTCTG	AGTCAGCATC	AACGAGTACG	TCAGCCTCAG	CAAGCACATC	960
AGCTTCTGAA	TCTGCATCAA	CCAGTGCCTC	AGCCTCAGCA	TCGACAAGCG	CCTCAGCTTC	1020
AGCAAGTACC	AGTGCGTCAG	CCTCAGCAAG	TACCAGTGCT	TCAGCCTCAG	CGTCGACAAG	1080
TGCGTCGGCC	TCAACCAGTG	CATCTGAATC	GGCATCAACC	AGTGCGTCAG	CCTCAGCAAG	1140
TACTAGCGCC	TCAGCCTCAG	CATCAACGAG	TGCGTCCGCT	TCAGCAAGTA	CTAGTGCATC	1200

1383

AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC AGCGCCTCAG CTTCAGCAAG	1260
CACCAGTGCG TCAGCCTCAG CAAGTACCAG CGCCTCAGCC TCAGCAAGCA CCAGTGCCTC	1320
AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA AGTGCGTCGG CTTCAGCAAG	1380
TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT TCAGCATCAA CAAGTGCTTC	1440
AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG AGTGCTTCAG TCTCAGCGTC	1500
AACCAGTGCC TCTGAATCAG CATCAACAAG TGCCTCGGCT TCAGCAAGCA CCAGTGCCTC	1560
GGCTTCAGCA AGTACTAGTG CATCGGCTTC AGCATCGACA AGTGCGTCTG AATCGGCATC	1620
AACGAGTGCT TCGGCTTCAG CATCAACGAG TCGGTCAGCC TCAGCAAGCA CATCAGCTTC	1680
TGAATCTGCA TCAACCAAGTG CG	1702

(2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 941 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

ACCAGTGCAT CAGCTTCAGC CTCAACAAGT GCTTCAGCCT CAGCGTCAAC CAGTGCCTCG	60
GCTTCAGCAA GTACCAGTGC GTCACTTCAG CAAGCACAAG TGCGTCACTT CAGCATCAAC	120
CAGTGCTTCG GCTTCGGCAT CAACAAGTGC CTCAGCATCA GCATCAACGA GTGCGTCACC	180
TCAGCAAGTA CTAGTGCATC AGCATCAGCA TCAACCAAGTG CATCAGCCTC AGCAAGTATC	240
TCAGCGTCTG AATCGGCATC AACGAGTGCA TCAGCATCAG CATCAACGAG TGCATCGGCT	300
TCAGCGTCAA CCAGTGCATC AGTCTCAGCA AGCACCAGTG CGTCGGCTTC AGCATCAACG	360
AGTGCCCTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TCGGTCAGCC	420
TCAGCAAGTA CTAGTGCATC GGCTTCAGCA AGCACCAGTG CGTCGGCTTC AGCATCAACC	480
AGTGCCCTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TCGGTCAGCC	540
TCAGCAAGTA CTAGTGCATC AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC	600
AGCGCCTCAG CTTCAGCAAG CACCAGTGCG TCAGCCTCAG CAAGTACCAG CGCCTCAGCC	660
TCAGCAAGCA CCAGTGCCTC AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA	720
AGTGCGTCGG CTTCAGCAAG TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT	780
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG	840

1384

AGTGCTTCAG TCTCAGCGTC AACCAGTGCC TCTGAATCAG CATCAACAAG TGCCTCGGCT	900
TCAGCAAGCA CCAGTGCGTC GGCTTCAGCA AGTACTAGTG C	941

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 869 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

CAGCAAGTAC TAGTGCATCA GCTTCAGCAT CAACGAGTGC ATCGGCTTCT GCGTCAACCA	60
GTGCATCAGA GTCAGCAAGT ACCAGTGCGT CAGCTTCCGC ATCAACAAGT GCCTCGGCTT	120
CAGCAAGCAC CAGTGCGTCG GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA	180
GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCCGCTT	240
CAGCAAGTAC TAGCGCCTCA GCCTCAGCGT CAACAAGTGC ATCGGCTTCA GCGTCAACGA	300
GTGCGTCTGA ATCGGCATCA ACGAGTGCGT CCGCTTCAGC AAGTACTAGC GCCTCAGCCT	360
CAGCGTCAAC AAGTGCATCG GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA	420
GCGCCTCAGC CTCAGCGTCA ACAAGTGCAT CGGCTTCAGC GTCAACGAGT GCGTCTGAGT	480
CAGCATCAAC GAGTGCGTCA GCCTCAGCAA GCACATCAGC TTCTGAATCT GCATCAACCA	540
GTGCGTCAGC CTCAGCATCG ACAAGCGCCT CAGCTTCAGC AAGTACCAGT GCGTCAGCCT	600
CAGCGTCGAC AAGTGCGTCG GCTTCAGCAA GTACCAGTGC GTCAGCCTCA GCAAGTACCA	660
GTGCGTCAGC CTCAGCGTCG ACAAGTGCGT CGGCCTCAAC CAGTGCATCT GAATCGGCAT	720
CAACCAGTGC GTCAGCCTCA GCAAGTACTA GTGCATCAGC TTCAGCATCA ACGAGTGCAT	780
CGGCTTCAGC ATCAACCAGT GCATCAGAGT CAGCAAGTAC CAGTGCGTCA GnTTCCGCAT	840
GCAACAAGTG CCTCGGCTTC AGCAAGTAC	869

(2) INFORMATION FOR SEQ ID NO: 370:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 750 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCAACAAGTG CCTCAGCATC AGCATCAACG AGTGCGTCAG CCTCAGCAAG TACTAGTGCA	60
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1385

TCAGCATCAG CATCAACCAG TGCATCAGCC TCAGCAAGTA TCTCAGCGTC TGAATCGGCA	120
TCAACGAGTG CATCAGCATC AGCATCAACG AGTGCATCGG CTTCAGCGTC AACCAGTGCA	180
TCAGTCTCAG CAAGCACCAG TCGTTCGGCT TCAGCATCAA CGAGTGCCTC AGCCTCAGCA	240
AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCCTCAG CCTCAGCAAG TACTAGTGCA	300
TCGGCTTCAG CAAGCACCAG TCGTTCGGCT TCAGCATCAA CCAGTGCCTC AGCCTCAGCA	360
AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCCTCAG CCTCAGCAAG TACTAGTGCA	420
TCAGCATCAG CATCAACGAG TGCATCGGCT TCAGCAAGTA CCAGCGCCTC AGCTTCAGCA	480
AGCACCAGTG CGTCAGCCTC AGCAAGTACC AGCGCCTCAG CCTCAGCAAG CACCAGTGCC	540
TCAGCTTCAG CAAGTACCAG TCGTTCAGCC TCAGCGTCGA CAAGTGCCTC GGCTTCAGCA	600
AGTACCTCAG CGTCTGAATC AGCATCAACG AGTGCATCAG CTTCAGCATC AACAAAGTGCT	660
TCAGCTTCAG CAAGTATCTC AGCGTCTGAA TCGGCATCAA CGAGTGCCTC CGCTTCAGCA	720
AGTACTAGCG CCTCAGCATC AGCGTCAACG	750

(2) INFORMATION FOR SEQ ID NO: 371:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 957 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

CCGGAACA GCTCTGGCGC TTGGTCTTGC CCAGCGTATT GCTAGTGGTG ACGTGCCTGC	60
GGAAATGGCT AAGATGCGCG TGTTAGAACT TGATTTGATG AATGTCGTTG CAGGGACACG	120
CTTCCGTGGT GACTTTGAAG AACGCATGAA TAATATCATC AAGGATATTG AAGAAGATGG	180
CCAAGTCATC CTCTTTATCG ATGAACTCCA CACCATCATG GGTTCCTGGTA GCGGGATTGA	240
TTCGACTCTG GATGCGGCCA ATATCTTGAA ACCAGCCTTG GCGCGTGGAA CTTTGAGAAC	300
GGTTGGTGCC ACTACTCAGG AAGAATATCA AAAACATATC GAAAAAGATG CGGCACTTTC	360
TCGTCGTTTC GCTAAAGTGA CGATTGAAGA ACCAAGTGTG GCAGATAGTA TGACTATTTT	420
ACAAGGTTTG AAGGCGACTT ATGAGAAACA TCACCGTGTA CAAATCACAG ATGAAGCGGT	480
TGAAACAGCG GTTAAGATGG CTCATCGTTA TTAAACCAGT CGTCACTTGC CAGACTCTGC	540
TATCGATCTC TTGGATGAGG CGGCAGCAAC AGTGCAAAAT AAGGCAAAGC ATGTAAAAGC	600
AGACGATTCA GATTTGAGTC CAGCTGACAA GGCCCTGATG GATGGCAAGT GGAAACAGGC	660

1386

AGCCCAGCTA ATCGCAAAAG AAGAGGAAGT ACCTGTCTAC AAAGACTTGG TGACAGAGTC	720
TGATATTTTG ACCACCTTGA GTCGCTTGTC AGGAATCCCA GTTCAAAAAC TGA CTCAAAC	780
GGATGCTAAG AAGTATTTAA ATCTTGAAGC AGAACTCCAT AAACGGGTTA TCGGTCAAGA	840
TCAAGCTGTT TCAAGCATTG GCCGTGCCAT TCGCCGCAAC CAGTCAGGGA TTCGCAGTCA	900
TAAGCGTCCG ATTGGTTCCT TTATGTTTCCT AGGGCCTACA GGTGTCGGGG TATCCGA	957

(2) INFORMATION FOR SEQ ID NO: 372:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 807 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

CAAAGCGCCT CAGCTTCAGC ATCAACAAGT GCGTCGGCTT CAGCATCAAC CAGTGCCTCG	60
GCTTCAGCGT CAACCAGTGC GTCACATTCA GCAAGTACCA GTGCTTCAGT CTCAGCATCA	120
ACAAGTGCTT CAGCCTCAGC ATCGACAAGT GCCTCGGCTT CAGCAAGCAC ATCAGCATCT	180
GAATCAGCGT CAACCAGTGC TTCGGCTTCA GCAAGTACCA GTGCTTCAGC TTCAGCATCA	240
ACCAGCGCCT CGGCCTCAGC AAGCACCTCA GCTTCTGAAT CGGCCTCAAC CAGCGCCTCG	300
GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GCGCCTCAGC CTCAGCATCA	360
ACGAGTGCTT CGGCTTCAGC AAGCACAAGC GCCTCGGGTT CAGCATCAAC GAGTACGTCA	420
GCTTCAGCGT CAACCAGTGC TTCAGCCTCA GCATCAACAA GTGCGTCAGC CTCAGCAAGT	480
ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTACGTCA	540
GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GTGCGTCAGC CTCAGCATCG	600
ACAAGCGCCT CAGCTTCAGC AAGTACCAGT GCTTCAGCCT CAGCGTCGAC AAGTGCGTCG	660
GCCTCAACCA GTGCATCTGA ATCGGCATCA ACCAGTGCGT CAGCCTCAGC AAGTACTAGT	720
GCATCGGCTT CAGCATCAAC CAGTGCCTCG GCTTCAGCGT CAACCAGTGC GTCAGCTTCA	780
GCAAGTACCA TGTGCTTCAT GTCTCAG	807

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1068 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

CATCGGCTTC AGCATCAACG AGTGCGTCCG CTTAGCAAG TACTACCGCC TCAGCCTCAG	60
CGTCAACAAG TGCATCGGCT TCAGCGTCAA CGAGTGCGTC TGAGTCAGCA TCAACGAGTG	120
CGTCACCTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCGT CACCTCAGCA	180
TCGACAAGCG CCTCAGCTTC AGCAAGTACC AGTGCGTCAC CTCAGCGTCG ACAAGTGCGT	240
CGGCTTCAGC AAGTACCAGT GCGTCAsCTC AGCAAGTACC AGTGCGTCAC CTCAGCGTCG	300
ACAAGTGCGT CGGCCTCAAC CAGTGCACTT GAATCGGCAT CAACCAGTGC GTCACCTCAG	360
CAAGTACTAG TGCATCAGCT TCAGCATCAA CGAGTGCACT GGCTTCAGCA TCAACCAGTG	420
CATCAGAGTC AGCAAGTACC AGTGCGTCAG cTTCCGCATC AACAAGTGCC TCGGCTTCAG	480
CAAGTACTAG CGCCTCAGCC TCAGCGTCAA CAAGTGCTTC AGCTTCCGCG TCAACCAGCG	540
CCTCGGCCTC AGCAAGTATC TCAGCGTCTG AATCGGCATC AACAAGTGCC TCGGCTTCAG	600
CATCAACGAG TGCATCAGTC TCAGCAAGCA CCAGTGCGTC GGCCTCAGCA AGCACCAGCG	660
CGTCTGAATC CGCATCAACC AGTGCCTCAG CTTAGCAAG TACCTCAGCA TCTGAATCAG	720
CATCAACAAG TGCATCGGCT TCAGCAAGCA CAAGTGCTTC AGCCTCAGCA AGTATCTCAG	780
CGTCTGAATC GGCATCAACG AGTGCGTCCG CTTAGCAAG TACTAGCGCC TCAGCATCAG	840
CGTCAACAAG TGCTTCGGCT TCAGCGTCAA CGAGTGCGTC TGAGTCAGCA TCAACGAGTA	900
CGTCAGCCTC AGCAAGCACA TCAGCTTCTG AATCTGCATC AACCAGTGCG TCAGCCTCAG	960
CATCGACAAG CGCCTCAGCT TCAGCAAGTA CCAGTGCGTC AGCCTCAGCA AGTACCAGTG	1020
CTTCAGCCTC AGCGTCGACA AGTGCGTCGG GCTCAACCAG TGCATCTG	1068

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 620 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

CAGCATCAAC GAGTGCTTCA GTTTCAGCGT CAACCAGTGC CTCTGAATCA GCTTCAACAA	60
GTGCCTCGGC TTCAGCAAGC CCCAGTGCGT CGGCTTCAGC AAGTACTAGT GCATCGGCTT	120
CAGCATCGAC AAGTGCGTCT GAATCGGCAT CAACGAGTGC TTCGGCTTCA GCATCAACGA	180
GTGCGTCAGC CTCAGCAAGC ACATCAGCTT CTGAATCTGC ATcAACCAGT GCGTCCGyTT	240

1388

CAGCGTCAAC CAGTGCGTCG GCTTCAGCGT CGACAAGTGC TTCGGCTTCA GCATCAACGA	300
GTGCGTCGGC CTCAGCAAGC GCAAGTACCT CAGCGTCAGC TTCCGCCTCA ACCAGTGCGT	360
CGGCTTCAGC AAGCACAAGT GCGTCAGCCT CAGCAAGTAT CTCAGCGTCT GAATCGGCAT	420
CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTCAGC CTCAGCAAGC ACATCAGCTT	480
CTGAATCTGC ATCAACCAGT GCGTCAGCCT CAGCATCGAC AAGCGCCTCA GCTTCAGCAA	540
GTACCAGTGC TTCAGCCTCA GCGTCGACAA GTGCGTCGGC CTCAACCAGT GCATCTGAAT	600
CGGCATCAAC CAGTGCGTCA	620

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 720 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

GTATTGGGGC GCCCCAACCT CTATGTGACT ACGGATTATT TCCTAGATTA CATGgGGATA	60
AACCATTTAG AAGAATTACC AGTGATTGAT GAGCTTGAGA TTCAAGCCCA AGAAAGCCAA	120
TTATTTGGTG AAAGGATAGA AGAAGATGAG AATCAATAAG TATATTGCCC ACGCAGGTGT	180
GGCCAGTAGG AGAAAAGCAG AAGAGCTGAT TAAGCAAGGC TTGGTGACGG TTAACGGCCA	240
AGTGGTGCGT GAACTAGCAA CCACTATCAA GTCAGGCGAC AAGGTCGAAG TTGAAGGTCA	300
ACCTATCTAC AACGAAGAAA AGGTCTACTA TCTGCTTAAC AAACCACGCG GTGTGATTTC	360
CAGTGTGACA GATGATAAGG GTCGCAAGAC GGTGTCGAC CTCTTGCCCA ATGTCAAAGA	420
GCGTATTTAC CCTGTGGGTC GTTTGGACTG GGATACATCA GGTGTCTTGA TTTTGACCAA	480
TGATGGGGAC TTTACAGACG AGATGATTCA CCCTCGTAAT GAGATTGACA AGGTTTATGT	540
CGCGCGTGTT AAAGGTGTGG CCAATAAGGA CAATCTCCGC CCCTTGACCC GTGGTCTTGA	600
GATTGATGGT AAGAAAACCA AGCCATAATA TATAGGTTTT GTAGCCTCTA CACCATAAAT	660
ATTTGCTAAT AAAAATACTG TATTATTACC CTCTTAAGGT GCGAAATTAT TCAAGTTCTT	720

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CGCCATTTCC CATCGTACCG CCGAAAATCC CAGCGCCTCA GCCATCAAAT ATCCTATCAA	60
CGTTCTCAAA AAAAGTGACC GCTCTCTCAT CATGTTTCCA AGTGGTAGCC GCCACTCAAA	120
CGATGTCAAG GGGGGCGCAC ACTskATTGC CAAAATGGCC AAGGTCCGTA TCATGCCGGT	180
TACCTACACC GGTCCCATGA CTTTGAAGGG CTTGATTAGC CGTGAACGTG TCGATATGAA	240
CTTTGGAAAT CCAATCGATA TCTCAGATAT CAAGAAAATG AATGATGAAG GCATTGAAAC	300
AGTCGCCAAT CGTATTCAAA CAGAATTCCA ACGTCTGGAC GAAGAAACGA AACAATGGCA	360
CAATGATAAA AAACCAAATC CACTCTGGTG GTTTATCCGC ATCCCTGCCC TCATCCTTGC	420
TATTATCCTC GCTATCCTAA CCATCATCTT TAGCTTTATC GCAAGCTTCA TCTGGAACCC	480
AGATAAGAAA AGAGAAGAAC TTGCATAGAA GAAATGAACC TTGGCCAAAC AGCTAAGGTT	540
TTCATTTATA TAGTAGATTG GwACTAGAAT AGTACACCTC TACTTCTAAA ACATTTTtag	600
AAATCGATTT GACTGTCCTG ATCGATTGTG CCTAATCTTA TTTCAATT	648

(2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 690 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

GTGCATCGCT TTCAGCATCG ACAAGTGCGT CTGAATCGGC ATCAACGAGT GCTTCGGCTT	60
CAGCATCAAC GAGTGCGTCA GCTTCAGCAA GCACATCAGC TTCTGAATCT GCATCAACCA	120
GTGCGTCCGC TTCAGCGTCA ACCAGTGCGT CGGCTTCAGC GTCGACAAGT GCTTCGGCTT	180
CAGCATCAAC GAGTGCGTCG GCCTCAGCAA GCGCAAGTAC CTCAGCGTCA GCTTCGCCT	240
CAACCAGTGC GTCCGCTTCA GCAAGCACAA GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT	300
CTGAATCGGC ATCAACGAGT GCGTCGGCCT CAGCAAGCGC AAGTACCTCA GCGTCAGCTT	360
CCGCCTCAAC CAGTGCGTCG GCTTCAGCAA GCACAAGTGC GTCAGCCTCA GCAAGTATCT	420
CAGCGTCTGA ATCGGCATCA ACGAGTGCGT CTGAGTCAGC ATCAACGAGT ACGTCAGCCT	480
CAGCAAGCAC ATCAGCTTCT GAATCGGCAT CAACCAGTGC GTCAGCCTCA GCATCGACAA	540
GCGCCTCAGC TTCAGCAAGT ACCAGTGCTT CAGCCTCAGC GTCGACAAGT GCGTCGGCCT	600
CAACCAGTGC ATCTGAATCG GCATCAACCA GTGCGTCAGC CTCAGCAAGT ACTAGTGCAT	660

1390

CAGCTTCAGC ATCAACGAGT GCATCGGCTT

690

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1003 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CGAGATTCTC TGGAGTTATG GATGTCGTTT CAATATGTGC ACGTTGGAAT GTTAGTGCTT	60
ATATGGGGGG AACAGAATCC TCTCTTGATT GAAGACAAGC TAGTCATTAG GCTGGTTTGT	120
CTTTTTGTCA ACTGTAGTGG GTTGATATAA TAGTATTAGT GAGTGGGATA AAAGTTTCAT	180
TTAGTTTATT CAGTACAAAT TTAACGGGTC AAGATTTATA TACTAGTGGT GTTTTTGGGG	240
CTGAGAGAAG TATCTTGATT TTATGTGTGG TTTTATACT TACAGTTGTT CTGCTCCAAA	300
GAGCTTGTAG AGAAGAATTA GCTCATAAAG GAGATTGATT ATTTTGATAT CAAAAAATG	360
CACAGGATAA CCTGATGCAT TTTTTTAGCG ACAATGCTTG CTACTTCCTT CTGTCGAATT	420
TAGACAATTT TAAACCCCAA TTATTCACCC CAAATCTAAA AACCATCCAG AATCCTTGCC	480
TTAGCTTAGA TCCTGGATGG TTTCTTTTTT CACCCAATGG GTGTTTTTTA CTAGACAAAA	540
AAGAGTTTCC CCTTTATGGT ATAAGTGTAG AAAAAACAC AAAAAGAAAG GAAACTCACA	600
TGAACAGTTT ACCAAATCAT CACTTCCAAA ACAAGTCTTT TTACCAACTA TCTTTCGATG	660
GAGGTCATTT AACCCAGTAT GGTGGTCTTA TCTTTTTTCA GGAAGTTTTT TCCCAGTTGA	720
AACTAAAAGA GCGGATTTCT AAGTATTTAG TAACGAATGA CCAACGCCGC TACTGTCGTT	780
ATTCGGATTC AGATATCCTT GTCCAGTTCC TCTTCAACT GTTAACAGGT TATGGAACGG	840
ACTATGCTTG TAAAGAATTG TCAGCTGATG CCTACTTTCC AAAATTATTG GAAGGAGGGC	900
AGCTTGCTTC ACAGCCAACC TTATCCCGTT TTCTTCCAG AACTGACGAG GAAACAGTCC	960
ATAGTTTGCG ATGCCTCAAC CTTGAATTGG TCGAATTCTT TTT	1003

(2) INFORMATION FOR SEQ ID NO: 379:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 738 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

1391

CCGATGATTC TGATTGGTTT GCTCTTTACT TTGCTGGGAA TTTTGAGGTA GATCTATGAT	60
TGAAATACTA ATTGTTTTAG CTATTATCCT ATCTCTTGCT TTGATTGTAT TGGTAACTAT	120
ACAACCCCGT CAAAATCAAC TATTTTCCAT GGATGCCACT AGTAATATTG GTAAACCAAG	180
CTACTGGCAG AGCAACACCT TGGTCAAGGT GCTCACTTTA TTGGTGAGTT TGGCTTTATT	240
TATTCTACTA TTAACCTTTA TGGTGATTAC TTATAAATAA AAGAAAACCTT CAGATATTCA	300
CCTTTTGTGG ATTGGTCTGA AGTTTTCTTT TTTATACTCA ATGAAAATCA AAGAGCAAAC	360
TAGGAAGCTA GCCGCackGC TCAAAACACC GTTTTGAGGT TGTAAGATATA ACTGACGAGc	420
GACTCAAAAC ACCGTTTTGA GGTGTAGAT ATAAGTACG AGcGACTCAA AACACCGTTT	480
TGAGGTGTG GATAGAAGTG ACGAGcGACT CAAAACACCG TTTTGAGGTT GTGGATAGAA	540
CTGACGAAGT CGcTCAAAAC ACCGTTTTGA GGTGTGGAT AGAACTGACG AAtgctCAA	600
ACACCGTTTT GAGGTGTGG ATAGAAGTGA CGAAGCgaaC ATATATACAG CAAGGCGACG	660
CTGACGTGGT TTGAAGAGTA TTACTGTCTA TATTTTGGT AAAAATCAAC TTTTACTTGG	720
ATGAAGGTTT TTTTTTTT	738

(2) INFORMATION FOR SEQ ID NO: 380:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 695 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

CCGTCTTATC AAAGAGGTTA ACAAAGGCAC CAAATTTCTC GATACGAACG ACTTTAGCAC	60
GGTAAACTTC ATCCACTTTG GCTTCACGAA CCAAACCAGC AATAATTTCT TTGGCACGGT	120
TAATAGCATC TTGGTCACTA GAGTAGATAG ACACATTTCC TTCTTCGTCT ATATCAATCT	180
TAACACCTGT TTCAGCGATA ATCTTGTCGA TGGTTTCTCC ACCCTTACCG ATGACAATCT	240
TAATCTTGTC CACATCAATC TTGATCGTAT CAATTTTCGG AGCAGTTGGA GCCAATTCTG	300
GACGAACTTC TGGAATGGTT GCTTCAATGA CATCAAGGAT TTCAAAACGC GCTTTCTTGG	360
CTTGAGCAAG AGCCTCCGTC AAGATTTCTG CAGTAATCCC TTGAATCTTG ATATCCATTT	420
GAAGGGCTGT AATCCCATCA CGAGTACCTG CAACCTTGAA GTCCATATCT CCAAAGTGAT	480
CTTCCAAACC TTGGATATCT GTCAATACTG TGTAATTATT TCCATCTGAG ATAAGCCCCA	540
TAGCAATACC AGCTACTGGC GCCTTGATTG GCACACCACC AGCCATAAGG GCAAGAGTTC	600

1392

CCGCACAGAT AGAAGCTTGA GATGAAGAAC CGTTTGATTC CAAAACTTCT GCTACTAGAC	660
GGATAGCGTA GGGGAATTCT TCCAAGCTTG GCAGG	695

(2) INFORMATION FOR SEQ ID NO: 381:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 691 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACATCTTAT CTAAATACAT GCTAATATAT TTAGATACAA ACATTCCAAC TTGATAATTT	60
TCACTCATCT TTCATCATTC CTTATACAAC TATGCAGTAT AAATAGAATA GTTTTCTCAT	120
CAGAATGAGA CTATTTTAAT ATTAGATCCC CAATTATTCA CCCCAAATCT AAAAACCATC	180
CAGAATCCTT GCCTTAGCTT AGATCCTGGA TGGTTTCTTT TTTCACCCAA TGGGTGTTTT	240
TTACTAGACA AAAAAGAGTT TCCCCTTTAT GGTATAAGTG TAGAAAAAAA CACAAAAAGA	300
AAGGAAACTC ACATGAACAG TTTACCAAAT CATCACTTCC AAAACAAGTC TTTTACCAA	360
CTATCTTTCG ATGGAGGTCA TTTAACCAG TATGGTGGTC TTATCTTTTT TCAGGAACTT	420
TTTTCCCAGT TGAAACTAAA AGAGCGGATT TCTAAGTATT TAGTAACGAA TGACCAACGC	480
CGCTACTGTC GTTATTCGGA TTCAGATATC CTTGTCCAGT TCCTCTTTCA ACTGTTAACA	540
GGTTATGGAA CGGACTATGC TTGTAAAGAA TTGTCAGCTG ATGCCTACTT TCCAAAATTG	600
TTGGAAGGAG GGCAGCTTGc TTCACAGCCA ACCTTATCCC GwTTTCTTTC CAGAACTGAC	660
GAGGAAACAG TCCATAGTTT GCGATGCCTC A	691

(2) INFORMATION FOR SEQ ID NO: 382:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 750 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

ATCTCTCTGC GTAATGGTCC TCAGATAACT CTGATGATGT GTGGCGATAT AGAACTGAGC	60
CAAGTTATGC CTAAAGGGCC TTAGGAATAG GAGCTTTCAC AAGCTTATCC AGATGATTAT	120
CTTTTACTCG TTATGGACAA TGCTATATGG CATAAATCAA GTACCTTAAA GATTCCGACT	180
AATATTGGCT TTGCATTTAT TCCTCCATAC ACACCAGAGA TGAACCCCAT TGAACAAGTG	240

1393

TGGAAAGAGA TTCGTAAACG TGGATTTAAG AATAAAGCCT TTCGAACTTT GGAAGATGTC	300
ATACAAGGAC TGGAGAAGGA GGTGATAAAG TCCATCGTTA ATCGGAGACG GACTAGAATG	360
CTTTTTGAAA ACAGATGAGT ATAAAAAGAA AGTCCTCATT TCAATAGAAA TCACGACTTT	420
CTGATGAATT TATAGTAAAA TGAAATAAGA ACAGGATAGT CAAATCGATT TCTAACAATG	480
TTTTAGAAGC AGAGGTGTAC TATTCTAGTT TAAATCCACT ATATTTGGGG AGTGATAGAA	540
AAGCCCTTCA TCAGCCAATC TACTTGTTCA GGTGCGAGAG CTTTGACATC CTTTTCTGTA	600
CTGGACCAAG TCAGTTTTCC GTTCTCAAAG CGTTTATATA ATATCCAAAA TCCTTGACCA	660
TCCCAGTAAA GAACTTTAAA GCGGTCTTTA CGTCCACCAC AAAAGAGAAA GACTTGATCG	720
GAGAAAGGAT CCAATTCAAA GTGGGTTTGG	750

(2) INFORMATION FOR SEQ ID NO: 383:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 738 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

TCAAATTCTT CGTGGTCCGC ATATCTnTCT TCGTACACGG CAGTCACTTG GTCTTTCCT	60
ACTCGAGTCG CAGCTTCACG GGCCAATTTC TCTTCTACTT GAACTGCCTT TTGGAGGTCA	120
CTGTTGTAGG CTGCAATGAT TTCAGCTTGC AATTCAGCAT CCACGTGAAG CAATTCCACT	180
TCTGCTTTTT CTTTACCGAC AGCAGCAACG ATTTCTTCTT GGAAGGCAAT CAATTCTTTG	240
ACAGCTTCGT GCCCTTTAAG GAGCGCTTCC AACATGATTT CTTCTGACAA TTCTTTGGCA	300
CCAGACTCTA CCATGTTGAT AGCGTGCTTG GTTCCAGCTA CTGTCAATTC AAGAAGAGAT	360
TGCTCTGCTT GTTCTTGACT TGGGTTGATG ATGATTTGGC CATCTACATA TCCCCTTGT	420
ACCCAGCAA TTGGTCCGTC AAATGGAATA TCTGAAATAG ACAGTGCCAA AGATGAACCA	480
AACATAGCAG CCATTGGTGC AGATGCATTT TCATCATAAG AAAGCACTGT ATTGATGACT	540
TGGACTTCAT TACGGAAACC TTCCGCAAAC ATAGGACGAA TCGGACGGTC AATCAAACGC	600
GCTGTCAAGG TCGCATCTGT TGAAGGACGT CCTTCACGTT TCATAAAGCC ACCAGGAAAC	660
TTCCCAGCCG CATACATTTT TTCTTCGTAG TTGACTTGGA GTGGGAAGAA ATCCTCAGTT	720
GCCATTTTCT GGGGATCC	738

(2) INFORMATION FOR SEQ ID NO: 384:

1394

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

CCCCCTATTT ACCGTGGACT AAAGTTGTAC AAGAAAAGTG CAAATAAGAA ATCTCCAGAT	60
TAGGAACTAT ATATGAGTTC TCTAGTCTGG AGATTTTTTCA ATAGACTTCG TTATTGGGCG	120
GTTACTTTTCG AAACTTTGAA AACTTCAAAA AACGGATTTT TATCGCTTTC AAATTCTTTT	180
GGGGTCAAAC TCAGTAACTT ATTCGCCTTG TAGACTTCAT GACGCTCAGG GTATACTTTC	240
AAGGTCCCAA ATAGCCAAGA ATCGTCAGCG ATATTATCTG AATCATCTCC TTCTTGTTCT	300
CCTTTAGTTC GCCTGAGGAC AGCCTTGACA CGCGCCAGAA TTCTCTAGGG CTAAAAGGCT	360
TGGTCAGGTA GTCATCAGCC CCTAATTCCA AGGCCAAAAC CTTATCAAAT TCATCACTTT	420
TCGCAGAAAC CATCATAATT GGAGTTTTGA CGCCTTTGGC TCTCAGCCGC TTACAAACTT	480
CCATGCCATC TAATTGTGGT AACATGATAT CAAGCAAGAT AAAATCAAAG GGTCTGTGTT	540
CTGCCAAAGC TAAGGCCTTC CGTCCATTTG TCACCAATTG AGTAGAAAAG CCTTCCTTAC	600
TTAAATGGTA GTCAAGCAAT TTCAGAATGT GTTCTTCATC ATCCACTAAT AAGACTT	657

(2) INFORMATION FOR SEQ ID NO: 385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

CCGCATCAGC ATCAACGAGT GCATCGGCTT CACGTCAACC AGTGCATCAG TCTCAGCAAG	60
CACCAGTGCG TCGGCTTCAG CATCAACGAG TGCCTCAGCC TCAGCAAGTA TCTCAGCGTC	120
TGAATCGGCA TCAACGAGTG CGTCAGCTCA GCAAGTACTA GTGCATCGGC TTCAGCAAGC	180
ACCAGTGCGT CGGCTTCAGC ATCAACCAGT GCCTCAGCCT CAGCAAGTAT CTCAGCGTCT	240
GAATCGGCAT CAACGAGTGC GTCACCTCAG CAAGTACTAG TGCATCAGCA TCAGCATCAA	300
CGAGTGATC GGCTTCAGCA AGTACCAGCG CCTCAGCTTC AGCAAGCACC AGTGCGTCAC	360
CTCAGCAAGT ACCAGCGCCT CAGCCTCAGC AAGCACCAGT GCCTCAGCTT CAGCAAGTAC	420
CAGTGCGTCA CCTCAGCATC GACAAGTGCG TCGGCTTCAG CAAGTACCTC AGCGTCTGAA	480

1395

TCAGCATCAA CGAGTGCCTC AGCTTCAGCA TCAACCAAGTG CCTCAGCCTC AGCAAGTATC 540
 AGTGCCTCAG CTTCAGCATC AACGAGTGCG TCAGCTGCAG CAAGTA 586

(2) INFORMATION FOR SEQ ID NO: 386:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 451 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

CGTCGGCTTC AGCATCAACG AGTGCATCAG CTTCAGCATC AACCAAGTGCT TCAGCTTCAG 60
 CAAGTACCAG TCGCTCGGCT TCAGCATCAA CGAGTGCTTC AGTCTCAGCG TCAACCAAGTG 120
 CCTCTGAATC CGCATCAACA AGTGCTCGG CTTCAGCAAG CACCAGTGCT TCGGCTTCAG 180
 CGTCAACGAG TCGCTCTGAG TCAGCATCAA CGAGTGCCTC ACCTCAGCAA GCACATCAGC 240
 TTCTGAATCT GCATCAACCA GTGCTCAGC TTCCGCATCA ACAAGCGCCT CGGCCTCAGC 300
 AAGTACAAGT GCTTCAGCCT CAGCATCAAC CAGTGCATCA GCTTCAGCCT CAACAAGTGC 360
 TTCAGCCTCA GCGTCAACCA GTGCTCGGC TTCAGCAAGT ACCAGTGCGT CAGTTCAGCA 420
 AGCACAAGTG CGTCAATTTA GCATCAACCA G 451

(2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

TCTCAGCAAG CACCATTGCG TCGGCTTCAT CAAGCACCAG CGCGTTTGAA TCCGCATCAA 60
 CCAGTGCTTC AGCTTCAGCC AAGTTACCTC AGCATCTGAA TCAGCATCAA CAAGTGCATC 120
 GGCTTCAGCA AGCACAAGTG CTTCAGCTCA GCAAGTATCT CAGCGTCTGA ATCGGCATCA 180
 ACGAGTGCGT CCGCTTCAGC AAGTACTAGC GCCTCAGCAT CAGCGTCAAC AAGTGCTTCG 240
 GCTTCAGCGT CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTCAGC CTCAGCAAGC 300
 ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCAGCCT CAGCATCGAC AAGCGCCTCA 360
 GCTTCAGCAA GTACCAGTGC GTCAGCCTCA GCAAGTACCA GTGCTTCAGC CTCAGCGTCG 420

ACAAG 1396 425

(2) INFORMATION FOR SEQ ID NO: 388:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 572 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

AGAGGATCCC CGGATCCTCA GTCGCTGAGA TAACTCCTTT GGGCTTGTTT ATCATGTAGT	60
AGACAAACTC TTCATACTCC AACACTTGCC CATTTTATGC GAATCTCATC TATTTTTTCT	120
TTTTTTTGCA ATTTAGCTGA TTTTCTTTT TTACCATTTA CAGTCACGCG CCCAGCCTTG	180
AGCAAGTTTT TGACCTCAGT CCGACTTCCC ACCGCACAGG CAACTAAAAA TTTATCTAAT	240
CTCATAGAAC TATTATATCA TATCAAAAGG AGGCTAGTAC AATGACCAAC CTCCTTTTCG	300
TTTCATACTC TTCAAAAATC TCTTCAAACC GCGTCAACGT CGCCTTGCCG TATATATGTT	360
ACTGACTTCG TCAGTTCTAT CTGCAACCTC AAAACAGTGT TTTGAGCTGA CTTCGTCAGT	420
TCTATCTGCA ACCTCAAAGC AGTGCTTTGA GCATCCTGCG GCTAGTTTCC kAGTkTGCTC	480
TTTGATTTwC ATTGAGTATC AGATTTAGGA AATTAAGTTC CTCGkCTCCA AAAAakAGCT	540
AAAACAATCA AGGCTCCTAA AATCGCTGGG AT	572

(2) INFORMATION FOR SEQ ID NO: 389:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 505 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

CAACAAGTGC CTCGGCTTCA GCATGCACAA GTGCTTCAGC TTCAGCATGT ACCTGAGCGT	60
CTGAATCAGC ATCAACGTGT GCGTCCGCTT CAGCATGTAC TGCTGCCTCA GCATCAGCGT	120
CAAcAwGTGC TTCGGCTTCA GCGTCAACGA GTGCGTCTGA GTCAGCATCA ACGAGTACGT	180
CAGCCTCAGC AAGCACATCA GCTTCTGAAT CTGCATCAAC CAGTGCGTCA GCCTCAGCAT	240
CGACAAGCGC CTCAGCTTCA GCAAGTACCA GTGCGTCAGC CTCAGCAAGT ACCAGTGCTT	300
CAGCCTCAGC GTCGACAAGT GCGTCGGCCT CAACCAGTGC ATCTGAATCG GCATCAACCA	360
GTGCGTCAGC CTCAGCAAGT ACTAGCGCCT CAGCCTCAGC ATCAACGAGT GCGTCCGCTT	420

1397

CAGCAAGTAC TAGTGCATCA GCATCAGCAT CAACGAGTGC ATCGGCTTCA GCAAGTACCA 480
GCGCCTCAGC TTCAGCAAGC ACCGG 505

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GCTAAGACTA CCTCATTAGG GGCATAGGCT GCTAAAATAA CTGCAGCTGT GGTTAATGAC 60
AATACTGTAC TTTTTCAT TTTAATTCCT TACATATTTA TATAACTTCC AATAGATAAT 120
AAACTTTAAC TTTGCTAGCC TTTGTTATAA AAAGTTTAC TAAGTATTAT CTAGGAAATA 180
GAGTAGTACA TTTATATATA ATTGTTATCT CTCTATAAAA ACAGTATATC ATTTAAAAAA 240
ATTTAAGTCA AAAAAATTAA CATTAGTTAA TTTATTTTTT AGCACACATT AAAAAATAAG 300
ATTAGTACTC AATGAAAATC AAAGAGCAAA CTAGGAAACT AGCCGCAGAT TGCTCAAAAC 360
AGTGTTTGA GGTGTAGAT GGAATGACGT AGTCAGCTCA AAACACTGTT TTGAAGTTGT 420
GGATAGAACT GACGAAGTCG GTACCGA 447

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 572 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

AGCACTTGTC GTTGAATTCT ACAACAAAAT GTTGTAATAT TTTATTGAAT AAGATAGGCC 60
TTGATATTAA GCACTTTGGG ACGTTCCTCC TTAGTGCTTT TTTGATTTCT CTTAGTATCC 120
AGCTATAATC GTTGAGACAT AACTAGACCG ATATAGTCCA AAGTGATATA GTAAAATGAA 180
CCAAAAATAG TACACAATGT GGTATAATCC TTTTATGGCA TATTCAATAG ATTTTCGTAA 240
AAAAGTTCTC TCTTATTGTG AGCGAACAGG TAGTATAACA GAAGCATCAC ACGTTTTCCT 300
AATCTCACGT AATACCATTT ATGGCTGGTT AAAGCTAAAA GAGAAAACAG GAGAGCTAAA 360
CCACCAAGTA TAGTGTATTG AATCTATAAC AGTACACCTT GGCTGCTAAA ATATTTCTAT 420

1398
AAATTAATTT GACTTTCCTG ATAGAGATGT TCACATCTTA TTTCAAATA CTATATAAGT 480
TCTATAATCT CTTTATAAGA TTGCCCCATC AGACAAAATA GAACGATTG AAGGCGTTTA 540
TGATATTTAG CTGTACGAGA GTCTTTTAAA AG 572

MISSING UPON TIME OF PUBLICATION

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person approved by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PUT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant, any request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by the applicant in the individual case.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the International publication of the application.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapse, the microorganism shall be made available as provided in Rule 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever two dates occurs earlier.

SINGAPORE

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for international publication of the application.

NORWAY

The applicant hereby requests that, until the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegians Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Registration), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

ICELAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected in the art.

What Is Claimed Is:

25 1. Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID NOS:1-391, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID NOS:1-391.

30 2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a degenerate variant thereof.

35 3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

40 4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

 5. A computer-based system for identifying fragments of the *Streptococcus pneumoniae* genome of commercial importance comprising the following elements:

45 a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391;

 b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and

 c) retrieval means for obtaining said homologous sequence(s) of step (b).

50 6. A method for identifying commercially important nucleic acid fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.

55

60 7. A method for identifying an expression modulating fragment of
Streptococcus pneumoniae genome comprising the step of comparing a database
comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a
representative fragment thereof, or a nucleotide sequence at least 95% identical to
the nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a
nucleic acid molecule comprised of a complementary nucleotide sequence to said
65 target sequence, wherein said target sequence comprises sequences known to
regulate gene expression.

70 8. An isolated protein-encoding nucleic acid fragment of the *Streptococcus*
pneumoniae genome, wherein said fragment consists of the nucleotide sequence of
any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3, or a
degenerate variant thereof.

75 9. A vector comprising any one of the fragments of the *Streptococcus*
pneumoniae genome SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a
degenerate variant thereof.

80 10. An isolated fragment of the *Streptococcus pneumoniae* genome,
wherein said fragment modulates the expression of an operably linked open reading
frame, wherein said fragment consists of the nucleotide sequence from about 10 to
200 bases in length which is 5' to any one of the open reading frames depicted in
Tables 2 and 3 or a degenerate variant thereof.

85 11. A vector comprising any one of the fragments of the *Streptococcus*
pneumoniae genome of claim 8.

12. An organism which has been altered to contain any one of the
fragments of the *Streptococcus pneumoniae* genome of claim 8.

90 13. An organism which has been altered to contain any one of the
fragments of the *Streptococcus pneumoniae* genome of claim 10.

14. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the fragments of the *Streptococcus pneumoniae* genome depicted in SEQ ID NOS:1-391 and Tables 2 and 3 or a degenerate variant thereof.

15. An isolated nucleic acid molecule encoding a homolog of any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising steps of:

a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS:1-391 and Tables 2 and 3, including fragments thereof;

b) identifying members of said library which contain sequences that hybridize to said target sequence; and

c) isolating the nucleic acid molecules from said members identified in step (b).

16. An isolated DNA molecule encoding a homolog of any one of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced a process comprising steps of:

a) isolating mRNA, DNA, or cDNA produced from an organism;

b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Streptococcus pneumoniae* genome to prime said amplification;

c) isolating said amplified sequences produced in step (b).

17. An isolated polypeptide encoded by any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and depicted in Table 2 and 3 or by a degenerate variant of said fragments.

18. An isolated polynucleotide molecule encoding any one of the polypeptides of claim 17.

19. An antibody which selectively binds to any one of the polypeptides of claim 17.

130

20. A method for producing a polypeptide in a host cell comprising the steps of:

135

a) incubating a host containing a heterologous nucleic acid molecule whose nucleotide sequence consists of any one of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and depicted in Tables 2 and 3, under conditions where said heterologous nucleic acid molecule is expressed to produce said protein, and

b) isolating said protein.

Figure 1

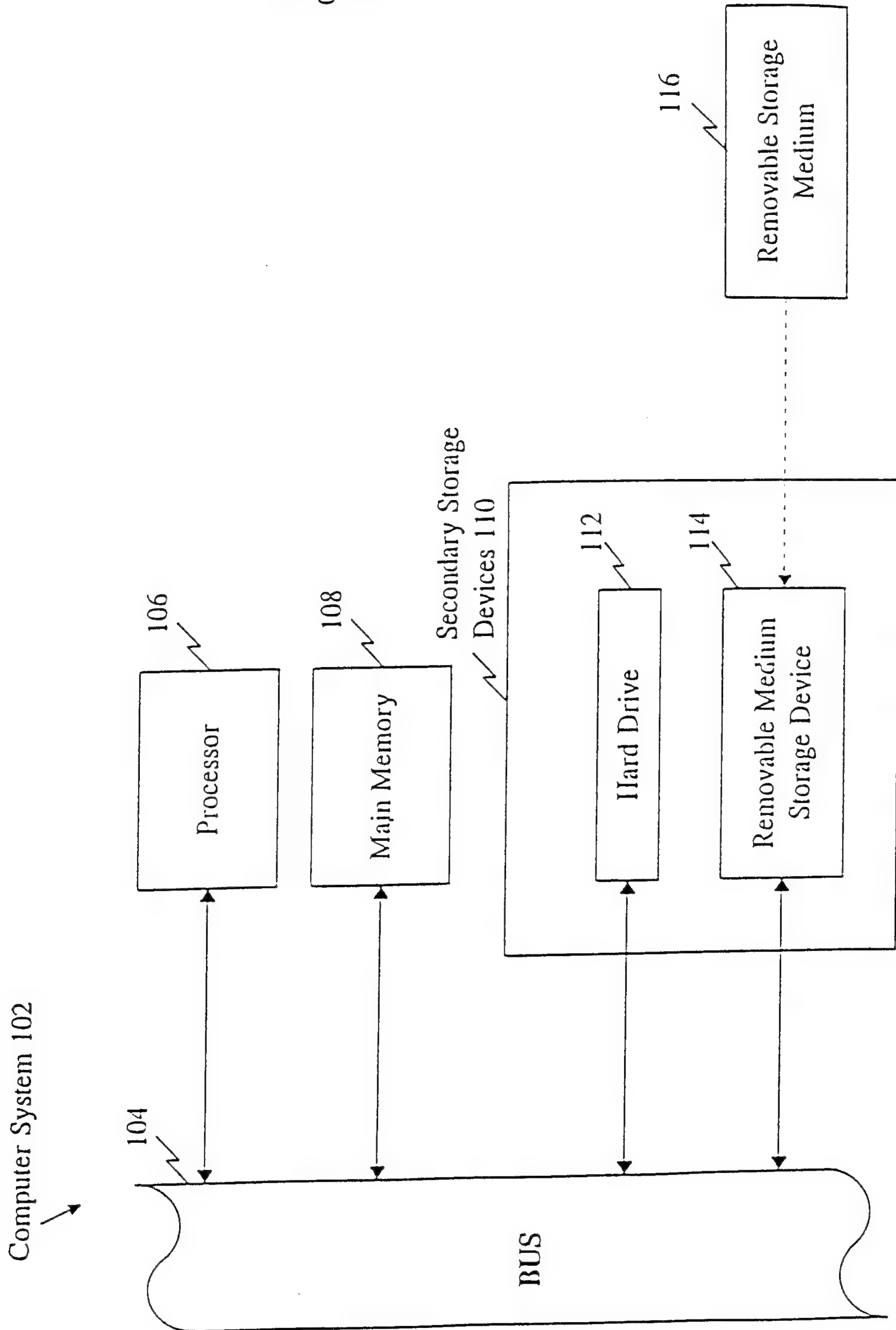
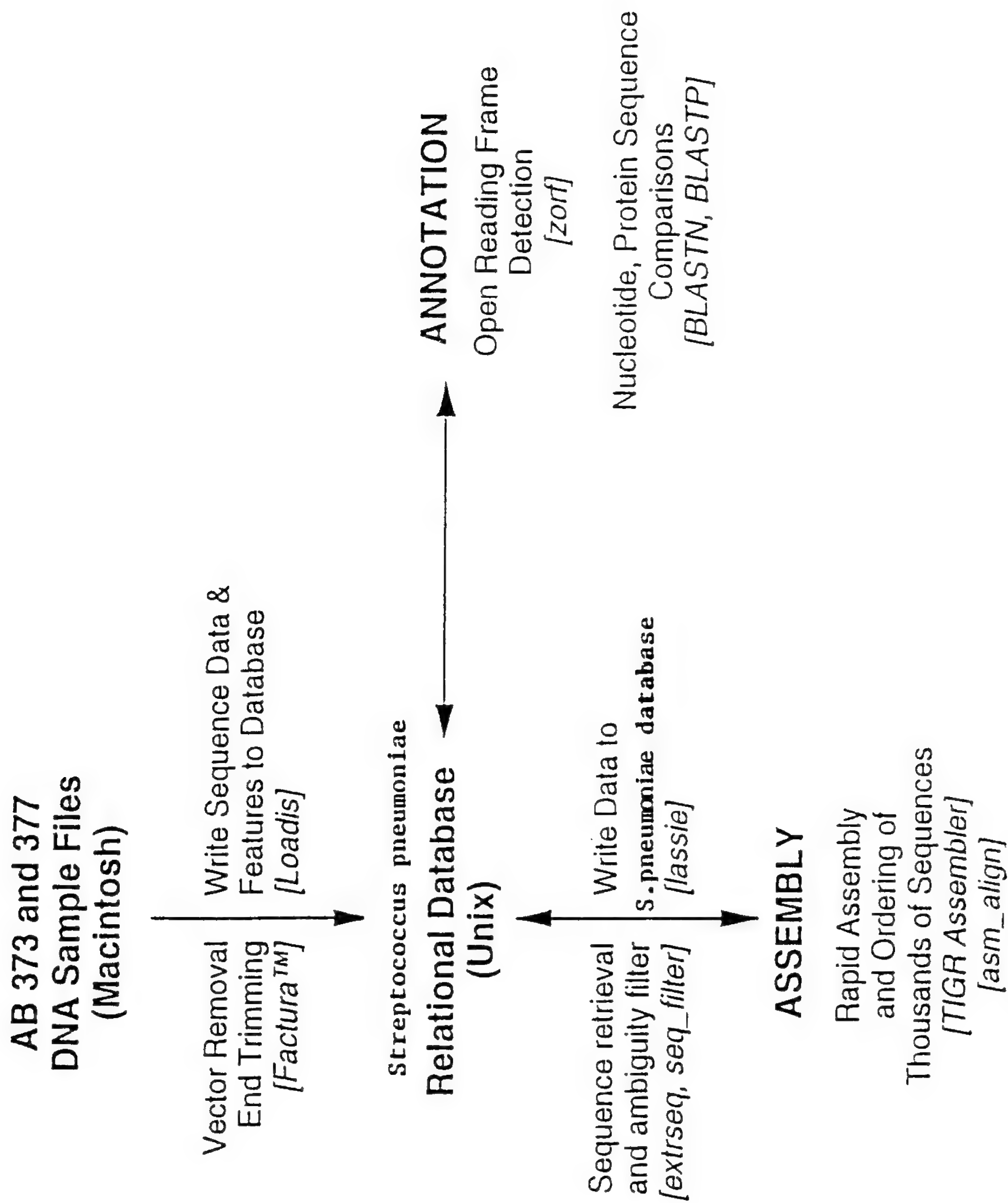


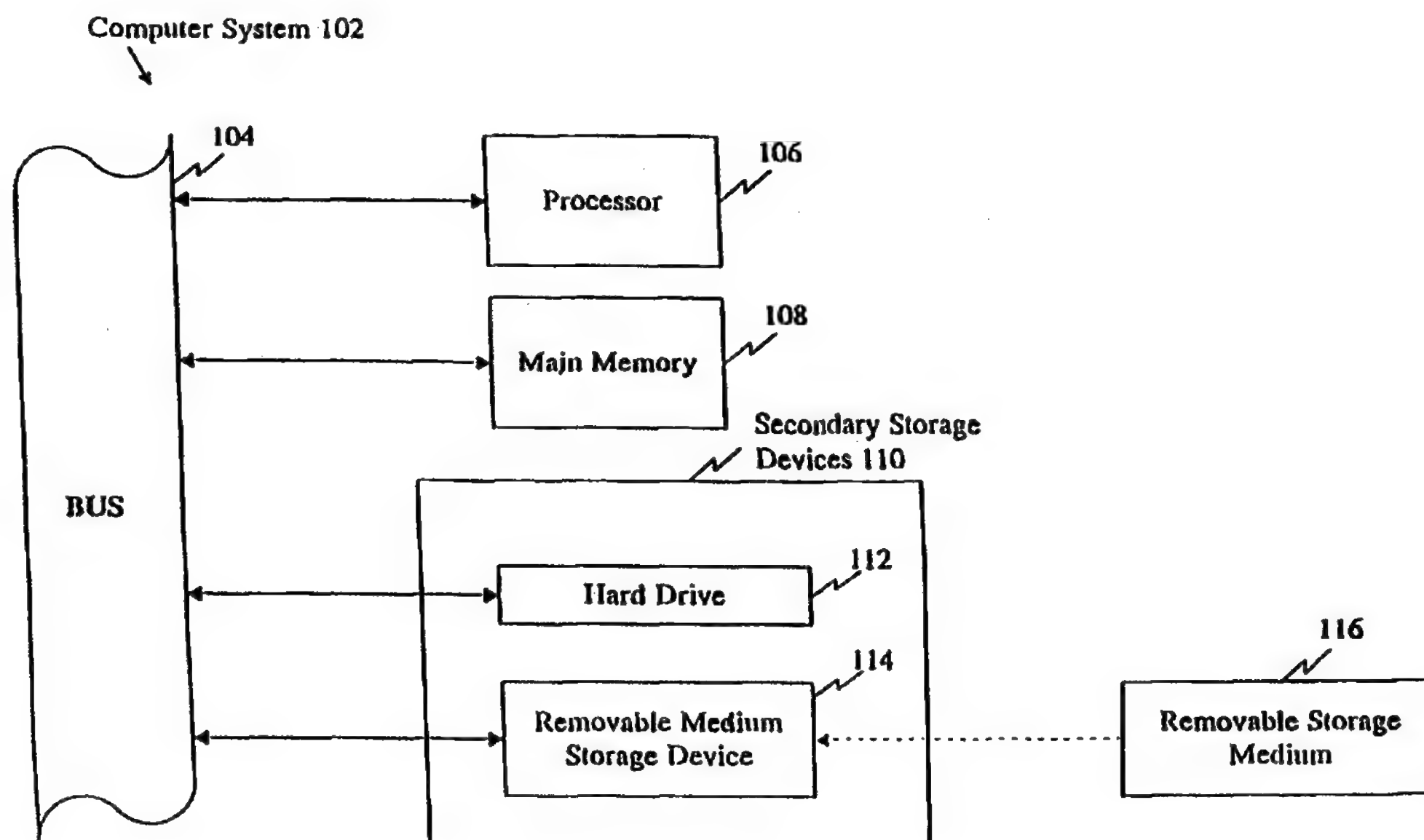
Figure 2





INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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(71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).			
(72) Inventors; and (75) Inventors/Applicants (for US only): KUNSCH, Charles, A. [US/US]; 2398B Dunwoody Crossing, Atlanta, GA 30338 (US). CHOI, Gil, H. [KR/US]; 11429 Potomac Oaks Drive, Rockville, MD 20850 (US). DILLON, Patrick, J. [US/US]; 1055 Snipe Court, Carlsbad, CA 92009 (US). ROSEN, Craig, A. [US/US]; 22400 Rolling Hill Road, Laytonville, MD 20882 (US). BARASH, Steven, C. [US/US]; 582 College Parkway #303, Rockville, MD 20850 (US). FANNON, Michael [US/US]; 13501 Rippling Brook Drive, Silver Spring, MD 20850 (US). DOUGHERTY, Brian, A. [US/US]; 708 Meadow Field Court, Mount Airy, MD 21771 (US).		Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
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(54) Title: *STREPTOCOCCUS PNEUMONIAE* POLYNUCLEOTIDES AND SEQUENCES**(57) Abstract**

The present invention provides polynucleotide sequences of the genome of *Streptococcus pneumoniae*, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 97/19588

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/31 C07K14/315 C07K16/12 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 96 33276 A (HUMAN GENOME SCIENCES INC ;UNIV JOHNS HOPKINS (US)) 24 October 1996 see claims 1-7	1-7
A	--- ALTSCHUL S F ET AL: "BASIL LOCAL ALIGNMENT SEARCH TOOL" JOURNAL OF MOLECULAR BIOLOGY, vol. 215, 1990, pages 403-410, XP000604562 cited in the application see the whole document --- -/-	1-7



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

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Date of the actual completion of the international search

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Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 97/19588

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	W.R. PEARSON AND D.J. LIPMAN: "Improved tools for biological sequence comparison" PROC. NATL. ACAD. SCI., vol. 85, April 1988, NATL. ACAD. SCI., WASHINGTON, DC, US;, pages 2444-2448, XP002060460 cited in the application see the whole document ---	1-7
A	WO 95 06732 A (UNIV ROCKEFELLER ;MASURE H ROBERT (US); PEARCE BARBARA J (US); TUO) 9 March 1995 see the whole document ---	1-7
A	WO 95 31548 A (UAB RESEARCH FOUNDATION ;YOTHER JANET (US); DILLARD JOSEPH P (US)) 23 November 1995 see the whole document ---	1-7
A	WO 95 14712 A (RES CORP TECHNOLOGIES INC) 1 June 1995 see the whole document ---	1-7
A	WO 96 05859 A (AMERICAN CYANAMID CO) 29 February 1996 see the whole document ---	1-7
A	WO 93 10238 A (US HEALTH) 27 May 1993 see the whole document ---	1-7
A	EP 0 687 688 A (UNIV OVIEDO ;UNIV LEICESTER (GB)) 20 December 1995 see the whole document ---	1-7
A	EP 0 622 081 A (UAB RESEARCH FOUNDATION) 2 November 1994 see the whole document -----	1-7

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 97/ 19588

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 1-4 could be, at least partially be considered as a mere presentation of information Rule 39.1(v), and claims 5-7 at least partially as a computer program, Rule 39.1(vi)PCT, the search has been carried out as far as possible in our systematic documentation.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see continuation-sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-7

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-7

Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID nos. 1-391, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID nos. 1-391; a computer-based system for identifying fragments of the *Streptococcus pneumoniae* genome of commercial importance comprising: a) a data storage means comprising said nucleotide sequence(s); b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and c) retrieval means for obtaining said homologous sequence(s) of step (b); a method for identifying commercially important nucleic acid fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising said nucleotide sequence(s) with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected; a method for identifying an expression modulating fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising said nucleotide sequence(s) with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression;

2. Claims: (8-20) partially

An isolated protein-encoded nucleic acid fragment of the *Streptococcus pneumoniae* genome, wherein said fragment consists of the nucleotide sequence of the fragment of SEQ ID no.1 depicted in Tables 2 and 3, or a degenerate variant thereof; a vector comprising the fragment of the *Streptococcus pneumoniae* genome SEQ ID no.1; an isolated fragment of the *Streptococcus pneumoniae* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frame of SEQ ID no.1 depicted in Tables 2 and 3 or a degenerate variant thereof; a method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the open reading frame of SEQ ID no.1 and Tables 2 and 3 or a degenerate variant thereof; an isolated nucleic acid molecule encoding a homolog of SEQ ID no.1; an isolated polypeptide encoded by SEQ ID no.1 and depicted in Table 2 and 3; an antibody which selectively binds to any one of said polypeptides, a method for producing a polypeptide in a host cell comprising a) incubating a host containing a heterologous nucleic acid

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

molecule whose nucleotide sequence consists of SEQ ID no.1 and depicted in Table 2 and 3, under conditions where said heterologous nucleic acid molecule is expressed to produce said protein, and b) isolating said protein;

3-392. Claims:(8-20) partially

Idem as subject 2 but limited to each of the sequences of SEQ ID no. 2 to 391;

For the sake of conciseness, the second subject matter is explicitly defined, the other subject matters are defined by analogy hereto.